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ABSTRACT BOOK

1

The six percent solution revisited

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Australia's strange marsupials were for many years viewed as 'inferior' or 'second-class mammals' because of their universal habit of producing only tiny, helpless young, attributed to their lack of a 'true' placenta capable of nourishing a larger offspring. Research initiated on the quokka wallaby by the late Harry Waring led to a well-spring of studies on their reproduction, nutrition and ecology and a deeper understanding of their alternate mode of survival in an environment very different from that inhabited by other mammals in the northern hemisphere. The legacy of these pioneers has been built on by others and ongoing research on marsupials has made unique contributions to our understanding of placental function, blastocyst development and sex determination in mammals.

2

Comparative ecology of desert mammals

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Most of the world's deserts are relatively young, forming or expanding during the Miocene and becoming progressively more arid during the Pliocene-Pleistocene epochs. As conditions became more arid, mammal faunas adapted *in situ* or moved in from more mesic surrounding regions. Despite the phylogenetic diversity of founders in the different world deserts, the arid conditions have long been claimed to shape convergent similarities in the morphology, behaviour, ecology and physiology of the extant mammal faunas. Thus, bipedal locomotion, granivory and economy of water use characterize gerbils (Muridae) and jerboas (Dipodidae) in arid parts of Africa and Asia, kangaroo-rats (Heteromyidae) in North America, gerbil-mice (Cricetidae) in South America, and hopping-mice (Muridae) in arid Australia. Convergent similarities can be seen also in phylogenetically different rock-dwellers, burrowers and mammalian members of several trophic guilds. Yet, profound differences occur too. In this talk I will highlight ecological and behavioural differences that have been described recently in small mammals from different world deserts, and present detailed results on two groups—rodents and dasyurid marsupials—from long-term studies in Australia's most extreme arid region, the Simpson Desert. Australia's central deserts have been a graveyard for medium-sized and many small mammals over the last two centuries, and now are dominated, uniquely, by insectivores (dasyurids: 22 species) and omnivores (rodents: 15 species). Many dasyurid marsupials persist at low densities (< 1 ha^{-1}), conserve energy and water by extensive use of torpor, have fixed breeding seasons, and appear to selectively hunt particular prey at different times depending on the prevailing conditions. Small dasyurids do not construct burrows, and instead make temporary use of the burrows of other desert dwellers. They adopt a mobile strategy that allows them to track shifts in key food resources across the desert landscape. Directed movements can exceed 10 km. Rodents, by contrast, show large population fluctuations, oscillating between prolonged periods when they are almost undetectable ($<< 1$ ha^{-1}) to transient peaks when densities can exceed 100 ha^{-1}. These 'boom' and 'bust' cycles are driven by heavy episodic rains or floods. Rodents show flexibility in their social structures, diets, and timing of reproduction; most can breed at any time when conditions permit. Unlike their counterparts in other world deserts, Australia's desert rodents display exceptional mobility; home ranges may exceed 10 ha, and short-term movements of 5-10 km are not uncommon. No species are known to cache seeds or other food materials. Despite the convergent similarity in appearance of many desert small mammals, ecological and behavioural differences between them clearly can be large. The boom and bust cycles that characterize many Australian species are driven by the larger and more frequent rainfall events that occur in Australian compared with other world deserts, while high mobility and behavioural flexibility reflect uncertainty in when these events will occur. The boom-bust dynamic carries inherent risks: refuge patches that are used during bust periods are often degraded for other (largely pastoral) uses, while boom periods provoke irruptions of introduced predators. Careful management will be needed to ensure the continuity of extant desert faunas.

3

Marsupials: Microchip miracles

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Marsupials are only 6% of living mammals but have many characteristics that have taught us about the control of reproduction and development. A striking characteristic is that marsupials give birth to highly altricial young after a relatively short gestation period supported by a chorio-vitelline placenta. They deliver the smallest mammal at birth of any we know, at just 5 mg. They complete much of their development within the pouch, dependent on a long and highly sophisticated lactation. They can even produce milk of totally different compositions from adjacent mammary glands. Unlike all other mammals, their blastocysts have no inner cell mass, so the enigma of which cells are stem cells remains. They are also placental mammals, replete with genomic imprinting of certain genes in their fully functional placenta, contrary to popular dogma that marsupials don't have a placenta! A major difference is the timing of their differentiation of sex, which all takes place post-natally, allowing easy manipulation of the process whilst the young is in the pouch. We discovered some unexpected findings that overturned the powerful Jost paradigm that sexual differentiation simply depended on hormones secreted by the testis when we demonstrated a number of hormone-independent sexual dimorphisms before the testicular differentiation. We now know that there are many other hormone-independent sexual dimorphisms, not only in mammals but also in birds. In addition, because of the post-natal gonadal development, we have been able to achieve testicular, prostatic and phallus sex reversal after treatment with oestrogen *in vivo* and *in vitro*. Finally, the long lactation, during which the composition of the milk changes dynamically to coordinate the specific growth requirement of the developing young has allowed us to examine the effects of fostering the young to a more advanced stage of lactation resulting in amazing growth acceleration and showing that the bioactives in the milk control the growth exquisitely regulating each stage of development. Marsupials may only be 6% of living mammals, but their unique biology provides novel perspectives for further understanding the evolution and control of successful mammalian reproduction and development. Acknowledgements: Supported by the Australian Research Council and the Australian National Health and Medical Research Council, and the efforts of many wonderful colleagues and students.

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African researchers show the world how to stop rats through developing ecologically-based rodent management

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The StopRats project carried out many EBRM studies. As examples, research on the evaluation of contraceptives on the fertility of *Mastomys natalensis* as well as the role of domestic predators on the foraging behaviour of pest rodents will be presented. *M. natalensis* were fed bait containing steroid hormones (quinestrol and levonorgestrel) at three concentrations (10, 50, 100 ppm) for seven days. Significant interaction effects of treatment and sex were observed ($F_{16,392} = 10.007$, $p < 0.001$), with higher acceptance of treated bait by females compared to males. Treatments significantly reduced the weight of male rat testes, epididymis and seminal vesicles with sperm concentration and motility also reduced. Although there were no significant differences in the weight of female rat uteri and ovaries, high rates of uterine oedema were observed among treated female rats. Trials with mate pairing showed there were significant differences ($F_{2, 86} = 3.28$, $p = 0.0423$) in pregnancy ($p < 0.05$). With respect to foraging behaviour, we tested whether the presence of domestic cats and/or dogs in rural homesteads would affect the foraging behaviour of pest rodents. We estimated giving up densities (GUDs) from established feeding patches at 40 homesteads across four agricultural communities. We found that the presence of cats and dogs at the same homestead significantly reduced activity and increased GUDs of pest rodent species. However, if only cats or dogs alone were present at the homestead there was no observed difference in rodent foraging activity in comparison to homesteads with no cats or dogs.

5

What can lemmings teach us?

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Strong population cycles characterise the dynamics of arvicoline rodents (voles and lemmings} in northern Fennoscandia. The peaks and migrations of Norway lemmings are the epitome of these fluctuations. Lemming peaks coincide with those of voles but there is not a lemming peak during every vole peak. Favorable winter conditions, soft powder snow and absence of warm spells, contribute to lemming peaks. There is a gradient in lemming dynamics from high mountains to lower ones and taiga. Peaks occur more often in higher mountains. These are characterised by high proportion of optimal wintering habitats, and winter breeding is essential for the population increase of lemmings. Therefore, lemmings are sensitive to the climate change. During great peaks lemmings can migrate deep into the boreal taiga zone, undergo few local cycles there in the rhythm of the local vole cycle, and then disappear. These large-scale migratory periods occur seldom. In Finnish Lapland, these major events, lemmings migrating 200 km into the taiga, occur twice or three times in a century. These kinds of large-scale movements need 2-3 years to develop and expand. The last great migration in Finnish Lapland occurred in 1969-70, even though some moderate migrations have taken place more recently. In the taiga lemmings encounter totally a new predator and parasite-pathogen world, which they may not have adapted to. The outbreak character and magnitude of lemming dynamics depends much on winter conditions, and how this affects the timing of lemming increase in relation of lowland vole dynamics, i.e. varying predation pressure.

6

Managing complex pests: Untangling the impacts of black rats on wildlife at the urban bushland interface

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Established invasive species pose a difficult management problem because over time they form complex interactions with local species and can replace the ecological role of lost natives. Pest removal to mitigate an impact on one target may therefore have unexpected impacts on other elements of the ecosystem. In this talk we explore the impacts of introduced black rats (*Rattus rattus*) living in peri-urban bushland around the harbour foreshore of Sydney, Australia. Black rats were introduced to the area 220 years ago and the local small mammal fauna are locally extinct. We conducted a 3-year replicated black rat removal experiment on 16x1 ha plots to examine the impacts of black rat predation on (i) artificial bird's nests, (ii) populations of garden

skinks (iii) invertebrate populations, and (iv) pollination of *Banksia* inflorescences. We found that black rat removal lead to greater nest survival and higher skink numbers, indicating rat predation was an additive source of mortality. However, the magnitude of impacts on skinks was akin to that of a native predator rather than an exaggerated impact typical of alien predators when benchmarked against known effect sizes. Rat removal led to increases in spider abundance, but also an associated decrease in the diversity of invertebrates in lower trophic levels. This result supports a role for black rats as an apex predator of invertebrate communities. Finally, black rat removal led to a decrease in seed set in Banksias. Together these results show that removal of long-standing pests with complex interactions leads to complex outcomes.

7

The search for non-lethal human-wombat conflict mitigation strategies has us digging for answers

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Human-wildlife conflict is a widespread and growing threat to conservation worldwide. It threatens a huge diversity of species and has far reaching environmental, health and safety, social and economic impacts. For many species, like the southern hairy-nosed wombat (*Lasiorhinus latifrons*), the scientific data needed to reduce conflicts and develop integrated management plans are lacking. Conflicts between *L. latifrons* and the agricultural sector have been ongoing for decades. Surveys of landholder opinions of *L. latifrons* across the species range found they can cause severe damage to infrastructure and crops. Despite the conflicts, there is strong support for their conservation, and the development of alternative non-lethal management options. Translocation was trialed as a non-lethal alternative, however it failed to reduce conflicts, as neighbouring *L. latifrons* quickly recolonised vacated burrows. In a bid to deter *L. latifrons* from conflict zones, we assessed whether avoidance responses were elicited by four treatments: dingo urine, dingo faeces, blood and bone (Brunnings PTY LTD) and compact discs (CDs). Field trials were conducted on active burrows, with remote cameras monitoring *L. latifrons* behaviour before and after the treatments were applied. Mixed effects models revealed a significant decrease in the number of visits to the burrows following the application of CDs, however *L. latifrons* quickly habituated to them. No other treatments significantly affected *L. latifrons* behaviour. Despite being ineffective, this research provides vital information to wildlife managers to aid in the future management of *L. latifrons* and guide further research into the use of deterrents.

8

A population dynamic model for planning control strategies of the domestic dog population in Santiago city, Chile.

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Unsupervised dogs in cities are a serious environmental problem in most developing countries. Although this problem is of a high priority, there is always a great deal of debate on its solution and a scarce management based on information from the basic ecology of this problem. In the city of Santiago de Chile, there is a population of one million of dogs, between owned and stray dogs, with the resulting problems of public health and safety. In fact, this serious problem has produced strong ethical controversies in the public opinion on the measures applied for controlling this population. In this study, we performed an analysis of existing information about the size and the structure of the dog population at Santiago City, Chile. Based on these results, we developed a population dynamic model that captures the growth of the street dog population. The model is a system of equations coupled in four states: owned dogs and street dogs (supervised and stray) and both divided between fertile and sterile states. These four states were chosen because it gives much more flexibility when evaluating management actions and allows the exclusion of time as an explicit variable (autonomous equation). The results strongly suggest a source-sink population structure, where the population of street dogs is strongly subsidised by individuals migrating from the state of ownedr dogs, which are abandoned or escape. Therefore, different scenarios are proposed in the population dynamics model that consider the potential strategies to be applied as public policies.

9

Can experiments on behaviour inform our understanding of macroevolution?

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Our ability to link microecology and macroevolution depends on whether we can study speciation and extinction with small-scale experiments. Such experiments will likely be most successful if they use metrics closely related to population growth rates while enabling behavioural choices that either enhance speciation or forestall extinction. I designed field experiments with meadow voles that combined observations of foraging behaviour and dispersal from rapidly deteriorating habitats. Voles emigrated from low to higher-quality habitat as expected, but did not match densities with those expected from supplemental food. Movement and giving-up densities suggest that the voles' habitat selection was modulated by sex-dependent differences in dispersal conditioned by additional components of fitness including predation risk. Even so, carefully designed behavioural experiments have a demonstrated ability to inform processes of speciation and extinction and thereby provide crucial insights into macroevolution and the conservation of Earth's biodiversity.

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Producing and scrounging can have stabilising effects at multiple levels of organisation

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That negative frequency-dependent selection can promote co-existence of strategies within a population is well established. There is some evidence that negative frequency dependence can also stabilise population size. Here, I will concentrate on one such game, producing and scrounging (PS), which some mammals are known to play. Using a Darwinian dynamics approach, I will show that producing and scrounging in a population can stabilise its abundance and stabilise the abundance of its prey. Furthermore, PS can facilitate the co-existence of two species which consume the same resource. It can also create an equilibrium point in a trophic chain. By contrast, other games which produce negative frequency dependent selection may have less impact. The presence of spite in a population can stabilise its interaction with its prey but this effect does not extend to other species (either competitors or predators). Altruism, on the other hand, can have a destabilising effect on the interaction between a species and its prey.

11

Non-positive abundance-range size relationships of small mammals in subtropical mountain ranges: Dispersal matters

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A pervasive positive abundance-range size relationship (ARR) has been challenged by recent studies which revealed negative and neutral trends in isolated systems (mountain ranges and islands). We expect that in a subtropical mountain range, small mammals should show a non-positive ARR due to geographical isolation and climatic stability (non-positive ARR hypothesis). Further, we expect a stronger non-positive ARR for species distributed at higher elevations (elevational distribution hypothesis) and with higher dispersal abilities (dispersal ability hypothesis). We examined the ARRs of small mammals in four mountains of southwest China and related species' mean abundances to range sizes. To test the elevational distribution hypothesis, we examined the relationship between mean abundance and elevational range centre and compared the ARRs between the montane and alpine group. To test the dispersal ability hypothesis, we compared the mean abundance and range size between glires (more vagile) and insectivores, as well as their ARRs. We found a negative ARR in three mountains and a weak positive ARR in the other. A positive correlation between mean abundance and elevational range centre was found in each mountain, so was a higher mean abundance of glires. Glires showed a stronger non-positive ARR than insectivores across mountains. The observed non-positive ARR is primarily driven by the prosperity of endemic species and poverty of widespread species given their different levels of specialization to subtropical montane habitats. Higher dispersal ability may cause a stronger non-positive ARR of small mammals in a mountain range where local dispersal is easier than regional dispersal.

12

The human influence on macroevolution and ecology of zoonotic diseases

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Human disturbances of intact tropical habitats combine with deep coevolution of diverse faunas and their pathogens to create the perfect storm for infectious diseases that are emerging and capturing headlines today. Pathogens possess unique vectors and features of infection, hence it is not easy to determine whether humans are perturbing a tightly evolved system, or whether humans function as just another victim of infection in an ecological dynamic. Indeed, most efforts to identify the source of zoonoses occur after humans are infected and it is difficult to predict zoonoses because spillover events are rare and infection prevalence in reservoir species can be low. We attempt to develop a predictive approach by studying *Bartonella* bacteria, which are prevalent in many mammalian taxa and are responsible for numerous human infections. Using a phylogenetic approach, we show that humans have frequently been exposed to *Bartonella*, most recently through spillover from commensal rodents in the genus *Rattus*. In general, rodents and domestic animals serve as the reservoirs or at least key proximate hosts for most *Bartonella* genotypes in humans and also in wild animals. Thus despite a long coevolution of *Bartonella* strains and their particular mammalian hosts, the recent expansion of humans and their commensals has left an imprint on these relationships so that neither geographic origin nor phylogenetic distance help to identify which pathogens may spillover into humans. Instead, a better indicator of future zoonoses may be found by investigating our own backyard.

13

Scales: Studies on the foraging ecology of desert rodents at different spatial and temporal scales, from micropatch selection to intercontinental consequences of macroevolutionary advances

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The traits of organisms are shaped by natural selection and can be viewed as adaptations. Foraging behaviours are among the most important of traits because they mediate the interaction of the organism and its environment and play crucial roles in managing the trade-off of food and safety. Here, I use behavioral indicators based on foraging theory to look at the consequences of scales in space and time. I focus on Allenby's gerbil, a small seed-eating rodent found on sandy substrates in the Negev Desert of Israel. Using a combination of experiments in the laboratory, outdoor enclosures, and the field, I quantified giving-up densities (GUDs) and quitting harvest rates of rodents exploiting depletable resource patches. In going from micropatches to macroevolution, I provide evidence for scales of habitat selection, risk management, the risk pump, possible ecotypes, mechanisms of species coexistence, scales of temporal partitioning, and intercontinental convergence and limits of convergence to community structure. Thus we can use foraging traits to reveal fitness consequences of optimal behaviors, and through that, the ecology of individuals, populations, communities, and more.

14

Further declines in populations of the Australian sea lion: Implications for the management of a unique pinniped

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The Australian sea lion is endemic to southern Australia and is unique among pinnipeds in having a non-annual (~18 month) breeding cycle that is temporally asynchronous across their range. They have the longest gestation period of any pinniped, protracted breeding and lactation periods, and females exhibit extreme philopatry relative to other pinnipeds. The evolutionary determinants of this unusual reproductive strategy remain enigmatic. Australian sea lions are demersal foragers, and their aquatic distribution is restricted to shelf waters off South Australia and Western Australia. The species was subject to sealing following European colonisation of Australia, from which it has not recovered. Current pup production per breeding season for the species is estimated to be ~3,000, across 70 breeding sites, with a mean and median pup production of just 43 and 19, respectively. A species-wide assessment indicates the population is declining by 2.6% per year. Surveys in South Australia indicate that declines have been ongoing for at least 1-3 decades and that pup abundance has declined by almost 25% over the last decade or less. Bycatch mortality in demersal gill-net fisheries has been identified as the major threat to Australian sea lion populations. Management actions introduced in the Commonwealth and Western Australian managed fisheries since 2010 should reduce that bycatch and its impact on populations. However, lack of ongoing monitoring means that the effectiveness of management measures introduced to mitigate bycatch and enable populations to recover cannot be assessed, with recent surveys indicating that populations are still in decline.

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Population demographics of southern right whales in South Australia based on 26 years of seasonal observations

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Population demographics of southern right whales (SRWs), *Eubalaena australis,* were assessed using 26 years of count and photo-identification data. Data were collected annually between 1991 and 2016 at Head of Bight in the Great Australian Bight Commonwealth Marine Reserve. SRWs were distributed within a 15x2km area and 10m water depth. SRWs occupied the site between May and October with maximum abundance between late-July and early-August. Up to 28% of calving females were present in mid-June and up to 61% remained in late September. The mean residence period was 65 days (range 1-99) for calving females and 15 days (range 1-51) for unaccompanied adults. Over the study years, 18-81 female and calf pairs were sighted per day, with a maximum of 172 animals counted on 16/08/2016. The estimated mean rate of increase in total SRWs was 5.5% (SD=2.5, 95%CI=0.03) per annum (1991-2016). The corresponding mean rate of increase for females accompanied by a calf was 4.9% (SD=1.9, 95%CI=0.03). The photo-identification database includes 1,186 non-calf individuals that included 459 reproductive females (providing 471 inter-annual calving intervals). The estimated mean calving interval was 3.3 years (SD=0.8, 95%CI=0.01) with high philopatry resulting in cohort structured breeding cycles and variation in annual abundance. The mean age at first parturition was 9.3 years (SD=2.1 95%CI=0.03, N=22). The mean date of calving was 16 July (range 19 June - 27 Aug). These population demographics and life history parameters provide key information for recovery assessments, species conservation planning and global comparative studies with other right whale populations.

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Atypical residency of short-beaked common dolphins (*Delphinus delphis*) to a shallow, urbanised bay in south-eastern Australia

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Short-beaked common dolphins (*Delphinus delphis*) are typically considered highly mobile, offshore delphinids. This study assessed the residency of a small community of short-beaked common dolphins in the shallow, urbanised Port Phillip Bay, south-eastern Australia. The ability to identify common dolphins by their dorsal fin markings and coloration using photo-identification was also investigated. Systematic and non-systematic boat surveys were undertaken between 2007 and 2014. Results showed that 13 adult common dolphins and their offspring inhabit Port Phillip Bay, of which 10 adults exhibit residency to the bay. The majority of these adults are reproductively active females, suggesting that female philopatry may occur in the community. Systematic surveys conducted between 2012 and 2014 revealed that the dolphins were found in a median water depth of 16 m and median distance of 2.2 km from the coast. The shallow, urbanised habitat of this resident common dolphin community is atypical for this species. As a result, these common dolphins face threats usually associated with inshore bottlenose dolphin communities. We suggest that the Port Phillip Bay common dolphin community is considered and managed separate to those outside the embayment and offshore to ensure the community's long-term viability and residency in the bay.

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Social influences and sex differences in the development of sponge tool use among wild bottlenose dolphins of Shark Bay, Australia

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Demonstration of social learning among marine mammals is challenging given the inherent difficulty of conducting detailed behavioral observations and experimental designs. Here, we examine social influences on the ontogeny of sponge tool use among Shark Bay bottlenose dolphins. Although sponge tool use shows strong patterns of vertical transmission and occurs at several sites in Shark Bay, only about 5% of the population uses sponge tools in the eastern gulf. Sighting records ($N = 30$ calves, 750 surveys) and focal follows ($N = 22$ calves, 250h) of female spongers and their dependent offspring enabled us to investigate maternal and non-maternal social influences on the development of sponging. Of 41 calves born to female spongers, 5% (1 of 19) of daughters and 45% (10 of 22) of sons did not become spongers post-weaning (> 4 years of age). Mothers of future spongers, compared with those that did not become spongers, tended to spend more time sponging when their dependent offspring were nearby (GLMM, $P = 0.07$). However, calves that became spongers also spent more time separated (> 10m) from their mothers than those that did not become spongers (GLMM, $P < 0.001$), likely because they both sponged independently. Of offspring that became spongers, daughters, more than sons, sponged at the same time as their mothers (permutation test, $P = 0.002$), even though they were rarely together when sponging. In sum, these results demonstrate that maternal foraging behaviour, sociability, and calf sex influence the likelihood of becoming a sponger.

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Changes in isotopic signatures suggest food web shift off the western Antarctic Peninsula

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The local warming occurring within the western Antarctic Peninsula (WAP) is causing some of the greatest environmental shifts on the planet. Over the past 140 years there have been profound biological and physical perturbations to the wildlife on the WAP. We examined whether trophic level shifts were evident in the top predators within this system and use stable isotope signatures as a proxy. Contemporary WAP leopard seals have different nitrogen isotopic values to other leopard seal populations, however historically WAP leopard seals had δ^{15}N values within the range of other western and eastern Antarctic populations. From our 140 yr record of leopard seal tissues ($n = 167$), we show that the δ^{15}N values of WAP leopard seal tissues have dropped significantly, and that this change occurs as a step around the 1980s. The magnitude ($2.6‰$ δ^{15}N) of change is ecologically significant as it reflects a drop of a trophic level within the contemporary WAP food web. Values suggest that leopard seals have shifted from eating vertebrates to krill. Over this same time period there was no shift in δ^{15}N of the WAP krill-feeding specialist, the crabeater seal, which supports the idea that the change in leopard seal δ^{15}N values is not due to a baseline shift in the nitrogen isotope values. Despite the century-long perturbation in the WAP, the top-predators, the seals, show a trophic downshift only in recent times, post 1980s.

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Project designs for running camera traps across small and large landscapes.

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Camera traps are great tools to measure the movement of animals across a narrow swath of land in front of the sensor, thus providing a sample of the animals that use an area. By running an array of cameras across a landscape, many samples can be accumulated and used to describe the local animal community. This workshop session on camera trap study design will address the question of how exactly cameras should be deployed to collect appropriate data to address research questions through quantitative analysis of occupancy, detection rate, or animal density. We will show examples of study designs for a short-term and long term monitoring of animals that use a protected area, as well as strategies for surveying large areas such as states or entire countries. We will discuss the spatial dependence of data and the appropriate minimum distance needed to keep samples independent. Finally, we will discuss the costs and benefits of working with citizen scientists to scale up data collection over large areas, and show how eMammal tools can help manage these volunteers, images, and data.

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What’s in your school yard? Using citizen science wildlife cameras to conduct authentic scientific investigations in the classroom

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The Next Generation Science Standards advocate for students to plan and carry out investigations, especially those developed by the students themselves. We have created a framework for students to ask and answer such questions using engaging mammal photos collected from camera traps run in their own school or neighborhood yards. This approach is embedded in the eMammal citizen science program. Students not only collect data for their education, but also make meaningful contributions to real scientific research on the distribution, behavior, and conservation of mammals. We have produced dozens of lesson plans covering a variety of ages and STEM topics that involve students setting up motion-triggered camera traps to collect photos of mammals, identifying the species using user-friendly software, and analyzing their data by hand or through automated website tools. The eMammal program naturally inspires student to come up with new questions from patterns observed in data, continuing the cycle of asking and answering questions.

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Data structure and management necessary for a camera trapping to serve as a conservation tool

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Images and metadata from camera traps can serve as an effective conservation tool, but the data must include location, date, and species, and be organized in a manner that allows comparison across projects and across time. Without this standard, camera trapping is a valuable research tool that can answer specific wildlife questions but does not fully leverage the data for conservation ends. Most individual projects are too narrow in their extent of place or time to monitor a species’ distributions. We advocate for a shared data structure that allows archiving data in a format it can be retrieved, compared, combined and reexamined by a broader conservation audience than the original intent. eMammal and Wildlife Insights are two digital repositories that share a Camera Trap Metadata Standard; an open data standard for storing and sharing camera trap data. The standard has a shared language of data units (image, sequence, deployment, plot, etc.) that is the foundation for a nested structure of data. The standard captures the minimal information necessary to share data between projects and offers a foundation for collecting the more detailed data needed for advanced analysis. This data standard is an important step in aligning camera trap surveys with best practices in data-intensive science. Ecology is moving rapidly into the realm of big data, and central data repositories are becoming a critical tool; the metadata standard is the first step needed for a shared, curated, repository of camera trap images and data.

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Managing volunteers and staff effectively for a distributed network of camera traps

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Camera trapping projects focused on data collection across broad landscapes experience limits of data management and staff coordination. eMammal facilitates three parts of this process; staff/volunteer coordination, quality control of metadata including animal IDs, and providing training, feedback and support to volunteers. The work flow is effective for professional staff, but is especially designed for volunteers who are distributed across multiple locations. Using the eMammal website, the Project Manager registers volunteers, verifies they have completed online training and testing, and assigns deployments. Field staff or volunteers use a desktop application to upload data and images to a cloud-based site (Amazon Cloud Services) where expert review is required before data flows into a curated repository. We have adapted the expert review process to sort images by species (for review by species-specific experts from outside project) or feed images into a crowd-sourcing platform (Zooniverse) prior to expert review. At the conclusion of the expert review, the volunteer receives an email with total detections, favorite images and notice of incorrect identifications. During a project in the eastern US volunteers improved their ID accuracy with subsequent deployments, achieved accuracy rates equal to paid staff, and increased their knowledge and interest in local mammals. Each project within eMammal has the capacity to conduct a discussion thread and a blog post for project members. Maintaining communication with volunteers is essential to sustaining interest among a broadly distributed network of volunteers.

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Killing mammal predators: An assessment of current management programs and methods.

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Throughout history, humans have considered mammal predators as threats to their wellbeing, industries, and subsistence and recreational hunting activities. Although attitudes have changed with the evolution of human societies and wildlife management programs, and predators have been recognised as playing an important role in the maintenance of wildlife communities and ecosystems, lethal control and eradication of mammal predators is still being promoted by today's governments, industries and special interest groups. On the basis of ecological and ethical considerations, this paper assesses a series of current mammal predator management programs, and their lethal and non-lethal methods. This paper also makes a series of recommendations to ensure the implementation of mammal predator management programs that are based on sound research protocols and scientific data, and are humane and ecologically and socially acceptable.

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The North American model of wildlife conservation: Through the eyes of the North American river otter

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Over the last decade the so-called "North American model of wildlife conservation" (NAM) has been widely portrayed as both a historical account of how wildlife was conserved in North America in the past and a prescriptive model for how wildlife should be conserved in the future. NAM is comprised of 7 primary elements, each depicted in a manner that supports and justifies recreational hunting and trapping as the "cornerstone" of wildlife conservation in North America. We are both intrigued and concerned that a hunter/trapper-centric approach has been put forth (marketed) as the primary dictum defining wildlife conservation. The basic precepts of NAM largely have been embraced within the wildlife profession in the United States (US), despite the general absence of meaningful scrutiny to assess the appropriateness of a hunter-centric approach for addressing the entirety of complex issues facing wildlife conservation issues in North America and beyond. We critically review NAM and its 7 elements in the context of conserving the North American river otter (*Lontra canadensis*) in the US, with particular focus on 3 of NAM's core elements: 1) wildlife as a public trust resource; 2) science as the basis for implementing conservation practices; and 3) elimination of markets for wildlife. Important to our discussion is a review of how science can be applied (sometimes inappropriately) to further specific management goals/agendas pertaining to the river otter. We argue that wildlife conservation is hindered and the "public trust" compromised when science and marketing are inappropriately integrated to achieve predetermined management outcomes.

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Is enemy's enemy always a friend? Vague implications of wild dog control on a native marsupial herbivore.

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At least 27 mammals have gone extinct in Australia since European settlement, which has been attributed to the human introduction of two invasive carnivores; red fox (*Vulpes vulpes*) and feral cat (*Felix catus*). The dingo (*Canis dingo*) is thought to control invasive mesopredator populations and thus benefit native species. The roles played by the dingo in the Australian ecosystem are still unclear with the majority of the continent controlling dingoes and their hybrids on a landscape scale as agricultural pests. Using the common brushtail possum (*Trichosurus vulpecula*) as a model species, we studied six sites in the New England Tablelands, northern New South Wales, where different wild dog control regimes are implemented. While predominantly arboreal, possums use the ground to move and forage which makes them vulnerable to predation by dogs, foxes and cats. Using remote cameras, GPS collars and giving-up density experiments, we investigated spatio-temporal patterns of activity and non-lethal effects of predation by both dingoes and invasive mesopredators. We also compared these patterns with the introduced European hare (*Lepus europaeus*), a strictly terrestrial herbivore of comparable size. Our preliminary results suggest that environmental and climatic factors as well as habitat structure may play a major role in shaping the predator-prey relationship. That implies that the conservation outcomes of wild dog control will depend on more complex mechanisms than simply regulating mesopredator populations and thus require thorough consideration in future management and conservation efforts.

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Diet choice of large carnivores (common leopard and Asiatic lion) and their coexistence in Gir NPLS, Gujarat, India

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The diets of the endangered common leopard *(Panthera pardus fusca)* and Asiatic lion *(P.leo persica)* were studied in the western part of Gir NPLS, Gujarat, India during the study period from 2009-2012. Scat analysis revealed that the diet of the two sympatric large carnivores overlapped considerably (O = 0.95). Prey contribution of ungulates was found highest for chital (ca. 38.57%) followed by sambar (ca. 21.42%) and nilgai (ca. 8.28) in the diet of leopard, and chital (ca. 44.58%), sambar (ca. 25.59%) & nilgai (ca. 18.21) in the diet of lions respectively. The contribution of domestic livestock was found unexpectedly low (ca. 4.86%) in the leopard's diet and ca. 5.48% of the lion's diet respectively. Prey killed by these large carnivores showed ca. 45% predatory competition between them. Seasonally, ungulates constituted ca. 66.44% of leopards' diet while 90.64% of lions' diet in the summer and 70% of leopards' diet and 88.57% of lions' diet in the winter. Livestock supported more of the summer diet of leopards compared to the lions, whereas other prey taxa were also found to be more important for the leopards by constituting 26.38% and 22.67% compared to the lions (ca.6.02 and 6.71%) during summer and winter respectively. Thus, scat analysis along with kill observations is a useful method to understand diet choices of two large carnivores and their coexistence for their long-term management and conservation.

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How to find the Achilles heel: Gene targeting in invasive mammal predators

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Apart from two species of bat, New Zealand has no extant endemic terrestrial mammals. Some live relatively commensally, while others are more parasitic on Aotearoa's native and unique birdlife, taking full advantage of their predator naivety and flightlessness. In response to the devastating impact on some species there are several well established national programmes to control invasive mammal predators, in particular possums, stoats and rats. This has led to the formation of the Zero Invasive Predators (ZIP) and Predator Free New Zealand (PFNZ) groups, dedicated to the formidable challenge of removing these mammal pests by 2050. A major hurdle to this initiative is the exponential cost, in terms of both finance and time, of removing the last few surviving individuals from an invaded area using current techniques. Hence there is an urgent drive for the development of new tools using novel technologies to assist in the complete elimination of mammal predators from regions. Here, I present our "Achilles heel" approach. In effect, we rely on comparative genomics to select genes central to critical physiological control processes for specific knock-out in target species only, using highly sensitive gene-silencing RNA interference (RNAi) techniques, in particular siRNA. Two cases are discussed, feral pigs and brushtail possums, each with their own set of unique challenges.

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Marsupial immune system development

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Unlike their eutherian counterparts, marsupials develop their immune tissues in a non-sterile environment shortly after birth. Neonatal marsupials are therefore reliant on innate and maternally-derived immunological strategies to survive microbial onslaughts until their adaptive immune system develops. To date, developmental studies of the marsupial immune system have largely focused on histological and immunohistochemical techniques. Gaps in our knowledge and understanding of the marsupial immune system remain. Current knowledge of the marsupial immune system and implications for marsupial conservation will be discussed.

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Ecological correlates of changes in the abundance of the main hantavirus hosts in Brazil

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One of the main species responsible for hantavirus disease transmission in Brazil is *Necromys lasiurus,* a rodent found in the Brazilian main biomes (savannas and tropical forests) usually living in and out of native forests. Here we investigated how this species responds to the landscape structure, habitat heterogeneity, climate and local rodent diversity. Our expectation was that landscape structure gathers the main correlates of the abundance of rodents, where areas with 1) predominance of agricultural matrix, 2) more contact areas between favorable habitat for reservoirs and remaining vegetation and would positively affect their abundance. We analysed data on areas where rodents were captured from a set of 278 inventories mainly located within the Atlantic Forest. Heterogeneity was calculated based on the supposed affinity of *N. lasiurus* for open agricultural areas and native vegetation areas. *N. lasiurus* was found in 35 sites and the main effects of predictors were the positive influence of habitat heterogeneity and the negative effect of precipitation on their abundance. Abundance peaked at intermediate to high levels of habitat heterogeneity at landscape scale. Local rodent diversity was not associated with *N. lasiurus* abundance, suggesting that landscape alteration is more important to determine abundance than other rodent species dominance effects. It would be interesting to test the influence of other trophic levels on this host abundance. This information helps to inform surveillance and prevention of hantavirus disease in the field and also contributes to understand potential factors influencing disease transmission risk.

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Hematological and chemistry parameters of eight juvenile spider monkeys (*Ateles chamek*) in captivity in the Amazonian forest of Peru

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Chemical immobilisation of eight juvenile spider monkeys in captivity (*Ateles chamek*) was carried out in the Taricaya Reserve located in the Amazon region of Peru for the purpose of health evaluation, sampling and morphometry. During this procedure the animals were thoroughly examined and samples of several types were taken per individual for further analysis. The analyses resulted in variations depending on the characteristics of each individual, however they yield data to establish basal parameters in the species. Rehabilitation projects allow a large number of evaluations to be performed on individuals, representing a pathway for research on threatened species. The present study aims to establish the evaluation of hematological, biochemical and morphometric and basal parameters of eight individuals of different sex but belonging to the infantile stage, the data then represent the evaluation even for a specific age and weight. It is important to collect the most data by having the opportunity to conduct research with threatened species.

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Do Neotropical bats play a role as potential natural reservoirs of Araraquara hantavirus?

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Bats (order Chiroptera) are known to harbor a large diversity of emerging pathogens, being second only to rodents. Viruses are the most abundant biological entities on the planet, and viruses that have their origin in the animal world cause most of the emerging diseases in humans. Viruses from bats can become important zoonoses, transmitted to domestic animals and humans via bats because of their ability to fly. Until 2012, there was only one report of hantavirus in bats. Then, it was thought that hantaviruses were rodent-insectivore borne pathogens. However new species of hantaviruses have been associated with bats, expanding the potential reservoirs and range of these viruses. To investigate if Neotropical bats harbor hantavirus, we captured 275 bats from February 2012 to April 2014 in south-eastern Brazil. From the captured bats, 53 individuals of different species were tested for hantavirus infection. It was possible to amplify a partial genome of S segment from the frugivore *Carollia perspicillata* and the common vampire bat *Desmodus rotundus*. The nucleotide sequences obtained showed high similarity with Araraquara virus, considered to be the most lethal genotype in the Andes virus clade, and perhaps in the world. Yet, we were able to find evidence of hantavirus infection throughout the organs, tissues and urine of *D. rotundus*. We report here for the first time in the Americas a hantavirus systemic infection in Neotropical bats, and we provide strong evidence that Neotropical bats may be playing a role as reservoirs disseminating lethal hantavirus.

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Untangling the koala stress syndrome: Understanding relationships between stress, disease and trauma in relation to clinical outcomes

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Anthropogenic induced environmental challenges such as habitat alteration and climatic warming can increase physiological stress in wildlife species. Wildlife species face multiple stressors so they require physiological and behavioural coping mechanisms for survival. The neuroendocrine stress response system provides physiological response to stressors in animals. However, it can become maladaptive under prolonged exposure to moderate stressors, such as environmental trauma and disease. This can lead to down-stream consequences on overall animal health and survival. The emerging theme of conservation physiology includes non-invasive physiological tools that can be applied to understand the stress biology of threatened and managed wildlife species. This research work focussed on the stress biology of rescued wild koalas (*Phascolactos cinereus*). The primary aim was to understand how environmental trauma and diseases influenced their physiological stress responses and the relationships between stress levels, clinical diagnosis, recovery and endpoint. Key stressors included chlamydia, physical demeanor (appearing flat or copious drinking), hit by car, dog attack, injury and burns. Diagnosis included chlamydia, infection, injury, burns, renal failure, inability to climb, respiratory illness, heat shock and diabetes. Chronically stressed koalas had generated significant allostatic load (elevated faecal glucocorticoid metabolites) and pathological state which required euthanasia. Noninvasive faecal glucocorticoid monitoring clearly reflected the diagnosis and recovery or endpoint of both mildly and moderately stressed koala patients. In conclusion, the stress biology of koalas should be studied in combination with clinical tests for environmental trauma and disease which may assist in more efficient stress management in koalas.

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Diet, body condition, and reproductive success: winners and losers in sea otter societies

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Sea otters exhibit marked individuality in prey choice when or where resources limit further population growth. Inasmuch as caloric content, search time, and handling time typically vary among prey species, the net rate of value (e.g., energy) returned from foraging should also vary among individual sea otters, thus producing the expectation of dietary covariation in fitness on the

one hand and selection for a dietary optimum on the other. Here we use Bayesian survival analysis to explore the effects of diet, mother's age and body condition on reproductive success (probability of pup survival), using data from a 38 year study of 310 tagged female sea otters in central California. Dietary patterns of individual sea otters aggregated into six clusters based on proportional abundance in the diet of 14 prey types. Average weaning success was similar among diet clusters. However, within clusters (and across the entire data set) there were positive relationships between female age, body condition and weaning success. Moreover, of the 189 adult females for whom we observed multiple (2 to 10) birth cycles, we found that individual females tended to vary consistently in terms of their likelihood of successfully weaning pups, even after accounting for effects of body condition and mother's age. Although fertility rate is essentially constant among adult female sea otters, most individuals fall into one of two classes: the winners (those who regularly succeed in weaning their offspring) and the losers (those who regularly fail).

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Maternal effects obscure condition-dependent sex allocation in changing environments

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Offspring sex ratios are predicted to vary with maternal condition where fitness returns are sex-specific, such as where one sex is differentially advantaged by extra investment. Studies in mammals tend to support the condition-dependent hypothesis, but results and effect sizes vary, suggesting constraints on maternal control. Maternal effects during gestation influence developing offspring and can cause lifelong physiological changes, which may be adaptive when anticipatory, with offspring ready to respond appropriately to certain environmental conditions, like predation risk. However, when a mismatch occurs between the pre- and post-natal environments, these effects may be detrimental if offspring are prepared for a different environment. Maternal effects do alter sex ratios in mice. Here we test whether this is due to an anticipatory maternal effect, by experimentally manipulating the gestational environment, and then breeding the female offspring in an environment that was either matched or mismatched to their environment during development. Females with matching environments displayed the predicted positive relationship between body condition and sex ratio, but females breeding in mismatched environments did not. Thus, the predicted condition-sex ratio relationship is obscured by anticipatory maternal effects when the environment changes, which may explain why some studies find unexpected sex ratio effects when developmental history is unknown. Furthermore, it may also contribute to unusual sex ratios seen in recently reintroduced or translocated populations which contribute to slow recovery rates, and effects may become more common with accelerating environmental change.

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Dose-response effects of deslorelin implants on contraceptive efficacy and health parameters in female Tasmanian devils (*Sarcophilus harrisii*)

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The selective use of contraception for endangered species breeding programs is a relatively new approach to wildlife management, but has many potential applications. The Save the Tasmanian Devil Program (STDP) uses contraception in their insurance metapopulation with the aims of equalising founder representation, controlling breeding within group housing situations, and preserving wild behaviours. Before this approach was taken, we conducted preliminary studies to ascertain the efficacy, duration of effect, optimal dosage, and any potential side effects of the proposed contraceptive on individual animals. This study assessed the dose-response effects of the Suprelorin® contraceptive implants containing a gonadotrophin-releasing hormone (GnRH) agonist, deslorelin, on female Tasmanian devils. Either one (n=5), two (n=5), or no (n=5) 4.7 mg implants were administered to the devils, with quarterly GnRH challenges used to test the hormonal responsiveness over two breeding seasons. There was an interactive effect of treatment group and month on the level of hormonal responsiveness ($P<0.001$), with treated females being suppressed relative to controls (with the exception of the mid-breeding season). At the end of the second breeding season, high dose animals were more suppressed than low dose animals, suggesting a dose-response effect. There was also an interaction between treatment and month on proportion change in body weight following contraception ($P=0.013$), yet there were no differences between treatment groups at each month. Contraception also had no apparent negative effects on general health measured by complete blood count analysis.

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How savanna vegetation influences rodent communities and foraging behaviors

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Elephants change savanna vegetation and at high densities reduce shrub and tree cover. The absence of elephants alternatively prompts increases in cover. Southern African savannas shift toward grass-dominated systems or shrub-dominated habitats, which impact rodent communities. As rodents are critical components of savannas, we sought to understand how and why they respond to different vegetation types. Using sites in Kruger Park (elephant presence) and in Swaziland reserves (elephant absence), we assessed how vegetation across a cover gradient shapes rodent communities. Kruger sites were open with limited woody cover, high grass, and low rodent diversity. Swaziland sites had higher cover levels, lower grass levels, and higher diversity. On average the community responded positively to both grass and woody cover, while individual species showed varied responses. Kruger's common species, *Mastomys natalensis*, responded positively to grass but negatively to shrub cover, matching Kruger's vegetation. We then tested whether fear of predation explains some species' decline in open grasslands. Loss of cover may increase perceived risks for rodents, shifting them towards "safer" covered habitats. We estimated rodent risk perceptions using Giving-up Density feeding trays placed across the cover gradient: inside a shrub, at the shrub's edge, and 3m away from shrubs. Rodents consumed more seeds under shrubs than further from shrub cover, suggesting that they perceive open areas as risky. Using camera traps, we monitored each species' foraging behavior and activity patterns. Most species primarily foraged under shrubs. *M. natalensis* foraged in all trays, appearing to thrive in open landscapes without fear.

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Elevational diversity patterns of small mammals in the Western Himalayas

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The Himalayas, located in the transition zone of three biogeographic zones, is a global biodiversity hotspot. Despite this, the distributions of small mammals in the western Himalayas are poorly known, with most surveys having been carried out over a century ago. We sampled non-volant small mammals along an elevation gradient from the Kashmir valley (1500 m) to the Tibetan plateau (5500 m) using a systematic methodology with standard Sherman and Tomahawk traps, in the Kashmir Himalayas, India. Using locally-weighted sums of squares and quadratic polynomial regressions, species richness of small mammals showed a bimodal peak at 2000 m and 3500 m, declining at lower and higher elevations. The areas where much overlapping of species occurs are the elevations where climate and vegetation change rapidly at the transition from mixed-broadleaved to conifers (~2200m) and the tree-line around 3300 m in the Western Himalayas. Murid rodents of the genus *Apodemus*, *Niviventer* and *Rattus* dominated the community in the lower elevations, replaced by voles of the genus *Microtus*, *Alticola* and *Hyperacrius* and *Ochotona* pikas in the alpine meadows, screes and Tibetan steppe. At least four species of *Apodemus* mice and four species of *Alticola* voles were sampled and subsequent genetic identification and phylogenetic analysis could potentially reveal new species in this region. Preliminary analysis of stable isotopes of carbon and nitrogen from fur samples show niche segregation among *Muridae* and *Arvicolinae*, possibly indicating a dietary transition from C_3 to C_4 plants mirroring the community turnover across the tree-line.

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Shifting habitat paradigms? Disagreement between the observed and predicted distribution of an expanding fisher (*Martes pennanti*) population based on previously documented habitat requirements

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Fishers (*Martes pennanti*) were extirpated from North Dakota, USA, during the late 19th century. However, there has been an increase in verified fisher sightings in the eastern third of the state over the past 15 years. Prior research supports old-growth forest as a habitat requirement of the fisher, but forested areas in North Dakota exist mainly as narrow, riparian strips and shelterbelts within a prairie/agriculture matrix. Thus, to verify the presence of fishers and to delineate their current and potential future distribution, we assessed verified reports and completed remote-camera field surveys and simulation modeling. Verified reports were concentrated in the northeast portion of the state and were less frequent farther south and west, which was consistent with remote camera detections collected in riparian forest over a 2 year period in the eastern 1/3 of the state. Simulation models, including Least-Cost Path (LCP) analysis and a spatially explicit population model, completed in program HexSim, did not accurately predict the observed pathways or distribution of fishers when they were parameterised with habitat requirements from published literature. However, when the strength of the requirement for forest habitat was reduced, LCP identified potentially important riparian corridors and HexSim scenarios predicted occupancy of large patches where populations were most likely to persist in the future. Overall, the results and predictability of the model would be greatly improved from additional behavioral and habitat studies in the region as habitat paradigms from prior research did not support the observed recolonization and distribution of fishers within the state.

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Demographic and behavioural characteristics of crop-raiding elephants in Sri Lanka: Can beehive fencing help mitigate human-elephant conflict?

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Human-elephant conflict (HEC), specifically crop-raiding, is a major conservation challenge. Many methods have been trialled to deter elephants from crops with varying success. One community-based deterrent demonstrating success in Africa is beehive fencing – a simple construction of beehives hung from pots and connected by wire, surrounding an area to be protected. However, it is not yet know if this deterrent will work in Asia. We present the first study to investigate beehive fencing as an Asian elephant crop-raiding deterrent, from a high HEC zone in Sri Lanka, where we have monitored hive occupations, crop-raiding, and farmer perceptions since 2015. We expect farmers to benefit from reduced crop-raiding and additional income generated through honey sales. We also investigate characteristics and social patterns of the local elephant population. Of particular interest is whether wild elephants exhibit individual personality traits, and whether these can be identified using ethological coding. To date, personality in wild elephants has been assessed only using items-rating, however this method requires long-term familiarity with individuals. We observed individually identified wild elephants in-and-outside protected areas, and coded behaviour during disturbance and non-disturbance periods, with preliminary analyses providing evidence of differences in boldness and aggressiveness between individuals and sexes. Many HEC studies focus on either the mitigation method or the crop-raiding behaviour of elephants. Simultaneously generating in-depth knowledge on both facets will enable a thorough analysis of beehive fence effectiveness, identification of other HEC hotspots that may benefit from beehive fencing, and help to facilitate appropriate expansion to other locations.

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The exploitation of anthropogenic resources by dingoes; more than just garbage and scraps

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The extent to which wild canids, including dingoes, rely on anthropogenic food resources in Australia appears to go beyond the direct use of garbage dumps and human-sourced waste. Wild dogs rely heavily on introduced species as food sources. We compiled data from 40 papers from the literature on dingo and wild dog diets to provide a comprehensive and objective record of the Australia-wide frequency of occurrence (FO) of introduced species in wild dog diets based on 27,711 scat and 1,522 stomach samples. All 40 papers reported evidence of introduced species in their diets, and showed that 24.8% of scats and stomach samples contained introduced species. Introduced animals recorded in the literature were swamp buffalo, camels, goats, hares, house mice, rabbits, sheep, black rats, wild pigs, foxes, cattle, deer and horses. Wild dogs consumed introduced species in relatively small amounts with the exception of the European rabbit (*Oryctolagus cuniculus*) which had the highest FO of 12.1%. The FO of livestock in wild canid diets was low, sheep and cattle being 0.26% and 4.93%, respectively. The direct consumption of human-provided food was recorded in just three papers, totaling 1.80% FO of the total wild dog diet. Dietary preferences of dingoes represent those of a generalist predator and over 200 distinct dietary items were detected. Wild canids appear to rely heavily on introduced species, but direct use of human-sourced food was rare and localized. Limitations of dietary analyses in Australia are discussed, including some general and country-specific problems that may be biasing the results.

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Threats to fishing cats and Indian smooth-coated otters in Godavari mangroves

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The Godavari mangroves are a mangrove wetland in India's Andhra Pradesh state. It is the second largest mangrove forest along the east coast of India after Sundarbans mangrove forest in West Bengal. Godavari mangroves cover an estimated area of 371 km^2 and also these mangroves supporting the largest number of fishing cats and smooth-coated otters in the east coast of India. As per the forest department census records, there is a deep decline of (>75%) in the population of both the species during the last decade. My study area includes Godavari mangroves and also mangroves adjoining 42 villages. To know the threats faced by fishing cats and smooth-coated otters in this region, I initially conducted an indirect questionnaire survey in mangrove forest adjoining 42 villages followed by sign survey at the creek fishing zones and also aquaculture influenced areas present adjoining the Godavari mangroves. According to the obtained information of both indirect questionnaire and sign survey I placed hide-outs at surveyed points and documented the kills of fishing cats and otters in this Godavari mangrove region and also while documenting the process of threats I documented standard 15 minutes of very rare video footage of fishing cats and smooth-coated otters in this region. According to the results of continuous 3 years of study (2014-2017), animal and human conflict, poaching, creek fishing, habitat destruction, and effluent water release into creeks are becoming the major threats for decline of these threatened species in this Godavari mangrove region.

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'Quenda-friendly' gardens; where urban wildlife conservation meets community engagement

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A large proportion of urban green space is residential gardens, which are becoming increasingly important habitat for urban wildlife due to continued clearing of native bushland. Within the City of Mandurah (~70 km south of Perth, Western Australia), the quenda (southern-brown bandicoot, *Isoodon obesulus fuscivente*r) is persisting in the urban environment, despite the potential threats of predation, habitat loss/fragmentation, and vehicle strike. There is anecdotal evidence that quenda frequently visit residential gardens in this area, but it is not known if some characteristics of these gardens are preferred or avoided by quenda. To determine what makes a 'quenda-friendly' garden, we surveyed a range of gardens surrounding known quenda habitat. Surveys included gardens that did, and did not, receive visits from quenda, as reported by residents. Remote cameras were used to confirm presence or absence of quenda within each garden. We measured attributes relating to vegetation structure (% canopy cover, % cover of dense vegetation), plant species diversity, presence of pet dogs/cats, size of gardens, and the location of gardens within the urban matrix (e.g. distance to nearest reserve). Identifying specific attributes that encourage the utilisation of residential gardens by quenda can increase the potential habitat and resources available for use by urban quenda. This work will allow the creation of an evidence-based framework that can be used by residents and local government to improve management

of urban habitat for wildlife. Encouraging ‘quenda-friendly’ gardens will benefit local wildlife and engage the wider community in the conservation of our native mammals.

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Weather drives population dynamics in common European forest and field rodents

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Voles of the genera *Microtus* and *Myodes* are distributed in many regions of the world. *Microtus* and *Myodes* species are particularly abundant in Central Europe where population dynamics are characterised by multi-annual fluctuations. Population outbreaks occur about every 2-5 years. They affect the ecosystem well beyond the small mammal community because of cascading effects through the food web, impact on soil composition, seed bank, etc. We used long-term time series (standard snap-trapping or active burrow counts) covering several decades of rodent abundance to assess effects of weather conditions on vole abundance and potential effects of long-term climate change on outbreak frequency. Analyses were based on boosted regression trees and classification and regression trees. Weather conditions were highly correlated to outbreak risk/abundance in common voles and bank voles. Results indicate bottom-up regulation in both species. Most of the relevant weather parameters connected to common vole abundance originated in the preceding winter and early spring. In contrast, there were delayed effects in bank voles and field voles, which responded to weather parameters affecting seed mast of forest trees in the previous year. Based on the A1B CO_2 emission scenarios we estimated the future occurrence of weather conditions that favour bank vole outbreaks. Results indicate that such conditions are likely to occur more frequently in the future than it is the case presently. This may also be the case in other rodent species if dynamics are similarly related to weather conditions. This can potentially cause ecosystem-wide effects at several trophic levels.

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Ecologically-based rodent management in SE Asia: Changing rules of engagement with agricultural intensification and extreme climatic events

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Rodents are one of most damaging pests of rice in Southeast Asia, with reported pre-harvest losses of 5-10% per annum. Based on a strong understanding of rodent pest ecology, it is known that the breeding seasons for the most important rodent pest species in Southeast Asia are closely linked to rice cropping seasons due to the abundant availability of food provided by the growing rice crop. Thus, ecologically-based rodent management (EBRM) strategies for rice ecosystems generally include synchronous planting and extended fallow periods to reduce pest population build-up. However, an increasing pressure to produce more food with less land and labor availability has led to intensified cropping frequency and changes to cropping systems that can pose challenges for EBRM. In addition, extreme climatic events, which are likely to become more frequent with global warming, can extend the availability of food for rodent pests due to significant changes to the rice production landscape. For example, crop damage due to severe flooding events can lead to asynchronous planting as farmers plant opportunistically with limited resources in an attempt to recover their losses as soon as possible. Due to such issues, there is an increasing need to manage rodent pests on a larger scale and develop strategies to deal with extreme weather events. In this paper, we provide an update on rodent issues in five rice-growing countries in Southeast Asia, including an overview of recently published studies, and conclude by exploring opportunities for targeted deployment of EBRM strategies.

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Management challenges of invasive mammals operating at different scales; the European brown hare, bank vole and greater white-toothed shrew in Ireland

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Ireland is a large (84,421 km^2) island, off an island (Great Britain), off a continent (Europe), with a depauperate yet unique mammal community. It is vulnerable to non-native species introductions and all mammalian guilds have been invaded expect the bats. The origin, spatial extent, expansion rates and impacts of two invasions will be compared; one involving a relative large (4 kg) mammal, the European brown hare (*Lepus europaeus*), and another involving two small (< 20 g) mammals; the bank vole (*Myodes glareolus*) and greater white-toothed shrew (*Crocidura russula*). European hares were intentionally released during the 1800s for field sport and now occupy a relatively small range (535 km^2) which expanded 3-fold between 2005 and 2012-13 (0.73 km year^{-1}). They are replacing an endemic species of conservation concern, the Irish hare (*Lepus timidus hibernicus*), through competition and hybridisation. The bank vole and greater white-toothed shrew were introduced during the early and late 20th century respectively; both unintentionally. They occupy a substantial range (32,700 km^2) and are expanding quickly (2-6 km year^{-1}) associated with the decline of the native woodmouse (*Apodemus sylvaticus*) and extirpation of the pygmy shrew (*Sorex minutus*). Due to their body size and scales of invasion they pose different management challenges. The native hare could be protected by culling the invader with eradication possible albeit difficult. The invasive small mammals are naturalised and impossible to remove but native small mammals may be protected by forward planning of landscape composition and land use change. Management strategies will be contrasted.

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Borrowed plant defences: Deterring browsers using a forestry by-product

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Herbivorous mammals can significantly damage important tree species, particularly at the vulnerable seedling stage. Harnessing the anti-herbivore defences evolved by some tree species could reduce the appeal of more preferred trees and thus their loss to browsing. We tested whether chemicals extracted from birch bark, a forestry by-product, could protect seedlings of Scots pine from ungulate browsers in Sweden. We quantified the responses by captive moose and red deer to extract application as a function of both the distance between seedlings and whether the extract was applied to all or alternate seedlings. Both moose and red deer consumed pine seedlings less frequently when seedlings were treated with extract. At inter-seedling distances equivalent to those used in forestry, red deer browsed untreated seedlings more frequently with treated than untreated neighbours (associational susceptibility), whereas moose browsed untreated seedlings less frequently with treated than untreated neighbours (associational refuge). Red deer used a finer scale of selection for choosing between seedlings, but moose consumed more untreated relative to treated seedlings overall (4:1 compared to 2:1 by red deer). We then tested the effectiveness of the extract to protect young pine trees from browsing by wild moose, red, fallow and roe deer in a mixed forest over winter. Treated trees were significantly less likely to be browsed; proximity to and species of the nearest tree were also important. Applied with an understanding of the foraging behaviour of resident herbivores, existing plant defence chemicals have the potential to significantly reduce herbivore damage in managed forests.

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Biodiversity outcomes for New Zealand’s major pest management regimes

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New Zealand’s native flora and fauna have immense biological, cultural and economic value, but are under major threat from invasive vertebrate pests. Predation by possums, rodents and mustelids, in particular, has caused many of New Zealand’s iconic native species to decline at an alarming rate. Approximately one third of New Zealand’s land mass is now under some form of vertebrate pest control, either through aerial delivery of toxic baits, or ground-based baiting and trapping operations. Quantifying the benefits of pest management activities for native biota is important for justifying the intensive efforts and resources invested by conservation agencies and other groups concerned with protecting and restoring ecosystems. To this end, we perform extensive meta analyses of published studies reporting native biota responses to pest control, along with data from unpublished outcome monitoring studies conducted across New Zealand. Our meta-analyses provide significant insights into the extent to which ecosystems respond to pest control, and allow a comparison of effect sizes across New Zealand’s different major control regimes.

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Messing with the mind: Using unrewarding prey stimuli to reduce predator impacts

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We tested the idea that bird odour placed as ‘chemical camouflage’ around bird breeding areas can protect vulnerable eggs and chicks by reducing the hunting success of mammalian predators (Price and Banks 2012). Before birds settled in areas to breed, we randomly deployed readily-available generic bird odours, such as chicken or quail, in the environment at two 1,000 ha riverbed sites in the Mackenzie Basin of New Zealand’s South Island. Predators (cats, mustelids, hedgehogs) investigated the odours but received no food rewards. After several weeks, predators’ interest in investigating the odour waned. Presumably we deceived them into thinking that bird odours were not a profitable cue, thereby reducing predation pressure when birds began nesting. We anticipated that some predators would ‘re-learn’ that bird odour sometimes results in a reward, so additional use of generic bird odour during the nesting period reinforced for predators that bird odour was not always associated with food, and also created a confusing surfeit of real and similar bird odour. This camouflage technique may give birds enough time to breed successfully before predator learning resumes. We report preliminary results from laboratory and field trials that test whether predators ‘generalise’ bird odour cues sufficiently to modify hunting behaviour and, therefore, whether generic odours resulted in increased nest survival of threatened shorebird species.

Price, C.J. and Banks, P.B. (2012). Exploiting olfactory learning in alien rats to protect birds' eggs. Proceedings of the National Academy of Sciences of the United States of America 109, 19304-19309.

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Replacement and displacement driven by innovations, competition and extinctions

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A key innovation may allow one group of species to radiate and replace another, but the role of competition and background extinctions for the replacement process is vigorously debated and unclear. We used an individual-based eco-evolutionary model of a co-evolving competitive community to study these macroevolutionary processes. Evolutionary innovation was modeled as a heritable competitive advantage introduced in one of the co-evolved species. We demonstrate that replacement may occur by the adaptive radiation of a competitively superior group. Increasing the competitive advantage shortened replacement times, but there was no particular threshold advantage. Origination rates in new groups were comparable to extinction rates of the original groups, keeping the total number of species approximately constant over time. Extra background extinctions sped up the process, consistent with observed patterns in the fossil record that replacement is sped up during mass extinctions. The replacement process was mainly driven by evolutionary competitive exclusion. The old, inferior type had an elevated rate of extinction matched by an increased speciation rate of the superior type. Incumbency also played a role, but we found little support for a strict incumbent replacement scenario, where replacement is entirely driven by background extinctions of the old group and opportunistic speciations of the new group. Compared to adaptive radiation into an empty niche space, replacement was slow and relict species from the original group could linger in marginal and previously unexploited niche space that provided a niche refuge and prevented complete replacement. Similar patterns are also found in the fossil record.

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The comings and goings of giant mammals: An explanation based on climate and foraging economics

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The last 55 million years has seen the largest perrisodactyls, rodents, and marsupials come and go. Some indricotheres weighed perhaps 20 tons. Alternatively, the horse and tapir families have seen evolutionary trajectories of increasing size. Ruminants begin small and hit their stride of size and diversity some 20 million years ago. Proboscideans have simply lumbered along. The seemingly regular turnover of large mammal groups and species, or changes of body size within a species seem associated with warming and cooling periods, and/or vegetation transitions. All seem tied to carbon dioxide levels. Here we combine three lines of research present in the literature to explain ebbs and flows of large body masses, and transitions between perrisodactyls and artiodactyls. First, high carbon dioxide levels may favor woodier vegetation of lower nutritional quality. Second, in terms of foraging allometries, herbivore body size may represent a tradeoff between finding (favors smaller size) and handling food (favors larger size). Third, foragers should have higher giving-up densities (GUDs) on lower quality foods, and when temperatures are lower. Together these can produce sometimes opposing eco-evolutionary feedbacks. The general trending downwards of carbon dioxide may explain the transition from giant perrisodactyls to artiodactyl communities. Furthermore, mid-epochal rises in carbon dioxide may select for new, larger species of browsers. Finally, the Pleistocene ice ages may emerge from feedbacks of C_3/C_4 plant communities, temperature, carbon dioxide and subsequent body size evolution. Foraging economics, digestion physiologies, and vegetation-climate feedbacks may drive the comings and goings of giant mammals.

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Thoughts on the interplay of demographic stochasticity, fitness, and the niche concept

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G.E. Hutchinson's niche concept is an abstract mapping of one aspect of population dynamics (in particular a measure of absolute fitness) onto an environmental space. For continuously growing populations, the metric is traditionally assumed to be the intrinsic growth rate, r, at low densities (with units of 1/time). But at small absolute numbers, extinctions can occur for populations with a positive intrinsic rate of growth because of demographic stochasticity. Another familiar fitness metric, R_0 (the expected number of offspring produced per individual over their lifetime), arises when considering extinction risk. This alternative metric can influence the shapes of niche response surfaces. This talk will broadly aim at assaying the relevance of demographic stochasticity for concepts of both absolute and relative fitness in small populations, such as at range margins and in sink habitats, with an eye towards refinement of ecological niche concepts. These different fitness metrics also have implications for how we think about species' evolution, particularly in rapidly changing environments, and also arise in models of macroevolutionary dynamics.

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Attitudes towards wildlife conservation, New South Wales, Australia

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People's attitudes towards wildlife conservation are of particular importance as they have an impact on conservation outcomes. Major threats to Australian wildlife include exotic weeds, changing fire regimes, climate change, mining activities, grazing pressure, disease, habitat loss and introduced predators, which highlights the need for wildlife conservation in Australia. The attitudes of NSW residents towards wildlife conservation were captured to gain a better understanding of how people relate to the conservation of native Australian wildlife. Convenience sampling was used to recruit 312 NSW residents to participate in an online questionnaire in a cross-sectional study. An ‘ecoscientistic’ attitude was the most commonly held attitude, which means wildlife are appreciated for the role they play within our ecosystem. Furthermore, growing up around animals had a strong impact on wildlife attitudes. However, the type of attitude held is dependent upon the wildlife species in question. In particular, people showed a preference for conserving mammals. Despite the attitudes expressed in the questionnaire indicating strong conservation attitudes, the participants’ intention to engage in conservation behaviours was low. Rates of participation in conservation were low due to lack of time, money, knowledge and impact of health and fitness levels. Strong conservation attitudes were present in the NSW population, and should be harnessed to inform future policy and management decisions, especially for action that promotes conservation preferences for non-mammal species that are under-represented and endangered. Further research is required to identify how to overcome barriers to conservation action.

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eMammal: Citizen science camera trapping as science, conservation, and public engagement.

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Citizen science can engage the public with nature while also accelerating the rate of data collection, which is critical to track the rapid pace of modern environmental change. Camera traps are ideal tools for citizen science because their photographs can be verified by experts, and the unique animal pictures provide an enjoyable experience for volunteers. Although not a replacement for traditional museum collections, these archives of photo-vouchers can be accumulated faster, over larger areas, and are noninvasive. Through the eMammal project, we have developed field protocols, training modules, education materials, and the cyberinfrastructure to enable large citizen science camera trapping programs. We have worked with volunteers and scientists in 11 states to monitor over 11,000 sites on public and private land, recording 0.5 million detections in >700 camera-years of monitoring effort. These data have been used in peer review publications on invasive species, predator-prey relationships, population monitoring, and the impact of recreation on wildlife. We are now scaling up to work with citizens to run camera traps at 20,000+ sites across the state of North Carolina. Internationally, we are working with over 50 schools in four countries, documenting endangered species living on community land. The eMammal data management framework has also been useful for non-citizen programs, including surveys by governments and academics, contributing to a growing camera trap archive at the Smithsonian. Volunteers consistently report positive experiences from camera trapping, and surveys show they increase their knowledge and become stronger advocates for conservation by running camera traps.

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Using environmental drivers to model blue whale acoustic detection variability

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Blue whales are difficult to study using traditional visual survey methods due to their endangered status and secretive behaviour. Passive acoustic monitoring (PAM) provides an alternative approach to better understand the ecology and behaviour of these rare majestic animals. PAM is cost effective, providing long term sampling that is not affected by adverse weather conditions. We compare two distinct acoustic populations of blue whales living in temperate waters across separate ocean basins. Using the CTBTO’s (Comprehensive Nuclear-test Ban Treaty Organisation) hydro-acoustic network, we have access to 15 years of continuous recordings of ocean noise from Cape Leeuwin, off Western Australia and 9 years of recordings from Juan Fernandez Island, off Chile. Hydrophones at each site record ocean noise continuously and whale calls are located using automated detectors. In addition, satellite derived environmental data was obtained which included sea surface temperature, sea surface height and productivity (chlorophyll-a). Using the satellite data, we constructed models to determine which of the environmental variables best predicted whale calls. Our results show that blue whales responded to the inter-annual variability in environmental conditions. This has implications for the management and recovery of the species as we provide some insight to how they will adapt to changing conditions.

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Significance of elevated mercury concentrations in Australian sea lion, *Neophoca cincerea*, pups with endemic hookworm disease

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The Australian sea lion, *Neophoca cinerea* is an endangered pinniped species (IUCN Red List, 2008) occupying an upper trophic level within the marine ecosystem. As such, it is a useful indicator species of trace element and heavy metal (toxicant) concentrations. Anthropogenic sources of toxicants when at high concentrations can be associated with increased susceptibility to disease, mortality and reduced reproductive success. A specific objective of the recovery plan for *N. cinerea* is to investigate and mitigate potential threats, including pollutant exposure. In a population significantly impacted by endemic disease due to the intestinal nematode hookworm, investigating toxicant concentrations and their role in increasing susceptibility and severity of disease outcomes, is paramount. ICP-MS was used to determine the concentration of 13 elements, Hg, Pb, As, Se, Cd, Mg, Al, Co, Ni, Cu, Zn, Cr, and Fe in liver and hair samples collected from *N. cinerea* pups sampled at two South Australian colonies from 2006 to 2013. The concentration of mercury (Hg) in both liver (mean = 28.9 $\mu g\ g^{-1}$ dry weight; n=39) and hair (mean = 5.4 $\mu g\ g^{-1}$ dry weight; n = 199) were among some of the highest reported in pinnipeds and were associated with an increased age at which pups shed hookworm infection and reduced health status, likely due in part to the immunosuppressive effects of Hg. Toxicant concentrations, particularly Hg, are likely a significant risk factor for hookworm disease in *N. cinerea* pups. As such, monitoring toxicant concentrations is important for the conservation and management of this endangered species.

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Impacts of toxicants in the marine ecosystem on the health of Australian fur seals (*Arctocephalus pusillus doriferus*)

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Persistent organic pollutants (POPs) cause toxicity effects in a wide range of species. Species dominating the upper trophic level are particularly vulnerable to bioaccumulative toxic effects caused by environmental pollutants. An alopecia syndrome has been recognised at high prevalence (up to 50% of juvenile females) in Australian fur seals, *Arctocephalus pusillus doriferus,* at Lady Julia Percy Island (LJP), Victoria. Previous investigations suggest causality could be due to a pollutant acting as an endocrine analogue. The alopecic syndrome is a likely risk factor for juvenile mortality. To investigate whether POPs are associated with endocrine disruption and alopecia, we compare POP's concentration in the fur of alopecic (n=50) and non-alopecic (n=51) juvenile seals sampled at LJP, in fur collected from pups at LJP and three other colonies in Victoria and Tasmania (considered baseline colonies for comparison), and in blubber and fur samples collected from stranded fur seals in Victoria. The concentration of selected POPs including dioxin/furans (PCDD/Fs), polychlorinated biphenyls (PCBs), polybrominated diphenyl ethers (PBDEs) and perfluoralkyl compounds was determined using high resolution mass spectrometry or liquid chromatography-mass spectrometry. High levels of several POPs, including dioxins, were detected, indicating that pinniped pups are at risk of POPs mediated toxicity in-utero, at a particularly susceptible developmental stage. We discuss the significance of POPs concentrations in relation to the causality of alopecia and the conservation management of the marine ecosystem, and assess the usefulness of fur as a non-invasive biomarker to assess POPs exposure in this sentinel species.

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Health implications for dolphins with heavy metal contamination in South Australia: A case study of two species in Spencer Gulf

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Industrial and agricultural pollutants have resulted in high concentrations of heavy metals in the sediments and biota of Spencer Gulf. The present study examined 307 opportunistically-collected Indo-Pacific bottlenose and short-beaked common dolphins with the aim of identifying relationships between heavy metal concentration in kidney and bone (by ICPMS and ICPAES), indicators of pathology in bone and kidney, age, sex, collection locality and circumstance of death. The highest kidney concentrations of cadmium (134 mg kg^{-1} wet weight), zinc (93 mg kg^{-1}) and lead (11 mg kg^{-1}) were found in bottlenose dolphins. Several individuals had elevated concentrations of more than one metal. Lead was weakly correlated with age for bottlenose dolphins. Preliminary evidence was found for transfer of zinc from mother to neonate during foetal life and while suckling. Cadmium accumulation may begin soon after birth. Nephritis was the most often recorded kidney pathology, usually as a chronic condition. Bowman's capsule, in the kidney, was larger in dolphins from Spencer Gulf than elsewhere. Older dolphins had more skeleton pathology than younger ones. Degenerative lesions, which are normally associated with age, were more frequent in young bottlenose than common dolphins at similar ages. Extreme congenital skeleton pathology was observed in a bottlenose dolphin from upper Spencer Gulf and it had the highest cadmium and zinc concentrations. Multivariate analysis of results may reveal relationships between the studied variables. Bottlenose dolphins in northern Spencer Gulf are exposed to many threats, including heavy metals and their toxic effects.

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From land to water: The thermoregulatory role of fatty acids in the mammalian fat tissue

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The biochemical composition of adipose tissues plays an important role as physical barrier in mammalian thermoregulation. As fatty acid (FA) desaturation increases, adipose tissues can reach colder temperatures without solidifying. This is particularly important in bare-skinned animals and those inhabiting cold regions. We investigate how variation in FA desaturation relates to different thermal proxies. We calculate FA desaturation index for 48 mammalian species based mostly on literature values and compile a dataset of thermal proxies: Hair density, latitude and environment (terrestrial, semi-aquatic and fully-aquatic). To examine the relative contribution thermal factors play in the variation of FA desaturation, we use phylogenetic regression analyses along with a model selection approach. An interaction of environment and latitude is the model with the highest support. Adipose tissues in terrestrial mammals do not seem to have a thermoregulatory role. Fully-and semi-aquatic mammals have higher FA desaturation compared to terrestrial mammals. We show that as mammals re-invaded aquatic environments, FA modification became an important component of their thermoregulatory strategy. Semi-aquatic mammals have significantly higher levels of desaturated FAs when living in colder environments whereas terrestrial and fully-aquatic mammals do not. A high FA desaturation allows fully-aquatic mammals to maintain flexible blubber in cold environments, but surprisingly they do not modify FAs as they migrate through different latitudes. They probably regulate other blubber parameters instead. In semi-aquatic mammals, when fur is very dense the desaturation of FAs is low, and vice versa. Semi-aquatic mammals in colder environments tend to rely on blubber as an insulator.

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Spatial distribution of South American in-shore cetaceans

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In-shore dolphins are potentially the most threatened of South American's marine mammals because of their close proximity to human influences. South America is a global hotspot of marine mammal conservation but because of regional limitations, there is restricted on-the-ground information about the spatial distribution of cetaceans. To identify the species most at risk, we model the species distributions of five in-shore dolphin species; the Chilean, Comerson's, dusky, Franciscana and Peale's dolphins. To assess the main drivers of their distribution, we inferred species distribution models using spatial sighting data for eastern and western South America. We included six eco-geographical variables: bathymetry, habitat, sea surface temperature and distance to canyons, to the coast, and freshwater to assess the main drivers of spatial distribution. We also estimated the degree of spatial overlap between species and niche overlap models using the Schoener's *D* Test. We found that the main drivers for species with reduced distribution are the distance to the coast and freshwater, whereas the drivers for the species with a wider distribution range are the distance to the coast and bathymetry. According to our distribution analysis, we identify that the in-shore dolphin species most vulnerable to anthropogenic impacts are the Chilean, Franciscana and Peale's dolphins. Although many marine mammal species remain classified as data deficient under the International Union for Nature, our case study shows that SDMs together with historical distribution data and environmental variables, can be used to identify species most at risk, to target future research and management priorities.

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Data preparation and decisions for multivariate analysis of camera trapping data

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Camera traps are capable of generating large amounts of data on multiple species. One of the biggest challenges of working with those data is preparing them for analysis and deciding which covariates to use. This workshop session on camera trap data preparation will discuss methods of data manipulation and preparation for common analyses including occupancy, density and generalized linear regression with examples in Excel and R. We will also explore common procedures for choosing the most appropriate covariates for a multivariate analysis including assessment of collinearity, data visualization and univariate tests. We will show examples of step-by-step data preparation and decision making based on common analysis goals. We will also discuss common issues encountered with camera trap data preparation and analysis.

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Data analysis: Capture-recapture using R and MARK

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When individuals of a species can be identified on camera traps whether via natural markings or artificial marks, we are able to employ a robust set of models to analyze those data in a capture-recapture framework to estimate critical population metrics such as true abundance, density, survival and recruitment. Camera traps allow us to use capture-recapture, often without ever having to capture the animals thus saving time, money and reducing potential stress. This workshop session will introduce a suite of mark recapture models for use with camera trap data. We will provide examples of how to run common mark recapture models using Program R and Program MARK including closed capture models, spatially explicit capture recapture and mark-resight models. We will also discuss some of the challenges of using these models including sample size, capture heterogeneity, mark loss and computing power.

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It is about what you've got and how you use it

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In wildlife management, camera traps are precision tools that command the same level of regard and care that any data logger or bio-sampling tool is afforded. It is necessary that researchers and managers define their question (what do we really want to know?), select an appropriate method (how do I best answer my research/management question), choose the right tool (should I use camera traps?) and then use it appropriately (what settings are best, how can placement be optimised?). Contrary to popular use, camera traps should not be considered "set-and-forget" devices able to be deployed effectively by anyone who wants to collect wildlife data. Rather, it is crucial that users have a fundamental understanding of the functionality, basic physics and limitations of these devices so that the technology can be suitably exploited. A failure to understand key concepts, such as: how camera traps detect heat-in-movement and its relationship to the background temperature, functional animal's heat signatures, how site conditions e.g. weather and time of day affect detection, and how a fast shutter speed setting may improve identification, may result in spurious and/or substandard data. We will present an overview of the types of camera trap equipment available in the market, some of the basic functionality of camera traps, and describe the types of questions users should consider before deploying camera traps into the field.

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Data analysis: occupancy and co-occurrence using r scripts

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An objective of many camera trapping studies is to understand factors that influence the probability a species will occur at a location in space. Interspecific interactions can strongly influence how animals use space, and camera traps allow us to record detection / non-detection of many species within ecological communities. Recent advancements in occupancy modeling techniques have allowed scientists to simultaneously evaluate how both environmental factors and interspecific interactions influence the probability a suite of species will occur at a location in space. This workshop session will introduce users to recently developed multi-species occupancy models. We will first discuss basic sample design issues and identify how to properly format data for analyses. We will then outline a modeling strategy that proceeds by fitting sequentially more complex models of species interactions. Throughout, we will illustrate how to fit multi-species occupancy models within the R environment and will share code used to conduct example analyses with workshop participants.

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Conditioned taste aversion as a tool for reducing predation by wild canids

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Predator control has traditionally been used to solve the conflict between wild carnivores and humans for resources, leading many carnivore species to the brink of extinction. We are assessing the use of conditioned taste aversion (CTA) as a tool to reduce predation by wild canids. Firstly, we performed an experiment with penned dogs to identify suitable substances to be used as CTA agents in wild canids. We compared pre- and post-conditioning consumption of untreated food as a measure of CTA response. Levamisole (anthelminthic) and Thiram (fungicide) reduced food consumption in the conditioned dogs between 15% and 48% and between 23% and 32% respectively. Both substances generated CTA in dogs with no adverse health effects. A field experiment was performed in two localities with Thiram as CTA agent. Nine foxes were marked with GPS collars and ear tags and simulated partridge nests were monitored with camera-traps. A control area (n = 5 foxes) and a treatment area (n = 4 foxes) were delimited in each locality. During the pre-conditioning phase, nest predation rate was 27.1% and 22.6% in the treatment and control areas, respectively. Foxes were exposed to 60 mg kg^{-1} of Thiram during the conditioning phase. During the post-conditioning phase, no nest was preyed by treated foxes, whereas foxes in the control area preyed on 13.1% of nests. These results show that Thiram can be safely used as CTA agent to prevent nest predation by foxes. CTA opens new opportunities to mitigate conflicts between humans and predators.

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Feral cat activity, home range, and density, and what happened when cats were removed.

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Worldwide, feral cats (*Felis catus*) have contributed to some of the greatest biodiversity losses, and are listed as one of the worst invasive species. This is particularly evident in New Zealand where native fauna evolved without mammalian predators. Feral cats are predators of native species and are sometimes the focus of control operations. Knowledge of their activity patterns and home range can be used in pest management by indicating the best time for capture, and spacing of traps. We studied a population of feral cats on Ponui Island, New Zealand. Nine adult cats (6 male, 3 female) were live-trapped and fitted with radio transmitters from April 2015 to January 2017. Twenty eight motion-sensing cameras were also set up in a grid over the site to monitor cat movements and activity. Males had larger home ranges than females and showed greater home range overlap then females. Feral cats were most active at night, with a peak of activity in the first hour of darkness. The worst time for capturing was between 07:00-11:00 where cats were least active. Literature indicates that the home range size of feral cats tends to decrease linearly with increasing density. We tested this relationship by manipulating the density of the cat population by removing cats. This resulted in an increase in home range by one cat (first manipulation), and an invasion of cats (second manipulation). This knowledge will help customise management plans to better control these pests and reduce their damage to native fauna populations.

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Learned aversion to poison baits using a ‘self-training’ device in domestic dogs

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Accidental poisoning of domestic dogs is an unfortunate occurrence when using poison baits to control introduced pests such as feral cats, red foxes, and wild dogs. Risks to domestic dogs can limit the use of baiting by land managers and result in reduced control of predator species that decimate our native wildlife. We developed and trialed the use of a device attached to a non-toxic form of a poison bait to assess whether we could induce a learned aversion towards the baits in domestic dogs. Presentation of an electrified and non-electrified non-toxic bait occurred over several time points at day 0, day 1, week 1 and 5 weeks, 3 months and 6 months, at the dog owners’ property and *in situ* (i.e. conservation estate). This study of 25 domestic dogs has shown that a learned aversion to the non-toxic bait can be created in domestic dogs. Twenty dogs developed strong avoidance responses after presentation of a single electrified bait. Four dogs took more than two presentations of the electrified bait to develop aversion towards non-electrified baits. One dog repeatedly ate baits and did not show any aversion behaviour. Longevity of the training is still undergoing testing but the dogs continue to demonstrate a learned aversion to the non-toxic forms of the bait. To date the training has shown great promise to create a learned aversion to toxic baits by domestic dogs, thereby reducing the risk of accidental poisoning.

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Dispersal patterns affecting pack formation and breeding success in a monogamous and social carnivore, the African wild dog (*Lycaon pictus*)

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Despite the importance of dispersal in increasing fitness and population persistence, there is a lack of understanding how dispersal proximately affects mate choice (i.e. group formation) and ultimately affects fitness (i.e. breeding success). In this study we investigated long-term patterns of dispersal by African wild dogs in an enclosed population for 90 pack years and modeled how these affected dispersal age, pack formation and breeding success. Dispersal patterns were biased although this was sex-specific across explanatory variables. Females dispersed at higher annual probabilities, at younger ages, and in smaller groups than males. Natal dispersal (i.e. primary) occurred at a younger age for females than males, while female non-natal dispersal (i.e. secondary) occurred at older ages than for males, indicative of mate competition as a mechanism for dispersal in wild dogs. We found evidence suggesting that costs of early dispersal might be offset by emigration in larger groups. Contrary to predictions, younger individuals dispersed in smaller groups during their primary event but in larger groups during their secondary event. Optimal pack formation was not related to timing of dispersal, rather, pack formation was significantly dependent on larger dispersal groups and emigration in the mating and resource abundant seasons. More males, younger individuals, larger packs, larger dispersal groups, and emigration during mating and resource abundant periods resulted in increased fitness. Our results confirm that mate competition (especially among females), inbreeding avoidance and resource competition are important drivers of dispersal in this population of wild dogs.

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Conspecific competition and resource depression affect movement and home range establishment of translocated fishers (*Pekania pennanti*)

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Experience and information should be advantageous to residents of a home range but put invaders at a disadvantage causing them to establish their home ranges elsewhere. Conspecifics should avoid the home ranges of one another to ensure they are not altering resource availability, but encountering one competitor (e.g., dominant or of a different sex) may cause an individual to discount resource patches differently compared to if they encountered another conspecific. We tested the hypothesis that female and male carnivores responded differently to the presence of sex-specific competitors. We tested our hypothesis by selectively releasing newly moved fishers (*Pekania pennanti*) in the presence or absence of already established fisher home ranges during a reintroduced into northern California over 3 years from late 2009 to 2011. Using satellite transmitters (Argos) and land-based (VHF) telemetry we made daily observations of fisher locations, movements and area of their minimum convex polygons during their first 200 hundred time steps after release. Females that encountered the home range of any conspecifics moved further, had larger minimum convex polygons and settled further from their release locations than did females that did not encounter a conspecific home range. Males did not avoid, or appeared indifferent, to the home ranges of all conspecifics but males released in the absence of females moved more. Our results suggest that female fishers avoided conspecific competition from both males and females in accordance with our hypothesis. Males appeared motivated by the absence of females and by the type of sex-specific competitor they encountered.

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Seasonal spatial behaviour of pine marten *Martes martes* in a deciduous oak forest of central Italy

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Size and characteristics of home range are fundamental ecological parameters for a species and useful life-history variables for predicting the number of individuals that can occupy a certain area. In Italy, wildlife biologists have largely ignored spatial behaviour of the European pine marten, although this predator is present across the peninsula. We investigated the seasonal socio-spatial behaviour of pine marten in a sub-Mediterranean deciduous oak forest of central Italy, by radio-tracking 16 pine martens (eight males and eight females). To our knowledge, our research is the only published study on spacing pattern of pine marten in sub-Mediterranean deciduous oak forests and the first published radio-telemetry study on pine marten home range in Italy. Size, composition and stability of seasonal ranges (FK 95 and 50 %) were analysed in both sexes. Unlike reports in the literature for other European habitats, home ranges resulted similar in size and forest coverage in both sexes and throughout seasons. The only exception were females' territories whose size decreased in spring. Males and females occupied ranges stable in both position and size through the year, leading us to hypothesise that the sub-Mediterranean deciduous oak forest was able to meet resource requirements for both sexes and in all seasons. Our results provide useful information on the socio-spatial ecology of the European pine marten and may be helpful for conservation management of this species in southern Europe.

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Exploring the role of short-tailed shrews (*Blarina*) in the Lyme disease cycle in North America

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Human Lyme disease is a bacterial infection caused by members of the *Borrelia burgdorferi* s.l. complex that is transmitted primarily by ticks in the genus *Ixodes*. Since first reported in 1975 in Lyme, Connecticut, Lyme disease has steadily increased both in number of cases and geographic extent. Despite being restricted to eastern and midwestern states, Lyme disease is the 6th most common reportable disease in the US, with ~300,000 cases annually, of which only 10% are diagnosed because the spectrum of pathologies makes early diagnosis difficult. The forest-dwelling white-footed mouse, *Peromyscus leucopus*, is presently considered to be the main competent (amplifying) reservoir host, but our recent studies indicate the potential for a

significant role in transmission of *B. burgdorferi* by the short-tailed shrews in the genus *Blarina*. Of 362 ticks removed from *Blarina* caught in live traps in eastern Virginia, 360 were *Ixodes* spp. Tissues from 22 of 33 *Blarina* from eastern Virginia were positive for *B. burdorferi* s.l., as were 72% of tissues from 25 museum specimens of *Blarina* collected from 1963-1993. *Borrelia*-positive tissues from *Blarina* collected in Minnesota (n = 42, 79%) and Kansas (n = 19, 74%) further indicate the importance of understanding the role of the short-tailed shrew in the transmission of Lyme disease.

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Toxoplasma gondii in domestic dogs living near wild mammals. Is this a complication for conservation purposes?

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Carlos Botelho State Park (PECB) is a protected area of an important Atlantic Rainforest remnant in São Paulo State, Brazil, affected by the growth of surrounding neighborhoods and the increase of domestic animals freely roaming inside and outside the park. Overpopulation of free-ranging domestic dogs is an issue faced by many protected areas, resulting in intimate contact with wild mammals. This situation increases the flow of infectious diseases between them, posing a threat to the wild populations. *Toxoplasma gondii* is a parasite that infects warm-blooded animals and its definitive hosts are wild and domestic felids. Once one infected domestic dog enters the park it can infect a wild predator mammal and contribute to the disease dynamic. In order to implement interventions regarding the local domestic dogs we evaluated habitants of the surroundings of PECB, and antibody anti-*T. gondii* was detected in 28% (100/350) and 25% (101/396) of the animals from 2015 and 2016, respectively. Among the 252 dogs sampled on both years, 33 were positive. The dogs entering the park probably act as predators as well and the high *T. gondii* seroprevalence shows the spread of this agent at that preserved area. Those results will foster the buildup of a health management model for the surroundings of the park. Implementation of permanent public policies including joint actions to minimize the access of feral domestic dogs into the park and their contact with wild carnivores, such as neutering and health education campaigns, could enhance the survival of local wild species.

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Prevalence of black spot disease among bottlenose dolphins in Shark Bay, Australia.

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Dolphins, as apex predators which routinely appear at the water's surface, are a good candidate species to serve as a bioindicator of ocean ecosystem health. In this study, we analysed black spot disease (BSD), a poxvirus-like skin disease in *Tursiops aduncus,* using the 30-year longitudinal data set gathered in Shark Bay, Australia. Using photographic observations, we characterised Shark Bay dolphins as being infected with BSD if at least one photograph showed a BSD skin lesion. We analysed this incidence data to determine general characteristics and demographics of the disease. We found that the average age of a BSD-infected individual is 26.6 ± 34.8 months with the average symptomatic period lasting 134 ± 35.6 days. The overall prevalence of BSD in the entire Shark Bay population is 19.26%. Upon demographic analysis, no sex difference was observed in the disease but there was a large age effect, with dolphins aged 1-2 years (yearlings) getting the disease significantly more than both younger and older calves. BSD was rare among juvenile and adult dolphins (N = 68 calves, 4 juveniles and 3 adults). We hypothesise that the lower prevalence in youngest calves (< 1 year) is due to maternal immunity, while older individuals (> 2 years) have infection-acquired immunity. The low prevalence overall in Shark Bay compared to other populations with poxvirus present is a positive indicator that environmental protections and controls are functioning well to keep the bottlenose dolphins healthy although the potential for zoonotic transmission warrants further investigation in this population.

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Seasonal variation in occurrence of oxalate nephrosis in South Australian koalas (*Phascolarctos cinereus*)

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Many koalas (*Phascolarctos cinereus*) in the Mount Lofty Ranges population, South Australia are affected by oxalate nephrosis, characterised by renal calcium oxalate deposition and kidney failure. Environmental factors such as the hot, dry summer period of the Mount Lofty region may increase the occurrence of this disease, particularly since koalas primarily rely on the moisture content of eucalypt leaves to maintain hydration. This study investigated seasonal variation in occurrence of oxalate nephrosis in koalas and whether temperature, rainfall and/or eucalypt leaf moisture were significant factors. Koalas from the Mount Lofty population that died or were euthanased between 2008 and 2016 were necropsied and oxalate nephrosis confirmed with

histopathology (n = 65). Moisture content was determined in leaves from four species of dietary eucalypts collected seasonally over one year in the region. Deaths from oxalate nephrosis were significantly correlated with high mean maximal temperatures in the month of death ($P < 0.05$) and the month prior to death ($P < 0.005$), and low rainfall in the month prior to death ($P < 0.05$). Winter was the season when the lowest number of koalas with oxalate nephrosis was identified ($P < 0.05$). Average leaf moisture content was found to remain relatively constant across the year, varying from 60.3 ± 1.0% in autumn to 62.5 ± 1.0% in spring. Hence hot and dry weather was identified as an important environmental factor for increasing occurrence of death of koalas with oxalate nephrosis in the Mount Lofty region, likely due to increased evaporative water loss.

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Maximising nutritional status in captive marsupials

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For marsupials there is a lack of detailed data on their nutritional needs. Nutrition is fundamental to health status, and inadequate nutrition can lead to deficiencies, poor health and poor reproductive output. Macronutrient composition plays a role in food intake of carnivores, in the wild and in captivity. Research has shown species such as dogs (*Canis lupus familiaris*) target for high lipid diets, while cats (*Felis catus*) and mink (*Neovison vison*) target for high protein and moderate lipid diets (one a percent energy basis). The largest extant Australian marsupial carnivore, the Tasmanian devil (*Sarcophilus harrisii*) and one of the smallest, the fat-tailed dunnart (*Sminthopsis crassicaudata*) have been studied to determine their macronutrient preferences. Preliminary analysis has shown devils prefer protein while dunnarts prefer lipid. Their choices can be related to their dietary preferences and physiological/behavioural processes.

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Change in territoriality of Tasmanian devils following a strong population decrease caused by a transmissible cancer

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Tasmanian devils (*Sarcophilus harrisii*), which are endemic to the island of Tasmania, have declined by 85% in the 20 years since the emergence of an aggressive transmissible cancer, devil facial tumour disease (DFTD). The population of devils on the Freycinet peninsula has been monitored by live trapping since 1999, two years prior to the first case of DFTD in this area (2001). This particular year, VHF collars were deployed on adult animals before and after the mating season (February and May respectively). Fifteen years later, DFTD has reduced the devil population by nearly 90%, yet instead of driving its host to extinction, the tumour has disappeared from part of the area, now for three years. GPS collars were deployed in 2015 and 2016 to evaluate how the spatial organisation of the population changed in response to the epidemic. The first results suggest that home range sizes did not significantly change with the decrease in population, and males still use larger areas than females. Before the disease outbreak, devils showed minimal territoriality resulting in many individuals sharing the same area. Following the DFTD epidemic and population decline, there is stronger spatial avoidance, especially between individuals of the same sex. Linking this change in spatial organisation with live trapping records and genetic data will help us to understand how and why DFTD disappeared from the Freycinet peninsula. This unprecedented knowledge on the transmission of DFTD within wild populations of Tasmanian devils will hopefully help conservation strategies to save this emblematic mammal.

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Daily timetable of embryonic development and its implications for reproductive strategies in the common brushtail possum

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Detailed daily timetables of embryonic development of marsupials are rare and are confined to the Virginia and grey opossum (13.5 days), stripe-faced dunnart (10.7 days), agile antechinus (27 days). Less detailed timetables for other species are available. Many marsupial developmental timetables are characterised by developmental arrests during cleavage and the unilaminar blastocyst stages and these are used in reproductive strategies to ensure breeding success. This timetable of the brushtail possum was based on 183 specimens, of which 80 were timed from a plug, sperm in the urine or an observed mating (time 0) and the residue were wild-caught. Captive colony animals were monitored during oestrus and for several days around the expected day of birth. Samples were collected on each day, measured and photographed. Samples from wild-caught females were fitted into the timed samples. The gestation period pc was 15.5 days (range 15- 17 days) in captive colonies and showed evidence that oestrus could be extended for up to a couple of days but was mostly less than a day, several periods where maternal/conceptus interactions apparently occurred and no arrests during cleavage or unilaminar blastocyst stages. The direct development shown by the common brushtail possum, the marked synchrony of breeding in the autumn in NZ and the few developmental failures so that about 80% of females breed successfully in the wild suggest that the reproductive strategy used by the brushtail possum is to breed at the time of the year when survival of young is enhanced.

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Twenty years of primate conservation studies: trends and biases

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The species extinction rate has been occurring at accelerating levels, such that scientists are concerned with identifying priority species and areas for conservation. Species that are better studied receive more conservation attention, so it is necessary to optimize our research efforts. However, factors contribute to some species being more studied than others. Our aim was investigate the biases and trends in allocation of research efforts on primate conservation, across species, themes and countries. We reviewed the literature for 20 years (1994 – 2014) from conservation journals and primatology journals, selecting papers with determined tags related to a primate conservation theme. We found 550 articles, and that theme has increased in the primatology, but not in the conservation, area. Fragmentation was the most addressed theme. Most of the authors are from universities and the research was conducted mostly in protected and unprotected areas. Most of the studies used an empirical approach, and were conducted in 49 different countries, with most published for the United States and United Kingdom. Of the studies from 55 different countries, Madagascar and Indonesia were those that had the most studies. The articles are related to 388 species, with *Pan troglodytes* the most studied. Allocation of research effort was motivated by time since description and species body size, but not by threatened status or size of distribution. Our results showed that the studies did not always reflect conservation needs. Primatologists need to rethink their priorities, to improve conservations efforts, focusing on conservation needs such as threatened species and important threats.

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Participatory conservation of the Indian pangolin (*Manis crassicaudata*) in coastal Maharashtra, India

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Hunting of the Indian pangolin is a known traditional practice in coastal Maharashtra. It would be done by a few skilled communities for their own consumption; it was a form of subsistence hunting. Pangolin meat would be consumed and the scales would be discarded, not sold. However, over the last few years, hunting for the wildlife trade has replaced subsistence hunting. In the last two years, four illegal consignments of Indian pangolin hunted in coastal Maharashtra have been confiscated by enforcement agencies. Sahyadri Nisarga Mitra initiated a participatory conservation effort in January 2016 to counter the rapidly decline of the Indian pangolin in coastal Maharashtra. One of the prerequisites of such a conservation initiative is sound understanding of the focal species. In this context Sahyadri Nisarga Mitra conducted a pilot social survey in 165 villages in Chiplun block of Ratnagiri district of Maharashtra state. In this survey, data were collected on the presence of the Indian pangolin in the recent period. Based on this information, a camera trap study has been conducted at 200 locations. In this paper our conservation efforts are described. World over there are very few systematic studies on pangolins. A naturally low population and the secretive, nocturnal nature of pangolins are often cited as the reasons for the lowly studied status. In this paper, our efforts for participatory conservation of Indian pangolin and subsequent learning are discussed.

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The role of in-situ speciation in the generation of biodiversity across the Indo-Australian Archipelago

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Island colonization followed by *in-situ* adaptive radiation has long been a fascination in biology, as it is thought to have generated the patterns of endemism we see on islands today. Nowhere is this more prominent than the Indo-Australian Archipelago (IAA), where four isolated biogeographic regions, separated by deep ocean channels, contain high levels of endemism. The rats and mice of the IAA (Rodentia: Muridae) are astonishingly diverse, both in species richness and niche breadth. Classical views predict that, following the arrival of an ecological generalist colonizer, subsequent speciation generates more specialist forms, increasing the overall ecological and morphological disparity within the resulting clade. We used a time-calibrated phylogeny for over 350 species of murids, along with measurements of body size and locomotor mode, to reconstruct the ancestral states at each instance of island colonization across the IAA. From these results, we test the prediction that clade age is positively correlated with ecological diversity, as indicated by locomotor mode and body size. Overall, we find increased locomotor diversity and body size in older clades, highlighting the role of *in-situ* island speciation in the generation of biodiversity.

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Contrasting the isotopic niche between small-mammal assemblages from habitats with distinct structural complexities

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Resource partitioning among small mammals mostly occurs through segregation on both food and spatial dimensions. Structurally distinct forests of the highly seasonal Brazilian savanna (Cerrado), such as the *cerradão* (dry woodland forest-WF) and the gallery forest (forests that surround water courses-GF), allow comparisons of small-mammal resource partitioning between areas with similar assemblages but distinct structural complexities. Using ^{13}C and ^{15}N stable isotopes, we described isotopic assimilation and compared the partitioning of isotopic niche of small mammals from both forest types. Considering the higher plant diversity and complexity of the GF, we expected a broader overall range of the isotopic niche for the assemblage and higher specific niche specialization in this forest type in comparison with the WF. Moreover, as small mammals are generalists and plastic foragers, we predicted that species that occur in both forest types would show a broader niche breadth in WF due to its lower complexity and potentially higher variability in resource availability along the year. The WF assemblage presented higher $\delta^{15}N$ range, increased general isotopic niche and decreased overlap in comparison to the GF assemblage, contradicting our initial expectation. These patterns indicate that the assemblages mirrored differences in plant isotopic signatures between forests. Rodent species occurring in both forests (3 spp) presented larger isotopic niche amplitude in GF, whereas marsupials (2 spp) did not show this same pattern, suggesting a larger plasticity on the use of food resources by rodents. Both resource availability and diversity influenced isotopic assimilation by small mammals in Cerrado forests.

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Functional responses of an apex predator and mesopredator to invading deer: dingoes, red foxes and sambar in south-eastern Australia

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Biological invasions by large herbivores involve the establishment of novel interactions with the receiving mammalian carnivore community, but understanding these interactions is difficult due to the large spatio-temporal scales at which such dynamics would occur. We quantified the functional responses of a native apex predator (dingo; *Canis dingo*) and a non-native mesopredator (red fox; *Vulpes vulpes*) to an invading non-native deer (sambar; *Rusa unicolor*) in south-eastern Australia. We predicted that the apex predator would exhibit a stronger functional response to increasing sambar abundance than the mesopredator. We used a state–space model to link two 30-year time series: (i) sambar abundance (hunter catch-per-unit-effort), and (ii) percentages of sambar in dingo (N = 4531) and fox (N = 5002) scats. Sambar abundance increased exponentially during 1984−2013. The percentages of sambar in dingo and fox scats increased during this 30-year period, from nil in both species in 1984 to 8.2% in dingoes and 0.5% in foxes in 2013. Dingoes exhibited a much stronger functional response to increasing sambar abundance than foxes. The prediction that invading deer would be utilised more by the apex predator than by the mesopredator was therefore supported. The increasing abundance of sambar during the period 1984−2013 provided an important food source for dingoes. In contrast, the smaller red fox utilized sambar much less. Our study demonstrates that prey enrichment can be an important consequence of large herbivore invasions, and that the effect varies predictably with the trophic position of the mammalian carnivores in the receiving community.

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Stable isotopes as a tool for conservation? Understanding human-primate conflict through seasonal variations of isotopic ratios.

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In the Central Karoo, small livestock losses to predators like jackals (*Canis mesomelas*) and caracals (*Caracal caracal*) are a chronic challenge to farmers and the leading cause of conflict with wildlife. Recently, farmers reported that chacma baboons (*Papio ursinus*) have added to their losses by targeting sheep. Here we use carbon and nitrogen isotopes ratio measured from hair of 33 baboons to assess whether animal protein constitutes a significant part of their diet. We then investigated variations in chronological values of stable isotopes in relation to seasonal variations in food sources using sequential analysis. The $\delta^{13}C$ and $\delta^{15}N$ results confirmed baboon’s largely vegetarian diet. Baboons mostly fed on C3 plants accessible near riverbeds. Invertebrates and C4 plants, including maize used by farmers to supplement the sheep, both contributed to a smaller portion of their diet. $\delta^{15}N$ values were higher for males than females, but remained very low in comparison to livestock $\delta^{15}N$ values. Only one individual showed significantly higher $\delta^{15}N$ values over time. Sequential analysis revealed marked seasonal variations for both carbon and nitrogen, strikingly homogenous among individuals. Variations in $\delta^{15}N$ values were likely related to short availability of preferred legume species following rain events. While the recurrence of drought events may have driven baboons toward alternative food sources when natural resources are scarce, only few individuals are probably involved in livestock predation. In the light of climate change, we emphasize the need for alternative management methods and discuss the use of stable isotopes as a tool for conservation.

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Preliminary results of the impact of human land use and landscape productivity on the density and dynamics of red fox in Norway

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In the boreal forest, the red fox (*Vulpes vulpes*) is a key species due to its many strong food web linkages and its exploitation of niches that form in the wake of human activities. A range expansion and population increase of red fox have caused major concern in Scandinavia, primarily due to imposed threats to a number of prey and competitor species. Here, we synthesize 12 years of transect snow-track data covering 27,000 km^2 to identify factors associated with their distribution and population dynamics. By the use of Bayesian hierarchical regression models, we evaluate the effects of landscape productivity and climate gradients as well as anthropogenic subsidization on red fox population size and density dependent growth structure. We found that landscapes with high human settlement density and high amounts of remains from moose (*Alces alces*) hunting held higher densities of red fox. Population mean return time and partial rate correlation function implied first order population dynamics, and the structure of density dependent population growth was associated with the amount of agricultural land in the landscape. Carrying capacity increased and populations were more stable in high-level agricultural areas, whereas density dependent population growth was more prominent in low-level agricultural areas. We conclude that human land-use is a dominant driver of red fox population dynamics in the boreal landscape and potential effects of regional-scale landscape productivity are overridden. We further argue that future research should focus on intrinsic, density dependent, factors such as social structure (e.g. competition and territoriality), fecundity and dispersal.

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Kin–bonds among bachelor males contributes to the evolution of a primate multilevel society

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In contrast to most mammalian social systems, a few primate species, including early humans, live in multilevel societies (MLS) in which multiple family units co-exist to form a breeding band of several hundred individuals and an associated all-male band (AMB). Although the primate MLS has importance for understanding the origin of human sociality, previous research has focused mainly on African papionins, revealing that the papionin MLS evolved from an internal fissioning process from a large multi-male/multi-female group. Based on a combination of social network analysis, satellite telemetry, and genetic investigation, we estimated the dynamic of interactions between bachelor males to restructure their affiliation patterns, and cooperative and tolerance behaviors, to form and maintain a large AMB in the golden snub-nosed monkey (*Rhinopithecus roxellana*). We found that bachelor males form stronger alliances when they approach breeding females. Using a novel HPMT mathematical model, we show that kinship was the most important factor facilitating alliance formation among AMB males, followed by age and dominance rank. We suggest that an 'arms race' between breeding males' collective defense against usurpation attempts by bachelor males, and bachelor males' aggregative offense to obtain reproductive opportunities, has selected for larger group size on both sides. This provides further support for the *R. roxellana* MLS having evolved from a fusion of a network of small, isolated family groups in an ancestral Asian colobine, as well as increasing understanding of human social evolution, because male-male affiliations are trademarks of small- and large-scale human societies.

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Wild rats are evidence of environmental changes in Asia through the late Quaternary

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In our recent study, we sought to explore the biogeographic history of the wild rats in Asia and to understand the long-term persistence of high species diversity in this region. The rat genus *Niviventer* is one of the dominant taxa in the local mammal communities from Southeast Asia to central China. The *N. andersoni* species complex (NASC) is highly adapted to middle to high elevations. In contrast to previous studies that have proposed regional refuges in the eastern or southern Hengduan Montains (HDM) and emphasized the influence of climatic oscillations on local vertebrates, we found that the HDM as a whole

acted as refuge for the NASC and that the historical range shifts of NASC mainly occurred in the marginal regions. Demographic analyses revealed slight recent population declines in Yunnan and south-eastern Tibet, whereas the populations of Sichuan and of the entire NASC were stable. This pattern differs greatly from classic paradigms of temperate or alpine and Holarctic species. On the contrary, *N. confucianus* is a dominant rat species with a wide elevational range in natural forests from southern to central and north of China. Inferring the demographic dynamics of this species uncovered dramatic population expansion in southwest, central and northern China that occurred since 0.5 Mya in the Late Pleistocene, but only slight expansion in Yunnan/Tibet. Environmental changes since the Late Pleistocene, particularly the decrease of predation and competition from the loss of megafanua, together with seed hoarding behavior, probably contributed to the dramatic population boom of this species.

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Multi-locus phylogeography of the rock-dwelling Cape rock hyrax *Procavia capensis* from southern Africa

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Mountains are a prominent feature of the African continent and, along with climatic and vegetation heterogeneity, have been suggested as major drivers of vertebrate radiations and phylogeographic structuring. Cape rock hyrax is a small mammal species associated with mountains and other rocky terrain. We used coalescent-based analyses of a multi-locus data set (mtDNA, two nuclear intronic loci and microsatellites) to tease apart life history traits and extrinsic factors that have shaped the intraspecific diversity, distribution and demography of this species in southern Africa. Rock hyrax gene trees show evidence of diversification during the late Miocene. Since this epoch, southern African biomes have experienced cyclic patterns of expansion and contraction linked to global and local climatic variability, impacting on small mammal speciation and intraspecific diversity. We confirm the presence of two unique parapatric mitochondrial lineages; however, the nuclear DNA data reveal secondary contact and introgression between these historically separated populations. We supplemented the genetic data with distribution modelling, leading to the identification of several important refugia for rock hyrax. These were identified mainly along the Great Escarpment and its associated mountain ranges. Although no discernible barriers to gene flow were evident from our study, we propose that rock hyrax diversification and population dynamics are driven by the availability of suitable habitat (rock crevices and nearby, abundant food sources), as well as factors such as social dynamics and disease outbreaks. The coalescent approach indicates that there is currently unrecognized diversity within the genus and species delimitation across the distributional range is warranted.

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Genetic and cytogenetic diversity in the *Cricetulus barabensis* species group

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Striped hamsters (*Cricetulus barabensis* species group) consist of four karyologically and morphologically distinct forms. Three of them are included today in a polymorphic complex *Cricetulus barabensis* sensu lato, which is widely distributed in steppe and semidesert zones of Siberia, Mongolia, the Far East, and China. At the same time, the last form - *Cricetulus sokolovi* - is a rare endemic species of the Gobi Desert and remains poorly studied. Molecular phylogenetic results have shown that the mean genetic distance between the *cytb* haplotypes of *C. sokolovi* and *C. barabensis* s. l. (8.1%) falls within a range observed for the congeneric sister species in Rodentia, while the distances between chromosomal forms in *C. barabensis* s. l. correspond well to an interspecific level (2-4%). Available molecular and craniometric data support the sister-group relationship of *C. sokolovi* with *C. barabensis* s. l. relative to *C. longicaudatus*. By contrast, cytogenetic (FISH) data highlight the outlying position of *C. sokolovi* within *Cricetulus*. The karyotype of *C. sokolovi* is highly rearranged, and the most parsimonious scenario of its origin implies at least four Robertsonian events (WARTs and fusions) and a centromere shift as a cause of the difference between the ancestral karyotype of *C. barabensis* s.l. and *C. sokolovi*. Considering a low level of the karyological differences between forms within *C. barabensis* s.l. these results demonstrate asynchronous rates of chromosomal evolution in different lineages of *Cricetulus*. The reported study was funded by RFBR according to the research project No. 16-34-60086 mol_a_dk.

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Using gene drive technology to control invasive mammal species in Australia: Are we ready?

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In Australia, invasive animals have been linked to the extinctions of native wildlife, and to significant financial impacts in agricultural assets. While there are current approaches to control invasive species, these efforts are self-limiting: they require ongoing management and cost over large landscapes, and often result in the short-term suppression of local populations. New and innovative approaches are warranted. Recently, the gene editing system CRISPR/Cas9 has been proposed as a potential

genetic tool that, among other applications, could be used to bias sex-determining genes in a target species to produce males and reduce the numbers of individuals over generations. This technology has the potential to be used by wildlife managers as a non-lethal alternative to control invasive species. While regulatory control and social acceptance are components that must be addressed, there is also a need to identify knowledge and research gaps based on the currently available information for each invasive species. Here we apply a conceptual framework based to an ecological risk model within the gene drive context to identify key requirements for undertaking work on four exemplar invasive mammal species in Australia (red fox, feral cat, rabbit, black rat). This framework, if applied, would allow an evaluation of the potential effects of a gene drive within a risk context. We consider the current biological information to evaluate the knowledge gaps in preparation for a more formal assessment of the use of gene drives as an additional strategy for the control of these and other invasive species.

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Post-control recovery of behaviourally homogenous pest populations: A case study of personality in wild house mice (*Mus musculus*)

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Animal interactions with wildlife management devices, such as traps or bait stations, rely upon an animal's behavioral decision to interact with the device. This decision is strongly influenced by an individual’s personality traits (consistent behaviour exhibited over time and context) and bias often arises as bolder animals more readily interact with devices, while shyer animals avoid detection. This bias is has significant implications to pest management if residual, un-trapped individuals are capable of rapidly repopulating, resulting from the removal of all but the extremely shy individuals from a population. It is unknown how such homogenous residual populations behave or whether its constrained behaviour will affect future population growth. As behavioural traits are partially hereditary, the populations may become behaviorally homogenised across generations, with an entire population becoming neophobic. Or they may be able to exploit the opportunities of a largely unoccupied behavioural spectrum; exponentially increasing in population size. We report on an experimental study of the implications of personality-driven biased pest removal on population recovery. Using standard personality screening protocols, wild-caught house mice were classified into bold, shy or mixed populations; each comprised of six founder individuals. Populations were released into semi-natural enclosures where limited food was dispersed in safe or risky areas. Over a nine-week period, we studied the founder and F1 generation behaviour, rates of population increase and changes in behavioural profiles. We discuss the implications of our results for other programs that may only target a proportion of the behavioural continuum when monitoring or managing wildlife populations.

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I don’t think we can be friends! Interactions between wallabies and feral goats at Avon Valley National Park; an operational perspective on management.

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Feral goats are a significant threat to native biodiversity in Australia. They are known to overgraze vegetation, cause land degradation, and compete with native species for resources. Goats compete with the threatened black-flanked rock-wallaby (BFRW, *Petrogale lateralis lateralis*) for access to caves and food resources, and have been implicated in population declines. In Avon Valley National Park, 50 km north-east of Perth, a small population of BFRW’s occur on granite outcrops, whilst western brush wallabies (WBW, *Macropus irma*) have been recorded across the wider park area. Using remote cameras, we investigated the interactions between feral goats, WBW’s and BFRW’s across the park. We placed 30 Reconyx (HC500) cameras in seven vegetation types throughout the park, and an additional 13 cameras focussed on the rock-wallaby habitat. There was little overlap between WBW’s and goats across different vegetation types in the park, suggesting disparity in areas utilised by goats compared to WBW’s. Both goats and WBW’s were recorded in wandoo woodlands, but goats’ preferred longer unburnt vegetation, compared to WBW’s that utilised younger vegetation. It is unclear whether these results demonstrate resource partitioning or avoidance. Goats showed a preference for the granite outcrops where the BFRW population occurs. An increase in goat activity over a 3 year period and a mild prescribed burn, preceded a large decline in the number of BFRW’s. The remote camera results were confirmed by targeted trapping. This information is being used to improve goat control measures in the park, including trapping and shooting programs.

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Costs of inflammatory and humoral immune responses in the subterranean rodent *Ctenomys talarum*: Linking immune variability and life history underground

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The immunological variation of wild populations in relation to life-history traits has recently become a central topic in evolutionary biology, given the critical contribution of immunity to an individual’s fitness. Specific induced defenses, which require substantial time and resources and are mostly beneficial against repeated infections, are expected to be favored in “slow-living” species. To test this prediction, understanding the costs and benefits of immunity is essential. Here, we evaluated the energetic costs of activating two different arms of immune defense (humoral and inflammatory) in the Argentine subterranean rodent *Ctenomys* *talarum* (tuco-tucos), a “slow-living” species. While a significant increase in oxygen consumption was verified when tuco-tucos mounted an antibody-mediated immune response against sheep red blood cells (SRBC), no significant energetic cost was detected during the inflammatory response triggered by phytohemagglutinin (PHA), which in tucos has components of the innate as well as the adaptive response. However, PHA-induced inflammation was negatively affected by infection with naturally-occurring gastrointestinal parasites and in animals under food restriction, suggesting that currencies other than energy are mediating the costs of inflammation in tuco-tucos. When both arms of defense were activated simultaneously, we found no evidence that the humoral response was favored over the inflammatory response, despite tuco-tucos’ slow pace of life. The relevance of other factors, such as pathogen exposure in the subterranean environment and the low basal metabolic rate of tuco-tucos, is discussed in relation to the immune variability exhibited by these rodents, and the implications for natural populations of wild mammals.

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Low mitochondrial DNA diversity in Gaur (*Bos gaurus gaurus*): Evidence from modern and ancient DNA

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The Gaur (*Bos gaurus gaurus*) is the largest ungulate found in South and Southeast Asian countries like India, China, Bangladesh, Bhutan, Nepal, Myanmar, Vietnam, Malaysia, Thailand and Cambodia. Largest population of Gaur is confined to India, but currently in all their distribution ranges, the Gaur population is declining and attained a status ranging from vulnerable to endangered. This study originated out of our three years of Gaur monitoring in Melghat Tiger Reserve, (MTR), one of the protected reserve created in early 1970’s for the conservation of tiger and also identified as one of the “Gaur Conservation area”. The MTR, is located at 21°26′45″N 77°11′50″ E in central India and covers an area of 1677 km^2 and inhabits 1000 Gaur, 1 per 100 km^2. We sampled 66 individuals from six pockets. ~300 bp of displacement loop (D-loop) was sequenced in 66 individuals. Single haplotype was obtained in 66 sequences generated from dung samples (KR233670). We also successfully generated a D-loop sequence from 50 years old Gaur trophy originating from Gaur of MTR displayed in our Zoological museum (sequence not submitted). Comparison of dung haplotype with ancient haplotype revealed that the ancient haplotype differs from dung haplotype by G>A transition at 1631 position with reference to GU324987 sequence in BLAST. Thus, retention of single haplotype in free-ranging wild population of Gaur points towards small founder female and inbreeding due to intense habitat fragmentation. Typing nuclear loci would shed more light on the population genetics structure of Gaur inhabiting MTR.

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Multiscale patterns of habitat use in the koala, a specialised arboreal folivore

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We examined the habitat use of the specialised arboreal folivore, the koala, in a fragmented rural landscape. Habitat use was studied at multiple spatial scales, from individual trees to the entire landscape. Koala presence was measured through scat searches, spotting individuals on transects and GPS tracking of individuals. At the landscape level, the proportion of patches with food tree species was most important. Soil type, although important for tree nutrient and toxin levels, were relatively unimportant in koala patch use. At the individual tree level, koalas used larger trees with more shelter during the day, and more food species trees during the night. We also examined the nocturnal tree use for the influence of leaf moisture, and concentrations of nitrogen, tannins, FPCs, terpenes and fibre. Using this multiscale approach enabled a comprehensive spatial and temporal understanding of habitat use in a highly specialised species. It also enables evidence-based conservation and management decisions on this iconic species in a fragmented landscape.

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Is the endangered northern quoll (Dasyuromorphia: *Dasyurus hallucatus*) one species or four? A morphological re-assessment.

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The northern quoll (*Dasyurus hallucatus*) is the largest marsupial predator in the arid monsoonal tropics of northern Australia. This endangered species is believed to have undergone serious declines due to a multitude of factors, including habitat fragmentation, altered fire regimes, predation from feral cats, and more recently very high mortality due to poisoning from ingesting introduced cane toads (*Rhinella marina*). As a result, northern quolls have been the focus of intense conservation efforts to mitigate the impact of toads. The four disjunct populations of northern quolls are not currently recognised as taxonomically distinct, but they were originally split into four subspecies; *D. h. exilis* (Kimberley, WA) *D. h. hallucatus* (NT), *D. h. nesaeus* (Groote Eylandt, NT) and *D. h. predator* (Qld). There is mounting molecular evidence to suggest that northern quoll populations are clearly structured and exhibit deep divergences that most likely predate post-European range contractions. The most genetically distinct population is the Pilbara, which was not included in the original subspecies description as no specimens were available at the time. Here we examine a suite of qualitative morphological characters of the skull and skins of specimens from each of the four northern quoll populations. Using a statistical approach we investigate the distinctiveness of each population and if they should be recognised as separate subspecies. Using previously published molecular data and our morphological data we discuss possible divergence dates for each population and the potential geographic origin of this species, as well as conservation implications.

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Dispersal and synchrony determine the slope of Taylor's law: Gompertz model analyses of Hokkaido vole populations

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Taylor’s law (TL) asserts that the variance in a population density is a power-law function of its mean: $\log(\text{variance}) = a + b \log(\text{mean})$. The slope b lies between 1 and 2 in most observed TLs, and an underlying mechanism determining slope b is one of major questions about TL. I showed in a previous study that densities of the Hokkaido vole satisfied temporal and spatial forms of TL, and demonstrated that time series generated by the Gompertz model reproduced the form of temporal and spatial TLs, but with slopes that were significantly steeper than the slopes estimated from data (Cohen and Saitoh 2016, Ecology 97: 3402-3413). In this paper, I analyzed effects of interpopulation dispersal and spatial synchrony of population dynamics on the slope b using the Gompertz model. When each population was independent, the spatial and the temporal slopes were higher than 2. When interpopulation dispersals were introduced, the temporal slopes were lowered to the interval between 1 and 2. However, the spatial synchrony was required to lower the spatial slopes.

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Geographical physiological variation in energy and water metabolism in Mongolian gerbils (*Meriones unguiculatus*)

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Mongolian gerbils (*Meriones unguiculatus*) have a large-scale distribution in Inner Mongolian of China, Mongolia and the Baikal region of Russia. Precipitation decreases from east to west along this geographic gradient, and the landscape consequently transitions from typical steppe to desert steppe to desert. Precipitation and primary productivity are considerable environmental variables to affect animal survival and distribution in this area. Geographic physiological variations which relate to energy and water metabolism are critical to animals’ local adaptation and distribution. Gerbils in a desert population had a lower resting metabolic rate (RMR) and total evaporative water loss (TEWL) than a mesic population. Serum metabolomics revealed that concentrations of five tricarboxylic acid cycle intermediates (citrate, cis-aconitate, α-ketoglutarate, fumarate and malate) were lower in a desert population than a mesic population. Gastrocnemius metabolomics and citrate synthase activity analysis showed a lower concentration of citrate and lower citrate synthase activity in the desert population. The relative medullary thickness (RMT), serum osmolality, vasopressin concentration, and renal expression of aquaporins (AQPs) did not have geographic variations, but showed phenotypic flexibility in renal morphology and osmoregulation when faced with seasonal environmental variations. Further, under extreme water scarcity, Mongolian gerbils could have a high efficiency for urine, faecal and evaporative water loss, and up-regulate renal AQP2 protein.

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The role of middens in white rhino (*Ceratotherium simum*) olfactory communication

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White rhinos transmit information about their sex, age, territorial and oestrous state via dung odours. White rhinos defecate communally in middens and it has been suggested that these middens act as information centres. However, it is uncertain which individuals are primarily transmitting information or who this information is intended for. We investigated the behaviour of white rhinos at middens and found that they were utilised predominately by adults. Territorial adult males visited and defecated more than any other individuals. Adult males investigated dung piles more than any other age or sex, and the majority of these piles belonged to territorial males and adult females (i.e. male-male and female-male communication). Adult females investigated the dung of non-territorial males more than adult males did, and also investigated the dung of other females as much as males did (male-female and female-female communication). There was a spatial aspect to defecating in middens, where territorial males defecated in the centre of the midden, while other individuals defecated around the periphery. Lastly, territorial males regulated their dung output, with a higher defecation frequency and smaller dung volume than any other adult. Ultimately, our results indicate that middens act as information centres, where the primary function seems to be for territorial males to transmit and obtain information (male-male and female-male communication). However, in addition, non-territorial males can assess female reproductive state, while females may be assessing the quality of all the males and even the number of other females that use a midden (male-female and female-female communication).

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The Ross seal in eastern Weddell Sea, Antarctica

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The Ross seal (*Ommatophoca rossii*) is the least numerous and least studied of the Antarctic ice-breeding phocids. Although listed as a ‘Specially Protected Species’ under the Convention for the Conservation of Antarctic Seals (CCAS), their current circumpolar population status remains largely unknown due to data insufficiencies regarding their abundances. This presentation deals with the distribution, density and percentage contribution of Ross seals, compared to the other pack ice pinnipeds encountered on the cruise track of the SA Agulhas II, bounded by 24°46.8’W and 0°43.2’W in the eastern Weddell Sea in December 2015 to February 2016. The ship-board survey results are compared with earlier ship-board surveys in the same general area (Hall-Martin 1974; Wilson 1975; Condy 1976, 1977) to ascertain the Ross seals’ current status off the Princess Martha Coast, Antarctica. Despite seasonal and annual differences in density of seals in pack ice ascribed to differences in pack ice density and extent, timing of censuses and the survey methods, crabeater seals still predominated by far in the eastern Weddell Sea in austral summer 2015/16. A relatively large population of Ross seals continued to be found in the pack ice off the Princess Martha Coast in mid-January 2016 at a density similar to what was considered to be high in the 1970s.

Condy PR (1976) *S Afr J Antact Res* 6:2–8

Condy PR (1977) *S Afr J Antarct Res* 7:10–13

Hall-Martin AJ (1974) *S Afr J Antarct Res* 4:34-39

Wilson VJ (1975) *S Afr J Antarct Res* 5:31-36

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Flying in circles: Abundance estimation of dolphins using distance sampling

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Population status for tropical dolphins in north Western Australia is unknown across most of their range. We used broad-scale manned aerial surveys to estimate abundance of three dolphin species in the Pilbara region of Western Australia. In 2015 the survey design included transects 5 km apart and extending offshore to the 20 m depth contour. We used a circle-back protocol, breaking from transect when a dolphin group was sighted, to confirm species identity and group size for groups > 5 individuals. We estimated minimum abundance of bottlenose dolphins (*Tursiops aduncus*) over an 18,950 km^2 survey area at 2,846 (CI 1549-5230) uncorrected for availability bias. The best distance sampling model included the factors distance, time of day, observer fatigue, glare angle, group size and group size/observer fatigue interaction. There were too few sightings of humpback dolphins (*Sousa sahulensis*) in the 2015 survey to estimate abundance and no snubfin dolphins were sighted. In 2016 we adapted the survey design to increase sampling intensity and survey effort where humpback dolphins had been sighted previously. In 2016 we recorded adequate sightings to produce a minimum abundance estimate of 273 (CI 184-405) for humpback dolphins over the 9,050 km^2 surveyed area. The best model for humpback dolphins included the factors distance, time of day, observer fatigue and group size. The few sightings of snubfin dolphins in 2016 precluded a population estimate of this species but future research will assess the viability and fidelity of this potential population through targeted boat-based surveys in the Exmouth Gulf.

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Applying the multistate capture-recapture robust design to assess metapopulation structure

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Mark-recapture study designs which accommodate heterogeneity in capture probabilities associated with individual animals moving between geographic sites can provide insight into mammal distributions in terrestrial and marine environments and the status and connectivity of subpopulations. Using a multistate closed robust design (MSCRD) approach, we investigated demographic parameters of Indo-Pacific bottlenose dolphin (*Tursiops aduncus*) subpopulations in coastal and estuarine waters of Perth, Western Australia, and the relationship between subpopulations in a metapopulation. Using year-round photo-identification surveys across multiple geographic sites, we accounted for heterogeneity of capture probability based on how individuals distribute themselves across sites and characterised the status of subpopulations based on their abundance, survival and interconnection. MSCRD models highlighted high heterogeneity in capture probabilities and demographic parameters between sites. High capture probabilities, high survival and constant abundances described a subpopulation with high site fidelity in an estuary, while low captures, permanent and temporary emigration and fluctuating abundances suggested transient use and low site fidelity in an open coastal site. Transition probability estimates varied between sites. Estuarine dolphins visited sheltered coastal embayments more regularly than coastal dolphins visited the estuary, indicating a key metapopulation dynamic. We demonstrated that spatially structured subpopulations in a heterogeneous coastal-estuarine environment contained distinct suites of individuals and differed in size, demographics and connectivity and the utility of extending mark-recapture studies to investigate metapopulation dynamics. The MSCRD approach is applicable to species consisting of recognisable individuals and is particularly useful for characterising wildlife subpopulations varying in their vulnerability to human activities, climate change or invasive species.

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Dolphin Watch: Trends in Indo-Pacific bottlenose dolphin *(Tursiops aduncus)* distribution based on long-term citizen science monitoring in the Swan-Canning River park, Western Australia

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Dolphin Watch was developed in 2009 from a government and university partnership for engaging community in collecting long-term scientific data on Swan-Canning River park bottlenose dolphins; river-health indicators requiring monitoring for securing their future in an urbanised and changing environment. Overall aims of *Dolphin Watch* are to improve the community's awareness and care of the River park, improve the knowledge-base for effective management of resident bottlenose dolphins, and demonstrate it is possible through cost-effective citizen science. The objectives here are to: 1) identify the extent of dolphin distribution within the River park, 2) identify long-term dolphin hotspots and their seasonal use for life processes, and 3) compare presence-only with presence/absence distribution models to explore the potential for presence-only monitoring. To date 1,034 citizen science volunteers have been trained. Over 22,500 monitoring surveys reporting dolphin presence/absence, group size, calf presence, behaviours, search effort, location, date and time have been submitted. Over the last half decade the mean number of dolphins sighted each year has remained stable at between 6-9 sightings day^{-1}. Consistent foraging hotspots were near the Swan River and Canning River entrances and the Narrows Bridge close to Perth's CBD. Dolphins occurred near the Narrows Bridge more often in autumn/winter, and in Fremantle Inner Harbour in autumn/winter/spring than in other seasons. Preliminary tests comparing presence-only with presence/absence models indicate similar outputs across most of their distribution. The program is ongoing; communication of its progress and science outputs benefits other projects worldwide through improved knowledge for designing and managing such programs.

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Looking without landing: Using UAVs to monitor fur seal populations

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Technical advances in monitoring devices are allowing managers and scientists to obtain quality information on ecosystem health with minimal disturbance to ecosystems and the wildlife they support. We rely on temporal and spatial indicators of ecosystem health, such as population abundance estimates, to understand and predict ecosystem change. This is critical for the achievement of conservation goals while supporting sustainable natural resource use. Obtaining abundance estimates can be logistically demanding and expensive particularly in offshore marine environments, and for some species, can cause significant disturbance. These constraints may lead to sub-optimal monitoring programs that reduce the frequency and/or precision of surveys at the cost of data quality or power in the resulting analyses. Using unpiloted aerial vehicles (UAVs) can be a solution to this dilemma and can improve the accuracy of estimates. With appropriate testing and ethical consideration; for many situations, UAVs can increase the frequency of surveys and enable more robust and reliable programs for monitoring ecosystem health. In this talk we demonstrate the process of testing and calibrating a UAV for monitoring abundance and body size of Australian fur seals at their largest colony. Two sizes of quadcopter with different gear at various altitudes above sea level were tested. We assessed disturbance levels in the seals and birds and optimised a methodology that allows effective and economical monitoring of this site. The benefits and disadvantages of such an approach will be outlined, as well as important considerations for those looking to incorporate similar methodologies in their research.

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Estimating abundance by combining camera trap and GPS tracking data: A case study using the Tasmanian devil

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Estimating animal abundance, N, or density, D, is difficult, especially when the target species is rare, cryptic or sparsely distributed. Historically, capture-mark-recapture (CMR) and distance-sampling (DS) methods have been used, but despite substantial research, shortfalls in theory and practicality still exist. Recent developments have focused on combining aspects of both CMR and DS theory (e.g., spatially explicit capture-recapture and trapping point transects). Here, we present a new abundance estimation technique that relies on camera trapping to obtain encounter rate information (i.e. individuals do not need to be uniquely identifiable) whilst concurrently tracking a subset of the population via GPS collars to obtain detectability information. Unlike CMR where the survey area isn't easily quantified due to edge effects, in this approach {N} can be easily converted into a readily interpretable estimate of D. A simulation study to assess bias in {N} under various home range shapes, and for differing sample size and distribution of camera traps in the survey region, was encouraging; relative bias was low ($< 1\%$) with small population sizes ($N = 20$) and decreased to essentially zero with increasing N. We applied this method to a population of Tasmanian devils (*Sarcophilus harrisii*), in Tasmania, Australia. In 2013, 42 cameras were deployed (with 67 detection events) and 7 devils were collared. In 2014, 31 cameras were deployed (with 106 detection events) and 12 devils were collared. Surveys whereby GPS tracking and camera traps are deployed concurrently are increasingly common – so this method potentially has wide applicability in situations when individuals cannot be uniquely identified from camera traps.

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Reserve size affects density of an African leopard (*Panthera pardus*) population

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The ability to decipher drivers of densities for large carnivores will be critical in understanding their ecological requirements and develop conservation strategies. In this study, we used 164 camera trap stations, covering ~740 km^2 over five distinct habitat types in the Udzungwa Mountains National Park and Kilombero Nature Reserve in Tanzania, to investigate drivers of density in one of the most widespread and adaptable large carnivores, the leopard (*Panthera pardus*). Data were modelled with an array of both biotic and abiotic covariates hypothesised to influence leopard density in a capture recapture framework. Results of stratified population models concluded that leopard densities declined with proximity to protected area borders and outranked prey availability, which was found to be the second most influential covariate explaining leopard density. We interpret these results of a negative effect on leopard population density as a direct effect of human activities, as Udzungwa is completely isolated and surrounded by agricultural development. Essentially this implies that protected area size limits leopard population size over prey abundance. Additionally, we found that leopard detectability was highest along water-ways and space-use was influenced the greatest by habitat type. Finally, the camera trap data found no exchange of individuals between habitat types despite being within the same protected area. Leopard density in the Udzungwa Mountains resembles that of exploited rainforest in West Africa and our study highlights the effects humans have on large carnivores deep into protected areas.

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A comparison of multiple spatial capture-recapture models for estimating mammal densities in a changing landscape

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Wildlife management is an adaptive process that requires accurate, precise, and frequent information on animal populations, particularly for species of conservation risk or in areas experiencing rapid environmental change. However, the information currently collected in many jurisdictions rarely meets these three criteria. Technological advances have led to increased use of camera traps to survey wildlife populations, a potentially cost-effective non-invasive alternative to standard survey methods. With the advent of spatial capture-recapture analyses as an emerging method of estimating population density it is critical to understand how different methods compare, especially when land managers may only have access to one survey method. This study used concurrent genetic, photographic and/or telemetry data of multiple mid and large sized mammal species to determine how parameter precision varied when using single and multiple data source spatial-capture recapture models. We found that sex-specific genetic spatial-capture recapture (maximum likelihood) models were quick and easy to run, yielding precise density estimates. Spatial count (Bayesian) models of unmarked populations were computationally intensive and frequently did not converge, even after high numbers of MCMC iterations, making it difficult to produce a reliable density estimate. Integrating multiple data sources in spatial-capture recapture models produced the most precise density estimates. This study highlights the challenge of applying complex models to low-density mammal populations, and stresses the need for continued evaluation of the most effective analytical approaches and survey designs, to better inform ecological conclusions and conservation management.

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Fuzzy logic modelling of snow leopard populations in response to threats from climate change

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Kazakhstan's snow leopard population represents a small but important component of the species range. The most recent population estimate, by Jackson et al. (2008), suggests that there are around 180-200 individuals. Prior to this study there were no reliable estimates of snow leopard numbers in Almaty State Nature Reserve. In total 40 camera traps were deployed for a total of 5,152 traps nights and yielded 50 independent capture events of snow leopards (with between 1 and 10 images per event), 275 capture events of primary prey and 68 capture events of secondary prey. The study capture rate of 0.97 independent capture events per 100 trap nights is at the higher end of the range experienced by other studies and mark-recapture modelling estimated 11-18 individuals in the study area which suggests density between 4.4 and 7.2 individuals per 100 km^2. Analysis of movement patterns suggests that individuals frequently crossed valley bottoms and used densely forested habitat in winter, which may indicated prey switching from ibex to forest ungulates. We developed a fuzzy logic model which aggregates a wide range of socio-economic and ecological data and provides a tool that can be used to inform the sustainable natural resource and landscape management decision-making process. Our model predicts the consistent negative impact of climate change (warming) at elevations below the tree line; this is particularly significant as the potential positive impacts for snow leopards at high elevation are slower to eventuate thereby increasing the habitat squeeze associated with climate change in mountain habitats.

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Do occupancy or detection rates from camera traps reflect population density? A case study example with white-tailed deer in North America

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Camera trapping is a powerful tool for studying mammal populations over increasingly large spatial scales. Density estimation is a commonly desired outcome, but most approaches only work for species that can be individually recognized, and researchers are typically constrained to measures of site occupancy or detection rate instead; metrics that are presumed to be directly related to animal density. To test relationships between these metrics we estimated density, occupancy and detection rate of male white-tailed deer (*Odocoileus virginianus*) using the same set of camera trap data collected from 1,199 unbaited cameras at 20 study sites. We found a strong ($R^2 = 0.80$) positive relationship between detection rate and density and low ($R^2 = 0.27$) correlation between occupancy and density. We identified two sites, both urban parks, where the relationship between camera trap detections and density estimates did not correspond, presumably because of heterogeneous movement patterns. When paired hunted and unhunted parks were compared, estimate agreement was least for pairs with the highest differences in surrounding housing density. Ecological models explaining variation in occupancy and detection rate were similar, but different from density models, suggesting that the metrics are reflecting different ecological relationships. Detection rate performed well as a proxy for density across large scales but poorly at small scales while occupancy showed the opposite trend. Our results indicate that managers should not use detection rate and occupancy as proxies for density when comparing between areas where animals might be expected to move or behave differently, such urban vs. wild landscapes.

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Ethical considerations for the use of livestock guardian dogs as control tools

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Livestock guarding dogs (LGDs) are often considered a continuous, mild and non-lethal form of predator control. As such, they have enjoyed a reputation as a passive yet effective management tool, with minimal welfare impacts on predators and the ecosystem. In Australia, LGDs are used as a control tool to defend livestock from wild Canids (dingoes, domestic dogs, their hybrids and foxes); however, a full assessment of the welfare issues and impacts of this scenario has not been undertaken. This welfare assessment used a cross-disciplinary approach combining philosophy and science to integrate possible hypothetical scenarios with data from published literature. We adapted an established Five Domains Model of welfare assessment (originally devised by Mellor and Reid) to evaluate the use of LGDs as a control tool in Australia. This model focuses on nutrition, environment, health, behaviour and mental state. We constructed hypothetical scenarios and pursued their logical arguments; from the best-case scenarios to their welfare implications. Additionally, we manipulated the effects on the variables within the domains and assessed the interactions between theses variables. In each best-case scenario we constructed, there were unavoidable ethical issues currently being overlooked. Surprisingly, even under the best scenarios, LGDs still had considerable welfare issues and impacts on dingoes, comparable to strychnine poisoning. While we are not arguing for the cessation of LGD use in Australia, these welfare and ethical issues need to be addressed to more comprehensively defend LGD use.

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Diet and bite force in red foxes: Ontogenetic and sex differences in an invasive carnivore

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The red fox (*Vulpes vulpes*) inhabits the most expansive global range of any wild carnivore. Since their introduction to Australia over 150 years ago, foxes have presented a significant threat to livestock and persistence of native species. Their success as an invasive species reflects their highly adaptable ecology, with few specific habitat requirements and an opportunistic, generalist diet. Bite force is often used as a predictive indicator of an animal’s feeding ecology. We analysed skull morphology (size, morphometry, weight) to estimate bite force for a large sample size of animals collected through culling. Over half (57%) of the 540 animals we sampled were juveniles (<1 yo; dispersing from their natal sites). Most variation in skull morphometry was driven by age: adults had significantly more robust skulls than juveniles, with greater estimated bite force. Sexual dimorphism (body mass and body length) was reflected in longer, heavier skulls of males. Sheep carrion comprised 47–65% of stomach contents volume; however, adult females ate less sheep but had more mice and invertebrates in their diet than males or juveniles of both sexes. This dietary separation for adult females is likely to reflect feeding behaviour and space use patterns rather than bite force limitations because juveniles (both sexes) showed as much consumption of sheep carrion as adult males, despite their lower estimated bite force than adults. This result highlights limitations of inferring diet partitioning from skull morphology alone.

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Hiding in plain sight: Taxonomy and redescription of the savanna glider (*Petaurus sp nov.*)

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Biodiversity is being lost at an alarming rate, largely as a result of human activities. To combat this pattern of decline we need to define taxonomic units and identify undescribed species so that biodiversity can be effectively managed. Despite being well studied across much of their Australian range, the petaurid species found in northern Australia is surprisingly unknown. The species is currently classified as a sugar glider (*Petaurus breviceps ariel*), although molecular work revealed that it has closer affiliations to squirrel (*P. norfolcensis*) and mahogany (*P. gracilis*) gliders, both of which occur many hundreds of kilometres away on the eastern seaboard. Over the past 2 years we have trapped at locations across the top end, collecting tissue samples and morphological measurements from >40 animals. We have also measured ~298 petaurid skulls held in collections across Australia and redescribed the *P. b. ariel* type held at the British Natural History Museum. Phylogenetic and morphological analyses indicate that *P. breviceps* currently consists of at least two species (*P. breviceps* and *P. sp nov*). As well as establishing the identity of the savanna glider our research will investigate the existence of two additional distinct genetic lineages within the genus *Petaurus* and what this means for the current species and subspecies designations and distributions. Elucidating the taxonomic identity of this poorly researched glider will enhance our understanding of the unique biodiversity of northern Australia. This is of particular interest in the wake of small mammal declines that are currently being experienced in this region.

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Regionally characteristic mammalian genera as ecotourism flagships

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Ecotourism is recognised as a major means of funding conservation initiatives worldwide. While bird watching has become by far the leading subcategory of specialist ecotourism, mammalian-driven tourism varies from one region to another, and primarily targets larger mammals. Some of these are branded as typical of a given region, although this is not necessarily biogeographically accurate (e.g. some of Africa's "big five" are not African endemics). In mammals, narrow endemics are often smaller species, which are more difficult to see. Regionally-widespread mammals are on average both larger and often easier to see, although it is not necessarily the same species that occurs throughout a region. Here we argue that, even though a human construct (as is the case with all higher taxa), the genus level is easier assimilated as a brand, being often described by a single-word common name. We propose combining a measure of endemism and a measure of within-region ubiquity to produce lists of characteristic genera for each zoogeographic region, and using those genera that are suitable tourism targets as regional flagships. We provide examples for all of world's zoogeographic regions.

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Size matters: Does morphological variation translate to ecological differences in a marsupial glider?

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Defining the ecological niche of a species is vital for effective conservation management. Understanding variations in the habitat use, social structure and morphology of a species illustrate how the species is adapted to its environment and in turn, can predict the species' susceptibility to novel threats and disturbance. The small mammals of northern Australia have undergone rapid and catastrophic declines, highlighting the importance of understanding the ecological adaptations of species at risk. Recently, the marsupial glider occurring in the tropical savannas of the Northern Territory, was found to be an undescribed species. Our study forms the first investigation into the distribution and ecology of the savanna glider in the Northern Territory, specifically detailing its ecological niche. We will compare the habitat use, social structure and morphology of savanna glider populations at either end of their distribution through live-trapping, spotlighting and radio-tracking. Our results will establish the drivers of abundance and distribution of the savanna glider, and demonstrate the species' morphological and behavioural adaptations to environmental gradients unique to the tropical savannas of the Northern Territory. We will also discuss how the broad distribution patterns and socio-ecology of the savanna glider compares to other *Petaurus* gliders in Australia. Findings from this work will address whether the northern savanna glider is vulnerable to decline and inform the future conservation management of the species.

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Sparganosis: Emerging disease in wildlife

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Sparganosis is a parasitic disease caused by plerocercoid larvae of the tapeworm *Spirometra* sp. The first intermediate hosts are copepods; the second intermediate hosts are amphibians, reptiles, birds or mammals; final hosts are carnivores such as lynx and wolves. The disease is known mainly from Asia, and it was rarely reported in Europe. We investigated spread of this parasitic disease in mammal communities in two forests in north-eastern Poland. Three new paratenic hosts: badger, raccoon dog, and wild boar were identified. We found differences in infection prevalence between study sites as well as interspecies and interindividual variation in the infection intensity. Higher percentage of infected badgers and raccoon dogs was observed in Białowieża Forest (BF) than in Augustów Forest, which can be related to higher habitat humidity and species diversity in BF. The infection intensity was increasing with the age of the infected animals due to the longer exposure to the parasite. We also confirmed the presence of adult *Spirometra* sp. in final hosts, wolf and lynx, reported previously only once in BF, over 60 years ago. Moreover, we found *Spirometra* sp. plerocercoids in wild boar meat. The meat is not diagnosed for this parasite and since wild boar is an important game species in Europe, there is a substantial risk of infections in humans. It has therefore become a priority to inform the public of possibilities and consequences of *Spirometra* sp. infection and to intensify research on sparganosis. Study financed by the National Science Centre, project No. 2016/21/B/NZ8/02429.

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Sexual dimorphism of the immune system in eastern grey kangaroos (*Macropus giganteus*).

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Gender specific behaviour resulting in enhanced reproductive success can come at an immunological cost, with males in many species exhibiting lower immune responses than female conspecifics. We aimed to investigate the immunological difference between male and female eastern grey kangaroos and to measure the effect these differences have on overall host fitness and long term reproductive success. Immunological parameters include total and differential leukocyte counts, red blood cell counts, gamma globulins, haemoglobin, packed cell volume, total serum protein and albumin concentrations. Ectoparasite and endoparasite burdens were also quantified. Reproductive success was measured by number of offspring over a given time frame and testosterone concentration. Male kangaroos showed significantly higher ($p = 0.01$) total leukocyte counts, as well as higher absolute lymphocyte counts ($p = 0.004$). Female kangaroos had significantly greater ($p = 0.006$) ectoparasitic burdens. Results from analysis of reproductive success will be discussed. Immunological differences are the outcome of a complex interaction of factors including the immunosuppressive effects of pregnancy and lactation, testosterone in males, and different contact rates to pathogens. Understanding sexual dimorphism of the immune system enhances our knowledge of evolutionary processes driving the development of varied traits for enhanced reproductive success and survival. This not only contributes knowledge to the field of macropod research but has flow on benefits in managing the overabundance of kangaroos. With increased knowledge of kangaroos, effective evidence based population control strategies can be implemented to alleviate the deleterious effects of overabundance in both urban and rural settings.

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Tracking origin and interspecific transmission routes of influenza A in birds and marine mammals

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Influenza A virus (IAV) is found in a range of different hosts but mainly circulates in waterfowl, shorebirds, and gulls, which constitute the major natural reservoir. However, mammalian species can also harbour infection. IAV is regularly detected in marine mammals and have been the source of multiple epizootics over the past decades. Still, it remains unclear if infections are spill-over events, or if marine mammals serve as a reservoir host where IAV can be maintained, circulate, and undergo reassortment and/or mammalian adaptation. Little is known about the mechanisms of cross-species transmission and pathogenicity of some IAV strains. Harbour seals (*Phoca vitulina*) account for 50% of reported IAV infections in marine mammals, they host the most diverse assembly of IAV strains, and is the only species in which IAV is pathogenic with six epizootics since the late 1970s. Here we use genomic IAV data to track the spatiotemporal origin, investigate transmission routes of pathogenic IAV strains, and identify mutations in the IAV genome that may be associated with marine mammal adaptation and pathogenicity. Our study reveal that pathogenic IAV strains are of avian origin with multiple and rapid genetic changes associated with the cross-species transmission. IAV infections in marine mammals typically result from spill-over events from birds. Harbour seals appear to be a dead-end host and given the frequent occurrence of epizootics in harbour seals, but not in other marine mammals, it seems that IAV pathogenicity in marine mammals may be more related to host susceptibility rather than viral adaptation.

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Using contact networks to investigate Tasmanian devil facial tumour disease

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Tasmanian devils are under threat from a novel transmissible cancer – devil facial tumour disease (DFTD). This disease spreads between individuals via bite wounds and is almost invariably fatal. The nature of transmission means that the study of patterns of contact within devil populations is vital to fully understanding disease dynamics and how it spreads through populations. We investigate contact networks in a wild Tasmanian devil population and relate networks to bite wounds received by individuals. Bite wounds are vital as they represent those contacts which could lead to disease transmission. We utilise a novel technology, proximity loggers, to record contacts between devils at a distance close enough to bite one another, while through long-term re-trapping we are able to detect when animals pick up new wounds. When investigated in tandem, these facets allow determination of which interaction properties are important for disease transmission and can lead to an increased risk of infection. A more thorough understanding of DFTD and how it spreads through devil populations is critical to its ongoing management.

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Lessons learned in a wildlife disease study using a citizen science approach.

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Raccoons (*Procyon lotor*) are common mesopredators across most of North America. They serve as definitive hosts for raccoon roundworm (*Baylisascaris procyonis*), which is transmitted via fecal-oral contact and the consumption of infected intermediate hosts. When ingested by an intermediate host, larvae migrate through host tissues causing damage, particularly to the nervous system, rendering them more likely to be consumed by raccoons. A wide range of species can serve as intermediate hosts, typically these are seed-eating birds and mammals, but other species are susceptible to roundworm infection, including humans. Our goal was to conduct a survey of raccoons in west Michigan to estimate the local prevalence (i.e., percent infected) and intensity (i.e., number of roundworms per infected raccoon) of roundworm infection. In collaboration with computer science faculty and students, we created a free mobile app that enabled volunteer participants to crowd source the location of road-killed raccoons for our study. Approximately 800 biology faculty, staff, were asked to contribute in this way, reporting the location of road killed raccoons during their regular travels. We found the prevalence of raccoon roundworm was 69% (203/295 sampled individuals) in our local population. Mean intensity of infection was 31.3 ± 3.6 roundworms/infected raccoon). Juvenile and sub-adults were more likely to be infected with roundworms than were adult raccoons. I will highlight the costs and benefits of this crowd sourcing approach during my presentation.

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The evolution of Diprotodontia: Arrested radiation and the kangaroo insurrection

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Understanding the evolution of the marsupial order Diprotodontia (kangaroos, koala, wombats and possums) has been hampered by conflicting reconstructions across molecular and morphological data. However the relative phylogenetic performance of these sources of data has not been extensively tested. We show that ameliorating base composition biases in mitochondrial (mt) DNA brings close agreement with nuclear DNA, which is encouraging for inferring the affinities of megafaunal marsupials, for which mtDNA is more obtainable. Incongruence with morphological reconstructions was driven by functional/developmental correlations with diet and body size, which may be corrected for, in order to merge older diprotodontian fossils into the marsupial tree. Here we present the most complete (to-date) time-calibrated phylogeny of Diprotodontia based on nuclear and mtDNA. The diversification analyses reveal a faunal turn-over within the order Diprotodontia with Vombatiformes being replaced by macropods (kangaroos). They also suggest that the adaptive radiation of diprotodontians was initially rapid, until competitive barriers arrested their evolution, and limited niche overlap between families. One group, Macropodiformes (kangaroos) escaped this evolutionary captivity and appear to have since been displacing Vombatifomes (wombats and koala).

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Phylogenetic measures of marsupials in the world

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Marsupials are a suitable group for phylogenetic and spatial analysis, because of their complex biogeography and evolution. In this analysis we used different phylogenetic measures to identify spatial patterns, such as phylogenetic diversity (PD), phylogenetic endemism (PE) and Categorical Analysis for Palaeo and Neo Endemism (CANAPE), using a dataset of marsupials, to compare the results at two geographic areas and incorporate a dated phylogeny at species level for 282 taxa. Spatial analyses were conducted at a 100 km × 100 km grid scale. Our aim was to identify an evolutionary pattern using the current marsupial distribution using the different biomes of the Americas and Australasia. Randomization tests were employed to identify cells with significantly high or low values of phylogenetic diversity (PD), and CANAPE was used to identify significant hotspots of neo- and palaeo-endemism. Preliminary results show significantly high PD values along the eastern coast in Australia and Papua New

Guinea. CANAPE indicated hotspots of neo-endemism in Central, north portion of South America and the south-east coast in Australia, and hotspots of palaeo-endemism scattered through Australia and Chile. We concluded that PD, PE and CANAPE generally provided results for consistent patterns with other taxa, providing further evidence for the utility of phylogenetic measures in testing hypotheses about phylogenetic and biogeographical processes.

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Insights from recent advances in phylogenetics and phylogeography of Africa's endemic golden moles (family Chrysochloridae): Implications for taxonomy, biogeography and conservation

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Golden moles (family Chrysochloridae) belong to Afrotheria, an ancient clade of placental mammals that ranks among Africa's most enigmatic and endangered, but poorly studied endemic mammals. Two subfamilies, 10 genera and 21 species are recognized, of which 10 species are threatened (IUCN 2016). Nonetheless, unclear taxon delineations based on morphology, cytogenetics and limited molecular data have hitherto impeded conservation efforts. Within this context, we present a fully-resolved chrysochlorid phylogeny based on a concatenation of molecular (five genes) and multistate morphological and cytogenetic characters (32) using model-based Bayesian and maximum likelihood inference.These analyses uncovered genetically distinct lineages within two genera and cryptic lineages within three species, which form the basis of a revised Chrysochloridae classification presented here. As the phylogeny offers unique insights into the diversification of an old but range-restricted clade across the African continent, we used molecular dating to place the evolutionary radiation of chrysochlorids in the context of Africa's palaeoclimatic and geological history. We also present a novel molecular phylogenetic framework based on mitochondrial and nuclear genes for one of Africa's most threatened small mammals, *Neamblysomus julianae*, that is known from only three range-restricted and geographically isolated populations revealed three genetically unique lineages, one of which is highly divergent, which informed conservation planning for the species that should be aimed at conserving the integrity of each genetically unique population. Rigorous geographic sampling chrysochlorids, and species in general.

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The endemic New Guinean dasyurid marsupial genus *Murexia*. How many species?

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Five species are currently recognized within the endemic New Guinean dasyurid marsupial genus *Murexia*: namely *longicaudata, habbema, melanurus, naso* and *rothschildi* (Baker, 2015). The identity and inter-relationships of these species have been confused in the recent past by the use of separate generic epithets for some of them (*Micromurexia* for *habbema*, *Murexechinus* for *melanurus*, *Phascomurexia* for *naso* and *Paramurexia* for *rothschildi*). Our morphological studies suggest that a revision of the taxonomy of these dasyurids is required. A new molecular database that includes both nuclear and mitochondrial genes has been assembled for multiple exemplars of each of the five taxa to cover as much of their geographic range as is possible with available material. The resulting phylogenetic tree suggests that not only do the current five species form a monophyletic clade with at least three of the widespread species (*longicaudata, naso,* and *melanurus*) showing major genetic variation that is consistent with the distribution of different morphological forms.

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First multilocus phylogeny and species delimitation within *philippinensis*-group from rhinolophids

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For rhinolophids, a widespread and diverse family, there is a high level of morphological convergence, leading to problematic taxonomic identification and estimation of species diversity. In this study, we conducted a first multilocus phylogeny of *philippinensis*-group using sequences from four mitochondrial markers and five nuclear loci (four introns loci and one Y-linked locus). We reconstructed the phylogeny of *philippinensis*-group based on the concatenated mitochondrial dataset, concatenated nuclear dataset, as well as a concatenated multilocus dataset, respectively. Gene-tree and species-tree as well as alternative topology tests were used to reveal the relationship within *philippinensis*-group. The results showed that the main clades with evident genetic structure were highly supported. Analysis of those data showed paraphyly for *philippinensis*-group within rhinolophids. *R. macrotis* [small form], *R. siamensis* and *R. huananus* formed a clade for all datasets, suggesting they may be the same species. And *R. rex* and *R. paradoxolophus* mixed together, which can also be considered as the same species. The results are consistent with previous studies based on morphology analysis. Furthermore, topological discordance exists between different datasets. Paraphyly of *R. macrotis* relative to *R. macrotis* [small form] for concatenated mitochondria dataset is discordance with nuclear dataset. Divergence time analysis based on the mitochondrial cytochrome *b* sequence estimates that rhinolophids originated in Miocene. And *philippinensis*-group appeared a rapid radiation approximately 2.55 Ma during the early Pleistocene, which can be explained by climatic fluctuations in Pleistocene.

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The great escape: How large, carnivorous mammals move out of harm's way

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For decades, biologists have reported a steady decline in the population size of many of the world's most iconic, large marine and terrestrial mammals. Often, the primary threat to survival is attributed to anthropogenically-driven "habitat destruction" resulting from development, pollution, the degradation of critical resources, altered physical risks and exposure to predators, and climatic events among others. Hidden within these threats is the first line of defense by canids, felids, ursids, cetaceans and pinnipeds, which is to move out of harm's way. Despite its importance for survival, relatively little is known about the biology of escape in this mammalian group. We find that mounting an escape response requires extraordinary coordination of physiological processes in highly active carnivores. Furthermore, the response is complicated by the habitat in which the animal lives. For terrestrial mammals, escape typically involves species-specific behavioral responses ranging from freezing to flight with the level of speed and maneuvering dictating energetic costs. For example, African leopards (n = 5, *Panthera pardus*) instrumented with calibrated SMART accelerometer- GPS collars that recorded fine scale (5 min) energetics and movements demonstrated a 38% increase in the cost of locomotion depending on if the animal used a directed high speed gait rather than a slower, cryptic meandering trajectory across the landscape. In a study comparing the chase-escape energetics of instrumented canids (hounds, *Canis lupus familiaris*) and felids (pumas, *Puma concolor*) in the Santa Cruz mountains, the behavioral advantage of complex, anaerobic maneuvers by felids was apparent in successful escapes. Combined with a higher cost per stride for the felid (stride cost averaged 5.0 J kg^{-1} $stride^{-1}$ for hounds and 7.2 J kg^{-1} $stride^{-1}$ for pumas), these evasive maneuvers resulted in a level of energy expenditure that was 3.8 times higher for the animal being chased compared to its pursuer. The physiological costs of escape are even more complex for marine mammals due to the simultaneous, and at times conflicting, responses associated with diving, exercise, and fear. Such conflict is evident in the cardiac patterns of wild narwhals (*Monodon monoceros*), a deep diving Arctic cetacean. Narwhals wearing an electrocardiographic recorder-stroke monitor showed a paradoxical escape reaction in which an extreme level of diving bradycardia (heart rate = 3-4 beats min^{-1}) was superimposed on a high stroke frequency exercise response. As a result, escape dives required nearly twice the energy of routine dives to similar depths, and rapidly depleted on-board oxygen stores required for supporting aerobic processes. Clearly, acute responses to aversive situations can instigate significant physiological and energetic costs for mammalian carnivores, and will need to be scaled up to predict population effects. Today, as the incidence of unanticipated disturbance by human activities continues to increase on land and in the oceans, the cumulative effects of behavioral modification, reduced time to forage, and such physiological challenges and costs associated with escape responses may well grow into major contributing factors altering the population trajectories of wild mammals.

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The paradigmatic lion: From social biology to social media

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Views of the landscape from different vantage points, synthesising twenty years of experience with lions, their biology and conservation. This review explores some features of lion behaviour, and their ecological origins, as a basis for thinking about their interactions with people, some resulting pest problems and solutions to them. These perspectives lead to wider views of landscape ecology and continent-wide conservation. One of our study animals, nicknamed Cecil, attracted international attention from which much can be learned, raising the question of whether the Cecil Moment can lead to a Cecil Movement and, indeed, the wider notion of conservation-led development.

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Response of leopards at varying densities of tigers in Rajaji National Park (RNP), Uttarakhand, India.

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Understanding intra-guild competition is imperative as we are losing our large carnivores. Rajaji National Park (RNP) in India is bisected by Ganges into two parts, Eastern RNP (ERNP) and Western RNP (WRNP). Rapid development along Ganges has disrupted the connectivity between both sectors. Management interventions and connectivity from adjoining populations resulted in recovery of tigers in ERNP whereas lacking connectivity led to their decline in WRNP. The leopard occupies both sectors. Thus RNP provides a natural test/control to study responses of leopards in landscapes with varying tiger density. Leopard and tiger densities were estimated from camera trap pictures, on a capture-mark-recapture framework using spatially explicit capture-recapture models. Spatial use of both carnivores was appraised using density surface models. Prey abundance was assessed using line transect based distance sampling using Distance 6.2. The research shows that tiger density varied significantly in ERNP & WRNP. In spite of varying tiger densities, the leopard densities remained high in both sectors and didn't differ significantly. The prey density also didn't vary significantly between the two sectors. Leopards avoided high tiger intensity usage areas. RNP, located in the Terai Arc Landscape, is among seven “Priority One” landscapes for tiger conservation in the world. WRNP, facing the local extinction of tigers, has been recognized as a potential site for tiger reintroduction. Our study shows that leopards co-exist with tigers in ERNP. Thus, if the tiger is brought back in WRNP, it would be of great conservation and ecological concern to understand the leopard's response.

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Conservation inequality and the charismatic cat

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Conservation resources are limited, making it impossible to invest equally in all threatened species. One way to maximise conservation gains is to focus upon those species with particular public appeal, using them to generate funding and support that could also benefit additional, less charismatic species. Although this approach is already used by many conservation organisations, no reliable metrics currently exist to determine the likely charisma of a given species, and therefore identify the most appropriate targets for such campaigns. Here we use market research techniques on over 1500 people from five continents to assess the relative charisma of different mammals, which factors appear to drive it, and which species show unexpectedly high or low charisma. Highly favoured species were associated with striking colouration, large body size, carnivory and high IUCN threat status. The public preferred species with which they had affinity and familiarity, and show distinct preferences for large and threatened species of mammals in comparison to their less charismatic counterparts. Australian respondents in this survey stand out as exceptions. While clearly liking two charismatic felids in common with other survey respondents from around the world, Australians ranked species from their own region (Australia and South East Asia) more highly than did respondents in other regions.

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Dingoes, dogs and foxes: Roles they can play.

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There are two species of Canidae in Australia. Both are relatively recent additions to the vertebrate fauna, which is primarily marsupial. Dingoes and other free-roaming dogs (*Canis familiaris*) are adaptable, occupying niches in urban to alpine environments across the continent. The equally generalist European red fox (*Vulpes vulpes*) is widespread but its northern range is coincident with the fluctuating northern boundary of the rabbit. Dingoes and foxes are sympatric in many of Australia's diverse ecosystems and their functions are debated. Here we draw on data from previous and current research to review the ecological roles that the two eutherian carnivores can fill in Australian ecosystems. We discuss their co-occurrence and make suggestions for their management in relation to their impacts and interactions, appropriate scales of effective management and ethical considerations.

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Human-modified canids in human-modified landscapes: Genome-wide variability and phylogeography of free-ranging dogs in Eurasia

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Domestication can be described as the adaptation to living in close proximity to humans, and therefore domesticated species may be expected to thrive in human-modified landscapes. Indeed, the domestic dog is the most widespread and numerous canid, with the global population estimated at 1 billion individuals, 75% of which are free-ranging. We analysed genome-wide variability of free-ranging dogs across Eurasia, and found isolation-by-distance pattern, but no genetic structure. This is in contrast with grey wolves, showing strong genetic differentiation driven by habitat and prey differentiation. Domestication process has strongly modified the dietary niche of the dog as compared with their wild ancestors, and most free-ranging dogs at least partially rely on human-derived food sources, and occupy habitats were such food is available. Therefore, habitats and diet of free-ranging dogs are less differentiated across large geographic scales as compared with those of grey wolves, which in combination with continuity of human-modified habitats across Eurasia results in lack of genetic structure. Our analysis also showed that modern dogs have East Asian origin, and have spread across Eurasia during the Neolithic human migrations. Therefore, in Eurasia the dog has been an integral part of an agricultural landscape. The spread of agriculture led to a secondary contact between dogs and grey wolves, sometimes resulting in hybridisation, as suggested by genome-wide patterns of haplotype sharing. While such admixture is typically perceived as a conservation concern, in some cases dog-derived gene variants could have facilitated adaptation of their wild owners to living in human-modified landscapes.

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The power of exclosures

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It remains a challenge to quantify mammal-plant interactions including seed predation or herbivory of different body sized mammals and its consequences on tree community structure and diversity. Here we reviewed the results from different studies to demonstrate how exclosure experiments can be powerful methods to test various hypotheses in the Amazon. First, we quantified seed removal of *Astrocaryum* in dense groves and under solitary palms within and outside of large mammal (peccary, *Tayassudae*) exclosures. One major finding was that peccaries, more frequently, preyed upon seed in groves whereas rodents foraged more often underneath solitary palms. In a 7-year study, we used semipermeable exclosures to simulate large mammal defaunation and its consequences on seedling demographics. Results showed that seedling density, survival, and recruitment were higher in exclosures. Finally, we tested how mammalian seed predation affects forest community structure. We monitored the fate of 8,000 seeds from 24 different species in exclosures that were selectively permeable to small, medium, and large mammals for up to 4.4 years. Small, medium, and large mammals reduced survival time by 10.3, 15.1, and only 2 months, respectively. Small and medium-sized mammals reduced survival of 17 and 14 species respectively and changed beta diversity. Therefore, somewhat surprising, small and medium-sized mammals had a stronger effect on community structure and may promote species coexistence compared to large mammals. Short and long-term exclosure experiments can provide unique insights that contribute to our ecological understanding and may also allow to predict what changes to expect in over-hunted or empty forests.

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Saving northern quolls: Quantifying the risk of colonisation by cane toads (*Rhinella marina*) on Australia's Kimberley islands

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Coinciding with the invasion of the highly toxic cane toad (*Rhinella marina*), the endangered northern quoll (*Dasyurus hallucatus*) has suffered declines and local extinctions throughout its range in Queensland and the Northern Territory. At least fifteen islands in the Kimberley are important to the future viability of northern quoll populations as they are naturally isolated from mainland threats, including potentially from cane toad invasion. However, islands are susceptible to cane toad invasion; cane toads have been detected on at least 45 Australian islands. Adolphus Island in the mouth of the Ord River in the eastern Kimberley has already been invaded by cane toads, and this island harbours a northern quoll population. Estimating invasion probability is key to effective surveillance strategies, which can reduce impacts of invasions, as well as management costs. Cane toads reach islands through both human-mitigated and natural means such as rafting on debris in freshwater "plumes" ejected from rivers during extreme rainfall events, complicating invasion modelling. By incorporating ocean circulation modelling (OzROMS) and virtual particle-tracking software into predictive models of invasion, we use existing island cane toad invasions to estimate invasion probability attributable to various pathways, including the natural colonisation of islands. We also will predict the island-specific probability of cane toad invasion in future time steps throughout the Kimberley. Our research will help streamline expensive surveillance in a region that is not easily or cheaply accessible by humans in an effort to protect the endangered northern quoll.

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Small mammals in the Anthropocene: Climate change and long-term observations in semi-arid Chile

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We have conducted a large-scale experimental manipulation of vertebrate assemblages in semi-arid Chile for almost 28 years. Established to assess the relative influence of predation, interspecific competition, and herbivory on the structure and composition of a dryland biota, we selectively exclude vertebrate predators (mammals, raptors), the ecologically dominant degu (*Octodon degus*), both, or neither (control) from replicate 0.56 ha exclosures; in 2001 we converted degu exclusions to all-small-mammal exclusions. Whereas this research has documented only modest and transitory top-down regulation by predation and limited evidence for negative interspecific competition among small mammals, it has revealed subtle to strong influences of small mammals on ephemeral and shrub vegetation, as well as on soil mycorrhizae and bacteria. In contrast to the limited role of biotic influences on small mammals here, episodic high-rainfall/ENSO periods and resulting vegetative growth release small mammals from bottom-up regulation, allowing for demographic expansion. Since about 2002, both mean annual rainfall and interannual variation in rainfall have decreased. In response, degus have increased numerically at the expense of other small mammals, and now regularly comprise 60-85% of small mammal biomass, with cascading effects on plants. Degus are important prey for culpeo foxes (*Lycalopex culpaeus*), and analysis of culpeo diets over 23 years has documented the first Type IV functional response of a vertebrate to changes in prey numbers. This research underscores the value of long-term research in understanding the broader impact of transient or modest influences on the ecology and behavior of dryland mammals.

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Desert mammal populations are limited by introduced predators rather than future climate change

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Climate change is predicted to place up to one in six species at risk of extinction in coming decades, but extinction probability is likely to be influenced further by biotic interactions such as predation. Climate is a major abiotic driver for dryland species; the Australian central desert regions especially are not immune from climate change, with higher temperatures and an increase in the frequency and magnitude of extreme rainfall events already recorded over the last 100 years. Wildfire return intervals are also predicted to decrease due to climate change, making it imperative that we understand how both biotic and abiotic interactions shape ecological systems. Here we use structural equation modelling to integrate results from remote camera trapping and long-term (17–22 years) regional-scale (8,000 km^2) datasets for vegetation and small vertebrates (>38,880 captures) to explore how biotic processes and two key abiotic drivers influence the structure of a diverse assemblage of desert biota. Our models are used to predict how changes in rainfall and wildfire are likely to influence the cover and productivity of the dominant vegetation and the impacts of predators on their primary rodent prey over a 100-year timeframe. Our results show that, while vegetation cover will decline due to climate change, the primary influence on prey populations is top-down suppression. Introduced predators have the strongest negative effects on prey.

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Pictures, predators, and prey: Camera data and community dynamics after a fisher reintroduction

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Researchers are often concerned with how reintroduced organisms fare in their new environments, but often cannot document how the reintroduced organisms affect their new communities. Fishers (*Pekania pennanti*) are a model mammalian carnivore that has been translocated > 40 times across its range in North America. Fishers are specialist predators on porcupines (*Erethizon dorsatum*) in localities where they co-occur and may regulate their populations. Otherwise, they are generalists that consume, and affect, many types of medium- to small-sized mammals. Understanding how predators forage for and change the abundance and distribution of prey is important to manage and conserve them into the future. Subsequent to the reintroduction of 40 fishers over 3 years (2009-2012) to their former range in northern California, USA, we placed trail cameras at over 600 locations (yearly = 100 ± 41) for reasons including to estimate fisher reproduction and evaluate the spatial distribution of fishers through time. We deployed both baited and un-baited cameras for an average of 42.4 ± 33-52, distributed across years and seasons. We quantified the distributions and naïve occupancy rates of key prey species through time. The naïve occupancy rates of tree squirrels were highest for *Tamiasciurus douglasii* (0.53 ± 0.16), *Sciurus griseus* (0.41 ± 0.14), and *Glaucomy sabrinus* (0.08 ± 0.06) but were highly variable in time and space indicating fishers were not negatively affecting them after release. We will further evaluate specific habitat metrics for each of these species to evaluate how these overlap with habitat and prey selection by fishers.

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Avoiding the subject: The implications of avoidance behaviour for detecting predators

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Estimating predator abundance can be challenging. Many predators are inherently difficult to detect due to their low population densities, large home ranges and cryptic behaviour. Detection rates derived from camera traps are often used as indices of abundance, however many factors can influence a species' detection rate and the extent to which it might reflect the species' actual abundance. I investigated the relationships between detections, abundance and activity of two sympatric predators, the Tasmanian devil (*Sarcophilus harrisii*) and the feral cat (*Felis catus*). I used camera traps to detect devils and cats across the island state of Tasmania in southern Australia, where devil populations have progressively and variably declined since 1996 following the spread of the fatal devil facial tumour disease. Devil and cat detections on individual cameras were negatively correlated; however, this was unrelated to abundance. While cats and devils were detected at nearly all of the same sites, cats appeared to avoid devils over short distances, suggesting that negative relationships in detections at the camera scale may reflect fine-scale behavioural avoidance rather than suppression of abundance. These findings highlight the importance of understanding avoidance behaviour when designing camera surveys to detect predators and when using indices to infer interactions or numerical relationships among sympatric predators. These findings also provide a cautionary tale that highlights the need to consider alternative hypotheses to explain observed patterns, as the implications for species conservation and management outcomes could vary dramatically.

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Safe-guarding koalas against climate-change

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The koala is an iconic Australian species listed as threatened in both National and State legislation and is one of the world's flagship species suffering from climate change. Extreme weather events associated with global warming are increasing dangerously in Australia and represent an ongoing threat for koala populations. Increasing hot and dry conditions are causing droughts and heatwaves which lead to drastic declines in koala populations. Yet the importance of free water availability for koalas' survival during these extreme climate events is currently unknown. In collaboration with land-holders in the Liverpool Plains in New South Wales, we are investigating the use of artificial water stations as a mitigation tool for koalas during heatwaves and droughts. We are currently monitoring koala behaviour at several water stations using camera traps, as part of a long-term experiment to assess if and how the use of water stations changes over the months (winter *vs* summer) and during different temperature (heatwaves) and rainfall (droughts) conditions. Details about the visits to the water stations, including number of visits, time spent drinking and other behaviours displayed by koalas are quantified and related to temperature and rainfall. This is the first study documenting the use of free water by koalas in the wild and the possible benefit of water supplementation for koala populations.

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Climate warming is affecting mortality of weasels due to camouflage mismatch

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In Poland, two subspecies (morphs) of weasel *Mustela nivalis* exist, which differ in winter pelage colour, white in *M. n. nivalis* and brown in *M. n. vulgaris*. Weasels are vulnerable to attacks from other predators, thus cryptic coat colour may affect probability of detection, and in consequence, their mortality. We hypothesize that natural selection should favour one of phenotypes, according to prevailing weather conditions during winter. Analysis of trapping data from the Białowieża Forest, where both subspecies occur sympatrically, revealed that the proportion of *M. n. vulgaris* increased along with decreasing number of days with snow cover and increasing mean ambient temperature. Moreover, recently we observed increasing variation in timing of moult in *M. n. nivalis*, whereas in the past it was fixed and most probably regulated entirely by photoperiod. To demonstrate that white or brown winter pelage may change predation rates, we performed a field experiment using weasel models (white and brown) exposed against different background colours. This experiment revealed that contrasting models of weasels were attacked significantly more often by predators than those matching the background colour. Results of our study provide another example that in mammals, variation of phenotypic traits is big enough to enable rapid adaptations to changing climatic conditions.

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Rapid natural history characterization of endangered Southeast Asian mammals: Using fecal metagenomics and metabarcoding for the simultaneous study of diet, host genetics, parasites, and gut microbiome

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A large number of mammal species are in steep decline due to habitat loss, degradation and poaching. Yet, we know very little about their natural history, which affects our understanding of species ecology and conservation management. Here, we demonstrate that faecal samples are very useful for a rapid augmentation of our knowledge of natural history because as they contain DNA from the host, its diet, parasites, and microbes. Using a combination of direct shotgun sequencing (metagenomics) and PCR based amplicon sequencing (metabarcoding) we can study many endangered mammal species of Southeast Asia simultaneously. Our study of the critically endangered Sunda Pangolin (*Manis javanica*) in Singapore identifies a diet of >24 species of ants and termites based on faecal samples and gut contents. Furthermore, we show that the gut microbiome of pangolins in the wild differs from the microbiome of captive pangolins, with wild pangolins having an increased representation of Proteobacteria. We discuss the implications of our results for captive management of the species. We also describe the diet, gut parasites and host genetics of other Southeast Asian mammals including the Raffles' banded langur (*Presbytis femoralis*), Tonkin snub-nosed monkey (*Rhinopithecus avunculus*), black-shanked douc langur (*Pygathrix nigripes*), Indochinese silvered langur (*Trachypithecus germaini*), leopard cat (*Prionailurus bengalensis*), common tree shrew (*Tupaia glis*) and Singapore rat (*Rattus annandalei)*. All studies rely on recently developed techniques for the evaluation of Next Generation Sequencing data, and many datasets will continue to provide new insights as more plant and animal species are barcoded.

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Validation of a non-invasive technique using faecal glucocorticoid metabolites to measure stress in leopards (*Panthera pardus*)

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Leopards utilizing areas under different anthropogenic influences may be exposed to different environmental, physiological and psychosocial stressors. Given the elusive nature of the species, a non-invasive approach to monitor responses to stressors would be advantageous to date; however, no test system has been established to determine glucocorticoid concentrations in leopard faeces. The study aimed to examine the suitability of five different enzyme-immunoassays (EIA's) for monitoring adrenocortical function in the leopard based on faecal glucocorticoid metabolite (fGCM) analysis. After performing an adrenocorticotropic hormone (ACTH) stimulation test, examining gastrointestinal transit (GIT) time under different feeding regimes and investigating the stability of fGCM concentrations post-defecation, faecal samples were collected from free-ranging leopards in a peri-urban and conservation area. An EIA using an antibody against 5α-pregnane-3β,11β, 21-triol-20-CMO:BSA seems most suitable for assessing adrenocortical function in male and female leopards, with post-stimulation fGCM concentrations increasing by 331% (male) and 203% (female) respectively. GIT varied distinctly between the two different facilities tested, and fGCM concentrations post-defecation remain fairly stable for up to 6 days. Faecal GCM concentrations did not vary between the two study sites ($T_{7,37} = 187$, $p = 0.35$). Overall median fGCM concentration of female leopards were ~50% and ~250% higher compared to males at both sites, respectively. Females also demonstrated higher variability in individual fGCM concentrations compared to males, which might be linked to differences in reproductive status. The established method now adds to the tools available to address some of the wildlife management, conservation and human-predator mitigation measures for free-ranging leopards under different land use practices.

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Biogeographical divides in distribution of genetic lineages of small mammals in East African savannahs

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In the frame of phylogeographic studies of small terrestrial mammals in eastern Africa, we observed conspicuous spatial genetic patterns in multiple savannahs' taxa (either within species or among closely related species). Most frequently, the divides among main lineages were concordant with Eastern Arc Mountains (EAM) and with rift valleys filled by lakes Malawi and Rukwa. Importance of these biogeographical divides was analysed by a new approach based on graph theory, using genetic data from 12 genera and 37 species or intraspecific lineages of rodents and shrews. As expected, the algorithm clearly defined three assemblages of taxa separated by a Y-shaped divide Malawi-Rukwa-EAM. Geographic distribution of sister taxa suggests major division between communities of northern (i.e. north-central Tanzania) and southern savannahs. In the latter, the assemblage east of EAM and Malawi Lake is only an offshoot of more widespread western (Zambian) one. The results of comparative phylo(bio-)geographical analysis therefore clearly indicate the importance of EAM and East-African rift valleys in forming the communities of small mammals living in non-forested habitats. Due to different evolutionary ages of particular taxa (approx. from 300 kya to 3 Mya), and absence of obvious current barriers to gene flow among defined regions, we speculate that the observed structure is driven by repeated extinctions of savannah community at detected divides. Alternatively, the role of long-term differences in climate and vegetation of three savannah regions separated by the Y-shape divide cannot be ruled out.

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Sulawesi after Wallace: Multiple murine lineages support within island speciation across the northern peninsula of Sulawesi, Indonesia

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Within-island speciation may play a significant role in shaping biodiversity in a large oceanic island. Sulawesi is the largest oceanic island in the Indo-Australian Archipelago with most species evolved after crossing Wallace's Line. *Bunomys* is the best representative of a unique murine radiation and distribution on Sulawesi with one species being widespread and the other species restricted to particular part of the island. Here, we used phylogenetic analyses from five independent loci to determine the systematic relationships of species in the genus *Bunomys* and to test the monophyly of the genus with respect other endemic murine genera from Sulawesi. We used morphometric analyses and qualitative morphological characters to determine if *B. fratrorum* populations across the northern peninsula of Sulawesi represent distinct species. We found that *Bunomys fratrorum* thought to be endemic to the eastern half of the northern peninsula are distributed to the western end of the peninsula. Our phylogenetic analyses show that *B. fratrorum* was not related to the other genera of *Bunomys* and may support to resurrecting of the genus *Frateromys*. Using both phylogenetic and morphometric analysis, we determine *B. fratrorum* may represent two divergent populations across the northern peninsula. Phylogenetic differences across the northern peninsula support the evidence for the significance of within-island speciation in producing species diversity on Sulawesi.

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Southern hairy-nosed wombats (*Lasiorhinus latifrons*) in Western Australia; out of sight, out of mind

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Our knowledge regarding the distribution and abundance of southern hairy-nosed wombats (*Lasiorhinus latifrons)* (SHNW) in Western Australia (WA) is scant and out of date. A search of the scientific literature and public domain provides virtually no information on SHNW in WA. This is likely to have arisen because of the need to address other wildlife priorities with the available state-based research funding, and the remote location where the species is found. As a consequence, virtually all SHNW research has been undertaken in South Australia (SA) where the majority of the population is located. The deficit in research effort in WA impacts estimates of the overall species' abundance, which have omitted the WA population from their calculations. As a result, extant estimates of wombat abundance almost certainly understate the true situation. Using a combination of satellite imagery, field surveys and conversations with landholders, we surveyed the south-eastern region of WA to determine the distribution and abundance of wombats in the area. Our results show that there is a significant and expanding population of SHNW in WA. Wombats can be found in an area between the coast and the trans-continental railway line, from the South Australian border to around Caiguna; an area of ~ 20,000 km^2. The population density varies, but is highest near the SA border. Our initial abundance estimate suggests that there is likely to be upwards of 50,000 wombats in the state. The importance of this population is discussed in view of potential climate change impacts.

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Elevational patterns of non-volant small mammal species richness in Gyirong Valley, Central Himalaya: Evaluating multiple spatial and environmental drivers

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Elevational patterns of non-volant small mammal species richness and its causes were studied along a central Himalayan gradient, in China, for the first time. We conducted field surveys at each of twelve elevational bands of 300 m for two times throughout the whole wet season between 1800-5400 m asl. In all, 755 individual small mammals of 22 species were documented in 21,600 trap nights. The species richness pattern for non-volant small mammals along the elevational gradients was hump-shaped, with highest richness at 2800-3100 m asl. Environmental factors played more important roles in shaping elevational species richness patterns than spatial factors. Our study also demonstrates that no single key factor can explain all species richness patterns, and a multiple or interacting causal framework for elevational patterns of species richness along the elevational gradient seem to be supported.

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Which landscape size best predicts the influence of forest cover on restoration success for mammals? – A global meta-analysis on the scale of effect

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Landscape context is a strong predictor of species persistence, abundance and distribution, yet its influence on the success of ecological restoration for mammals remains unclear. Thus, a primary question arises: which landscape size best predicts the effects of forest cover on restoration success? To answer this, we conducted a global meta-analysis for mammals. Response ratios were calculated for comparisons between reference (e.g. old-growth forest) and disturbed sites (degraded or restored). Using an information-theoretic approach, mean response ratio (restoration success) and response ratio variance (restoration predictability) within each study landscape were regressed against the percentage of overall (summed forest cover) and contiguous (summed pixels of ≥ 60% forest cover) forest within eight different buffer sizes of radius 5–200 km (at 1 km resolution). The best buffer (landscape) size varied for: (i) overall and contiguous forest cover, and (ii) mean response ratio and response ratio variance. Mammals were influenced by contiguous forest cover only (5, 10 and 50–200 km radii). Overall, mean response ratio and response ratio variance were positively and negatively non-linearly related with both overall and contiguous forest cover, respectively. We reveal for the first time a clear pattern of increasing restoration success and decreasing uncertainty as contiguous forest cover increases. We also indicate preliminary recommended buffer sizes for investigating landscape restoration effects on mammals. When setting targets for ecological restoration, policymakers and restoration practitioners should account for: i) the landscape context, and ii) the uncertainty in restoration success, as it increases when contiguous forest cover falls below about 50%.

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Long-term monitoring protocols for established populations of threatened mammals: Faure Island, Shark Bay

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The creation of feral predator-free exclosures and islands has become a national focus for the conservation of critical weight-range mammals. During the planning stages, it is important to consider protocols for the long-term monitoring of the proposed species for translocation. This can be aided by considering lessons learned from existing exclosures and the populations of threatened mammal species within. One such example is Faure Island, a 5000 ha island located in Shark Bay, Western Australia. The pastoral lease over the island was acquired by Australian Wildlife Conservancy in 2000. The island was freed of introduced predators (cats) and grazers (goats) in 2001. A reintroduction program was initiated in 2002, with the translocation of burrowing bettongs (*Bettongia lesueur*) and Shark Bay mice (*Pseudomys fieldi*), followed by the translocation of banded hare-wallabies (*Lagostrophus fasciatus*) in 2004 and western barred bandicoots (*Perameles bougainville*) in 2005. As the populations of these species became established, it became increasingly difficult to monitor some species. Numerous methodologies have been trialed, including various trap arrays, spotlighting, camera trapping, scat plots and tracking plots. Final decisions on long-term protocols considered robustness of data, animal welfare, cost and practicality.

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Individual variation in the physiological stress response: Implications for studies of captive and free-ranging mammals

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In recent years, many researchers have used non-invasive methods to measure the physiological stress response of diverse mammals, by measuring glucocorticoid hormones and/or their metabolites in urine, faeces or hair. Such studies have investigated the physiological responses of mammals to numerous stressors, such as seasonal changes, social ranking, population density, translocation and acclimation to a new environment, the presence of or handling by humans (e.g. zoo visitors), to name a few. However, individual differences in the stress response may impact on studies investigating differences between treatment groups. Using examples from studies of koalas, possums and bandicoots, we will show that high variation between individuals can make interpreting group differences difficult, and discuss ways to account for this during the experimental design phase. We also argue that investigating the individual variation itself is a worthwhile scientific pursuit, particularly if it is related to differences in how individuals interact with and value the extrinsic biotic and abiotic environment.

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The role of individual differences in conservation: Effects on the success of threatened mammal re-introductions

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Post-release survival of re-introduced mammals can vary dramatically between individuals, with some animals surviving for many months, whilst others die soon after release. Studies have found that post-release survival may be related to individual differences in behaviour, or ‘personality’. In particular, individuals that respond appropriately to potentially risky or stressful situations when tested in captivity prior to release, are more likely to survive following reintroduction. We investigated individual differences in behaviour in wild-caught western quolls (*Dasyurus geoffroii*) housed in captivity, prior to their reintroduction to the Ikara-Flinders Ranges National Park in 2014 and 2015. Behaviour was recorded for eight tests, including a novel object test, a giving-up density test, and handling behaviour. Quolls were then radio-tracked for 6 months following release to determine survival, body condition, and dispersal patterns. Repeatable individual differences were identified in western quolls using the novel object test and handling behaviour. Here I will discuss how individual differences influenced post-release behaviour and survival, and make suggestions for how we may improve the success of future reintroductions by targeting individuals most suitable for reintroduction.

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How is diet related to personality and stress physiology of a mammalian herbivore, the common brushtail possum (*Trichosurus vulpecula*)?

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Individual behavioral phenotypes (personality traits) are predicted to influence an animal's diet and maybe linked to its stress physiology because different behavioral phenotypes perceive and react differently to similar stimuli. Here we studied free-ranging common brushtail possums to test whether their diets differ as a function of their personality and to interpret this relationship in terms of stress physiology. We predicted that pro-active (bold, exploratory, active) animals would have a higher quality diet because they had more diverse foraging opportunities, such as foraging more on the ground and in gardens where predation risk is higher. We studied 30 possums on the urban boundary with open eucalypt forest in Ku-ring-gai Chase National Park, Sydney Australia. We quantified the personality of each animal along three axes: exploration, boldness and activity; and collected their scats to determine diet using micro-histological and DNA barcoding methods. In a separate study with animals brought into captivity, we quantified stress hormone levels and compared these to personality traits. Our results show that the diet of individual possums is strongly influenced by personality (exploration, boldness and activity). Diet of exploratory individuals was twice as diverse as that of less exploratory individuals. Diet diversity was also related to boldness and activity. We report on the correlation with stress hormone levels across a proactive-retroactive continuum. Given that the personality of different animals leads to different choice of foods within the same landscape, we predict that herbivore impact on plant communities will vary according to individual phenotype.

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Stress, not personality, affects problem-solving by urban possums

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Behavioural flexibility, the ability of animals to modify behaviours in response to novel challenges, is thought to be a key determinant in the persistence of some species within the expanding urban landscape. Behavioural flexibility is often tested using food-motivated problem-solving tasks, and inter-individual variation exists in the capacity to solve problems. We investigated the influence of inherent individual characteristics (personality and physiological stress), and behaviours involved in the problem solving process (flexibility rate, behavioural variety, functional manipulation, and learning) on problem solving abilities within an urban population of common brushtail possums (*Trichosurus vulpecula*). We validated the use of a corticosterone enzyme immuno-assay on brushtail possums and quantified the personality traits of boldness, activity, and exploration. We found that although aspects of the stress response correlated with measures of personality, stress reactivity, but not personality, influenced problem solving. This influence was manifest via proximate behavioural mechanisms. Moreover, increased problem-solving efficiency over trials indicated that possums are capable of combining simple associative learning with some scope for higher order cognition to exploit novel food resources. We suggest that behavioural flexibility may confer fitness consequences within the urban landscape, allowing possums to exploit novel resource opportunities.

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Feeding around the bush: Supplementary feeding for dogs in Singapore forests

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Since its domestication more than 30,000 years ago, the domestic dog (*Canis familiaris*) has become the most abundant canid worldwide, estimated at 700 million to 1 billion in numbers. Of this, approximately 60% of dogs are found in rural areas and a large proportion is free-roaming, potentially exerting direct ecological influences on the native wildlife. Because dogs are often supplemented with human-derived food, supplementary feeding can translate to increased dog abundance (which leads to greater intensity of ecological interactions) and the food items may also be consumed by non-target species. Here, we examined the public's perception of supplementary feeding of dogs and the extent of supplementary feeding at the forested nature reserves of Singapore. Additionally, we investigated the community composition of non-target forest vertebrates that were attracted to common food items left out for dogs at forest interiors, edge habitats, and adjacent public-accessible recreational facilities using baited camera-traps. We found that the public generally did not support supplementary feeding of dogs for various reasons, and such feeding only took place at locations where dogs were found. The vertebrate communities attracted to food baits were significant dissimilar between forest interiors and recreational sites; camera-trap images also revealed that free-roaming dogs seldom recorded in forest interior sites. General recommendations with regards to supplementary feeding were made in relation to the findings of the study.

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Coping with the ubiquitous dogs: An integrative approach to managing disease in threatened Ethiopian wolves

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The Ethiopian wolf (*Canis simensis*) is the rarest canid in the world, with half a dozen surviving populations at constant risk from dog-related diseases, such as rabies and canine distemper virus. Intensive vaccination of neighbouring domestic dogs in the Bale Mountains has proved insufficient to fully prevent these viruses from spilling over into the wolf population, due to the large numbers of sympatric dogs and their high turnover. Where outbreaks have been detected in the wolves, responsive parenteral vaccination has been the key disease management approach. A new strategy for an integrated disease management is urgently required to protect the wolves, and also achieve ‘one health’ spill-over benefits to humans, livestock, dogs and other wild carnivores. We describe mortality patterns and analyse long-term demographic data to disclose the crucial role of pack formation in wolf population recovery. We assess the spatial and temporal dynamics of viral pathogens, their transmission from reservoir free-ranging dog populations to wildlife, and consider the effectiveness of preventive oral vaccinations. Using simulation models to test alternative disease management strategies we present some recommendations for the future management of disease in Ethiopian wolf populations.

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Mesocarnivores in human-modified habitats: A movement ecology approach to understanding adaptations for survival.

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In the increasingly human-dominated landscapes of India, the survival and long-term persistence of mammalian carnivores is a key conservation challenge. This is especially the case for species that survive in the semi-arid savanna biomes of central India. Much of the conservation research focus in India lies in the study of large herbivores and carnivores, yet smaller mammalian species are key components of ecosystems. Some small carnivores exist in human-modified landscapes, often venturing close to settlements and other infrastructure. However, we still lack an understanding of the behavioural strategies that permit effective commensalism and ecological conditions that permit coexistence in fragmented human-modified landscapes. We used a movement ecology approach to understand how multiple species of mesocarnivores survive in heavily human-modified landscapes. We fitted GPS collars to Indian foxes (n = 15), golden jackals (n = 7) and jungle cats (n = 8), with fixes every 15-60 minutes. Our results show that species such as the Indian fox are heavily dependent on remnant native vegetation for daytime resting, using agricultural fields and fallows for foraging, but without a fixed route preference. On the other hand, jackals show a strong habitat preference for irrigated cultivation and a strong "spoke and node" pattern of foraging. Jungle cats are the most generalist, using native vegetation, irrigated agriculture as well as human settlements for foraging. For all three species however, daytime resting locations are in either natural or cultivated dense vegetation patches. Our results suggest that these species can survive in such environments provided there are relatively undisturbed daytime resting refugia.

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Patterns of carnivore distributions and human-carnivore conflicts: Sympatric wild canids in India as a case study

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Protected areas constitute a mere 4% of India’s land area. Many species of carnivores inhabit unprotected human-dominated landscapes. Wild canids in India exemplify this issue, but are among the least-studied carnivores, globally. We conducted sign and questionnaire surveys in 2015-2016 across *c.*7000 km^2 of the Kanha-Pench forest corridor in central India. Using an array of 128 52 km^2 grid cells, we examined distribution of wild canids, and human-canid interactions in the region. We focused on the dhole, Indian fox, Indian jackal and Indian wolf. We also included the striped hyena, because of similarities in their ecological requirements. Results from sign surveys and occupancy models indicated that wild canids occupied large parts of the landscape, ranging from 16% for dholes to 82% for jackals. Combining interview surveys of 675 local people and multi-state occupancy models, we estimated probability of conflict ranging from 33% for dholes to 87% for wolves. In general, scrub forests and terrain heterogeneity were important for canid occurrence. Presence of free-ranging/feral dogs and agricultural lands also influenced occupancy patterns of these carnivores. We further explored the influence of land-use, anthropogenic factors, and livestock-holding by households on patterns of conflict. Results from our study provide insights on the ecology of these five data-deficient carnivores in human-dominated landscapes. We propose that prioritisation and zoning of areas could facilitate persistence of carnivores in this multi-use landscape. Based on our results, we provide (1) species-specific management recommendations and (2) innovative methods of communicating such results with local people, wildlife managers, and popular media.

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The past and future fate of the world’s island mammals

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As for other taxonomic groups, and relative to their land area, islands support a disproportionately large share of the world’s mammal species, but also a disproportionate share of mammal extinctions and threatened mammal species. The extinction-proneness of island species is exemplified by the loss of two Australian island-endemic mammal species in the last decade. Island species tend to be susceptible to novel threats because of their typically small population sizes, limited genetic variation, predator naivety and life history characteristics. Somewhat conversely, islands have also provided conservation security for some mammal species that have disappeared from their formerly extensive mainland ranges due to threats introduced to mainland areas but not yet to islands. We review the fate of the world’s island mammal species over the last few centuries relative to that of the mammal fauna of mainland areas, and describe the factors that have most influenced that fate. We quantify and summarise the current conservation state of the world’s island-endemic mammals. We conclude that the dismal rate of extinctions of island-endemic mammal species is likely to continue into the future unless there is more concerted attempt to enhance island biosecurity, spread extinction-risk, eradicate priority pests from priority islands, and engage better with island communities.

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The role of islands and fenced areas for mammal conservation in Australia

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Islands have been critical for conserving Australian mammal species, which have proven highly susceptible to impacts from pest species (cats, foxes, rabbits, other herbivores) introduced after European settlement. More than on other continents, these pests have subverted native mammal populations, causing multiple species extinctions. At least 8 mammal species survived this invasion shock only because of naturally-occurring populations on islands that remained pest-free. Other species survived on the mainland only precariously, and populations on pest-free islands provide some insurance against extinction. The value of islands for avoiding mammal extinctions was recognised as early as the late 1800s, with rates of island translocations accelerating during the past 40 years. The construction of barrier fences on the mainland to exclude cats/foxes, and protect native species (‘mainland islands’) began from the 1990s. Both approaches have been critical to the conservation of Australia’s mammals (and other species), although each has constraints that limit implementation and/or require specific management focus. To describe the past, and potential future, contributions of ‘island-arks’ to Australian mammal conservation, we compiled information (from multiple sources) on the presence/absence of cats, foxes and threatened mammals across all Australian islands and fenced areas. We examine the value of island-arks for the persistence of species with varying susceptibility to cat/fox predation; we compare the contributions of islands and fenced areas to species’ persistence; and compare the contributions of n aturally-occurring and translocated populations to species’ persistence. Finally, we identify ‘gaps’ in representation of threatened species across island-arks.

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Minimising Australian mammal extinctions through strategic planning of safe havens

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Translocations to areas free of introduced predators (offshore islands, mainland fenced exclosures) have become a key management action for conserving Australian mammal species, many of which are highly vulnerable to predation by introduced foxes and/or cats. Multiple safe havens create multiple safe havens, further reducing the risk of extinction. However, creating safe havens is expensive, with an ongoing legacy of maintenance and biosecurity. Consequently, the safe haven approach is broadly viewed as an emergency intervention used to secure species from extinction. To date, the existing safe haven network is highly decentralised where conservation agencies have created safe havens independently of one another. Consequently, species representation is highly disproportionate, with some species are represented in several safe havens, and other species in none. Creating new safe havens strategically could rectify unequal representation, ensuring a minimum level of security for all threatened taxa vulnerable to foxes/cats, while minimising the number of costly new projects. In an Australia-wide prioritisation for creating new havens, we identified 106 taxa whose persistence strongly depends on representation within safe havens. We assessed the vulnerability of each taxon to foxes/cats, and characterise their current population structure. Potential new safe havens were prioritised based on the expected reduction in extinction risk across the suite of threatened species, improving representation within the network with a minimal number of new fences. This approach provides a tool for assessing the merit of new additions to Australia's safe haven network, pursuing the dual goal of minimal cost and improved representation.

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The use of Western Australian islands for fauna reconstruction

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Fauna translocation has become an important management tool for reversing the decline of many native species, and within Western Australia, translocations to islands have been more successful than those to the mainland or to fenced enclosures. Most of the 12 translocations of native fauna to WA islands have involved single species with the primary aim of improving the conservation status of the species. The reintroduction of a suite of “ecosystem engineers” to assist in restoring island ecological function has been promoted as an additional benefit of fauna translocations. While there have been programs underway for several years to reintroduce (and introduce) native mammals to WA islands, it is only more recently that the opportunity to reintroduce several species has arisen. The Montebello Islands group, off the Pilbara coast, formerly had three mammal species and two bird species that went extinct following the introduction of feral cats, black rats and atomic explosions. Two mammal species and two bird species have been returned successfully to the island, and another mammal species will be re-introduced in 2018/19 to complete this fauna reconstruction project. Planning is now underway for a more ambitious island fauna reconstruction project. Over the next 13 years, 12 species of mammal and one bird species will be translocated to Dirk Hartog Island in Shark Bay. In addition to improving the conservation status of several threatened species, and returning ecosystem processes to help restore soil profiles and promote vegetation regrowth, this project offers unique opportunities for conservation research and ecotourism.

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Presence/absence of an apex predator and body size dictate the magnitude of resource-driven population fluctuations in desert mammals

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There has long been debate over the primacy of top-down (consumption) and bottom up effects (primary productivity) as forces controlling population fluctuations of mammals. In deserts, rainfall driven fluctuations in food availability are often considered to be more important drivers of the population dynamics of mammals than predators’ top-down effects. Here I report the effects that the presence/absence of an apex predator, the dingo, has on population dynamics of mammals in Australia’s Strzelecki Desert. Results show that primacy of top-down and bottom-up effects as drivers of mammals’ population fluctuations scales with their body size and the composition of predator assemblages. Populations of herbivorous kangaroos (> 20 kg) and introduced mesopredators (4-7 kg) the red fox and feral cat increased with the availability of food resources in the absence of dingoes but showed negligible responses to increased resource availability where dingoes were present. Conversely, populations of small mammals (< 1.5 kg) increased with the availability of food resources in the presence of dingoes but showed muted responses to resource pulses where dingoes were absent. My study shows that that predators can decouple bottom-up effects and that top-down and bottom-up effects can have primacy on different species within desert mammal assemblages. This can occur because the strength predators’ top-down effects scales with body sizes of both predators and prey.

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Conservation implications of livestock grazing for threatened small mammal species in Australia’s arid and semi-arid rangelands

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Livestock grazing in arid and semi-arid rangelands (drylands) encompasses a greater area than any other land use. Australia supports the largest area of managed grazing land worldwide. Evidence for direct and indirect effects of grazing on small mammal species in rangelands is often inconclusive or mixed, with variation in responses among species. I review the evidence for the influence of livestock grazing systems on small mammals in Australian drylands broadly. I examine the threat posed by grazing to three species that are considered Vulnerable or Presumed Extinct in New South Wales: southern ningaui (*Ningaui yvonneae*), stripe-faced dunnart (*Sminthopsis crassicaudata*), and plains rat (*Pseudomys australis*) in view of their ecology and behaviour.

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Do differing habitat preferences promote coexistence for semi-arid mammal species?

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Arid and semi-arid mammals experience irregular rainfall and resource pulses from year to year. Consequently, some species fluctuate in persistence and abundance between years, while other (often coexisting) species remain relatively constant. In the semi-arid mallee environment of Eyre Peninsula South Australia, two dasyurid marsupials, the mallee ningaui (*Ningaui yvonneae*) and the sandhill dunnart (*Sminthopsis psammophila*), are sympatric and exhibit a similar life history strategy. However, *N. yvonneae* is relatively common and stable in abundance, while *S. psammophila* is considered rare and its abundance fluctuates both temporally and spatially. We were interested in ascertaining whether habitat preferences and use by these species differed, and whether this might help explain variability in their temporal and spatial abundances. We used data obtained at two spatial scales; broad-scale trapping at 11 sites (using pitfall and aluminium box traps) and fine-scale (direct) observations of foraging. Observational data were collected by recording behaviour and movements while animals foraged at night time, with the aid of fluorescent chemi-tags affixed to individuals. Habitat data were collected at each scale, and generalised linear modelling was used to understand habitat preferences. The combination of data from broad and fine scale habitat use may provide insights into the drivers behind population abundance in these dasyurid marsupials, and afford valuable information to consider when managing areas for the persistence of mammal assemblages.

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Defining the refuges of a threatened desert rodent when resources are scarce

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Recent research has focused on how small mammals persist in environments with high temporal unpredictability in the availability of resources. In areas such as the Australian arid zone, where irregular and unpredictable resource pulses drive small mammal population dynamics, some species persist through long periods of low resource availability in drought refuges. Refuges are small discrete areas in the landscape that provide a relatively consistent supply of resources for survival and reproduction throughout these low-resource times. We investigated the spatial scale and dynamics of populations of a threatened native rodent, the plains mouse *Pseudomys australis*, in cracking clay refuge habitat in central Australia during a period of low resource availability. Using live- and camera-trapping data collected over two years, and spatial modelling techniques, we assigned boundaries to the refuge areas and found that *P. australis* fluctuated both spatially and numerically over the study period, but stayed largely within the cracking clay refuge areas. Our research suggests that this refuge-using species is, for the most part, confined to cracking clay during periods of low resource availability and that this restricted habitat type forms the boundary of refuge areas. The assignment of boundaries, based on readily defined and spatially predictable landscape attributes, allows for more targeted and efficient management of these small areas to promote the persistence of this threatened species.

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Climbing into the canopy: Arboreal camera trapping proves effective for broadscale surveys of the Critically Endangered Leadbeater's possum, *Gymnobelideus leadbeateri*

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The Critically Endangered Leadbeater's possum is a small, cryptic, arboreal marsupial restricted to the montane ash forests in Victoria, Australia. Threats to this species include extensive bushfires and timber harvesting. To rapidly locate new possum colonies to implement conservation actions, we have undertaken broadscale surveys across the species range, using remote cameras mounted in trees to detect Leadbeater's possums at night while they are foraging. The major challenge of camera trapping for this species is they rarely come to ground and they are non-gliding, so foraging occurs only in densely connected layers of the forest. This layer varies in height with forest age. To overcome these issues, cameras were installed using specialist arborists, allowing us to be flexible when surveying across forest age-classes. From November 2014 to April 2016 we surveyed 289 sites, resulting in 18,581 camera trap-nights and over 466,000 images. Leadbeater's possums were detected at 148 (51%) of these sites. They were recorded in all sampled forest age-classes, including fire regrowth from major bushfires in 1939 and 1983, and timber harvesting regrowth. All new colonies have now been protected with a timber harvesting exclusion zone, resulting in 1,865 ha of forest reserved. Arboreal camera trapping has proven effective at detecting Leadbeater's possum and has allowed a large number of sites to be surveyed to inform and improve its conservation management. Arboreal camera trapping is a potentially useful technique for anyone conducting research on arboreal mammals.

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A scalable approach to wild animal monitoring using distributed autonomous sensing systems

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Camera traps have enabled significant insights into wild animals' lives through the collection of image-based information which now routinely include high quality day and night imagery due to continuing advancements in camera technologies. However, the effective range of a camera trap is restricted by its short range motion sensor and highly manual and logistical burden to recover and analyse data. This typically limits their utilisation to small areas of coverage, or the need for attractants within the sensor's range. Through our research into humanely deterring vertebrate pest animals, we need to address issues of scalability (coverage area), detection range, and in situ animal classification for real-time pest management. Our approach employs a combination of inexpensive, low-power, 'detection nodes' with motion sensors and wireless radio communications capability, operating in collaboration with a ''supervisor" that has high quality thermal and colour cameras and also has wireless communications capability. This combination provides low power, scalable coverage for triggering long range, high quality thermal and colour video recording. Additionally, this allows for onboard, in situ animal classification. Examples where our approach can be utilised include game trails, farmland, and landscape-transition boundaries, covering larger areas than practically possible with the stand-alone motion based sensor approach. Further to the discussion of the potential benefits and challenges of our approach, we present results from early instantiations of our system deployed in peri-urban, bush and agricultural domains.

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Assessing the accuracy of mammal identification from camera traps

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Camera traps are a powerful and increasingly popular tool for mammal studies. However, like all survey techniques, camera traps have their limitations. While researchers recognise constraints associated with experimental design or the cameras themselves, photo mis-identification is often neglected. Identifying mammals from camera trap photos can be unreliable and potentially influenced by the expertise of the observer, yet few studies have examined this source of error. We evaluated the effects of observer experience, confidence, animal body size and uniqueness on the accuracy of mammal identifications from camera trap images. Between 20 December 2016 and 22 February 2017, an internet survey was conducted, consisting of 20 questions regarding observer experience and 60 camera trap images to be identified. Images were sourced from surveys in northern Australia and included 25 native mammal species, ranging in size from the delicate mouse (< 15 g) to dingo (> 10 kg). A total of 176 people participated in the survey with experience ranging from none to > 40 years of mammal trapping. There was surprisingly little relationship between the accuracy of mammal identification and levels of experience or confidence. Accuracy was highest for unique species (such as the echidna) and lowest for small indistinct species (such as rodents and dasyurids). There was also a positive relationship between accuracy and body mass. Our results highlight that development of computer-assisted identification is needed, particularly for studies where similar-looking mammals co-occur. However, in the interim, integration of camera traps with conventional survey techniques (e.g. trapping) can aid positive identifications.

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Improving detection probabilities for the Critically Endangered Leadbeater's Possum (*Gymnobelideus leadbeateri*) using arboreal camera trapping

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The Critically Endangered Leadbeater's possum is a small, cryptic, arboreal marsupial largely restricted to the montane ash forests of Victoria, Australia. To rapidly locate colonies of Leadbeater's possum for protection from timber harvesting, we adapted an arboreal camera trapping approach to survey 289 sites across the species' range from 2014-2016. We worked with arborists to place cameras set opposite bait stations in trees up to 47 m above ground. Two or three Reconyx cameras (models HC500, HC600 or PC900) were used per site, located < 150 m apart, for 3–4 weeks duration. The large survey effort using a standardised method allowed modelling of detection probabilities for Leadbeater's possum. We examined the effects of survey length, number of cameras per site, season, camera model and camera height. Covariates including camera height, tree height, and season had a negligible influence on detectability. Detection probabilities associated with the three different camera models were generally similar. Survey length and number of cameras had the greatest influence: after 21 days of sampling with a single camera, detection probabilities were 0.37–0.54. After 28 days sampling with three cameras per site, detection probabilities increased to 0.87–0.95. Deployment of three baited camera traps for at least four weeks result in a very high probability of detecting Leadbeater's possums at sites where they occur. These findings have led to a more efficient method of locating Leadbeater's possum colonies, improving conservation management of this species.

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Hot lunches for herbivores: How herbivorous diets interact with thermoregulation.

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The diet of mammalian herbivores poses a number of challenges unique to having an herbivorous diet, and at the same time thermoregulating. I will present mechanisms by which thermoregulation is influenced by herbivorous diets, especially through the action of plant secondary compounds. Using the Australian marsupial possum-eucalypt study system, I will provide evidence for temperature dependent toxicity in wild folivores consuming plants rich in plant secondary compounds. I will also show that plant secondary compounds can uncouple mitochondrial oxidative phosphorylation interfering with energy metabolism and leading to excess body heat production. Furthermore, since a mammal's ability to thermoregulate depends on sensing the thermal environment and responding appropriately, the binding of plant secondary metabolites to thermoreceptors can disrupt this process. Balancing of nutrients, and consuming a high fiber diet also interacts with thermoregulation in mammals consuming plants. I will discuss these phenomena in mammalian herbivores in general and how the interaction between plant based diets and thermoregulation means nutritional ecology and patterns of herbivory will likely change in a dynamic way as our climate changes in the future.

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Red squirrels decline in abundance in the boreal forests of Finland and NW Russia

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Recent global warming and other anthropogenic changes have caused well-documented range shifts and population declines in many species over a large spatial extent. Most large-scale studies focus on birds, large mammals, and threatened species, whereas large scale population trends of small to medium-sized mammals and species that are currently of least concern remain poorly studied. Large-scale studies are needed, because on smaller scales important patterns may be masked by local variation and stochastic processes. Here, we utilized snow track census data from Finland and NW Russia to estimate population growth rates of the Eurasian red squirrel (*Sciurus vulgaris* L) during 17 years in an area of over 1 000 000 km^2. We also studied the effects of summer and winter temperature change and loss of canopy cover on estimated red squirrel population growth rates. Our results suggest that red squirrel populations have declined in most parts of the study area, the only remarkable exception being SW Russia. These results are in concordance with previous studies suggesting that still common and least concern species may be declining, but is in contrast to the common pattern of northern populations of boreal species increasing under global warming. The estimated population growth rates are in synchrony over vast areas, suggesting also that the underlying reasons operate on a large scale. However, we find no evidence that the decline is caused by loss of canopy cover or changes in summer temperature, which was used as a proxy for the level of cone crop.

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Ecosystem modifiers create cache sites with microclimate that reduces seed release

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The evolution of seed caching is influenced by availability and perishability, which are related to climate. Future value is a major determinant of caching strategy and is likely influenced by perishability. Animals should select sites that reduce pilferage, promote relocation, and retard seed degradation. Across coniferous forests of North America, red squirrels (*Tamiasciurus hudsonicus*) are ecosystem modifiers that maintain iconic larderhoards within conspicuous piles of cone scales known as middens. We test the hypothesis that middens function as cool, moist sites that promote cone storage, deter seed germination and reduce seed dispersal. We assessed external and internal microclimates and forest structure, and detailed consequences of midden microclimates to cone opening. Our results delineate the adaptive nature of larderhoarding in middens. Midden internal microclimate is related to surface conditions, which are influenced by forest characteristics. Cone opening increased with temperature and decreased with moisture. Middens serve as cool, moist locations that retard perishability and facilitate cone storage. Small differences in temperature have important impacts on cone opening and efficacy of cone storage. Furthermore, global change is predicted to result in microclimates that may not be conducive to cone storage and suggest the broader vulnerability of animal caches to climate change.

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Long-term population dynamics of tropical dry forest small mammals: Global climate disruption and conservation

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Understanding the consequences of biotic and environmental variability on the population dynamics of mammals is fundamental to assessing the impacts of direct and indirect anthropogenic actions, as global climate disruption. Long-term studies of small mammals in temperate ecosystems have elucidated the roles of climate or interspecific interactions in their dynamics. However, the lack of long-term studies in the tropics is a major impediment to generalise between these species and ecosystems. We analyse the population dynamics of seven small mammals from two contrasting adjacent tropical dry forests in a protected area in western Mexico. We modelled the population dynamics using an 18 year live-trapping database, evaluating the effects of intra- and inter-specific interactions, climate, and primary productivity. Our analyses showed effects of both biotic and abiotic factors on the dynamics of all species. Intra- and inter-specific interactions negatively affected five and two species, respectively. Precipitation caused positive effects on every species, either by directly enhancing their survival (five species) or by triggering changes in primary productivity (two species). Extreme climate events left intense signals; either positively, for two invasive species inhabiting these forests, or causing population declines for another species and temporarily extirpating the dominant one. Our results suggest dramatic interactions between the sharp precipitation reductions and the higher probability of extreme climate events - both predicted by global climate disruption models - and other anthropogenic pressures that these forests are suffering from (habitat loss, over-exploitation). We show how well-preserved forests are resilient sources to prevent these - the World's most endangered - forests from annihilation.

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Biological validation and practical application of hormones in non-invasive samples collected in the field: The evaluation of health and fecundity of wild populations

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The collection of non-invasive biological samples for the purpose of evaluating adrenal or reproductive hormones from free-ranging Australian mammals has been limited to date. This may be due to challenges associated with sample collection and validation as well as limited knowledge of these techniques. Metabolism, route of excretion and structure of the eliminated hormone metabolites can vary significantly between species. Therefore, regardless of sample type or hormone, a research program must start with a robust, biological validation process to ensure the sample collection, storage, processing, analysis and data evaluation methodologies are sound. Factors that will be reviewed include suitability of sample type, effects of environment exposure and sample storage on hormone stability, designing biological validation tests (e.g. using ACTH challenge or pregnancy to confirm biological relevance), determining excretion time delays, sampling intervals and sample numbers as well as testing different methods of sample processing, analysis and immunoassay antibody specificity to find the best fit for your species and research study. The potential application of these techniques are endless but, for example, a single faecal sample has been used to confirm pregnancy in species such as the ghost bat and dugong, allowing conservation biologists to better evaluate population fecundity towards improving population monitoring and management. With a good research plan, non-invasive hormone analysis can be a powerful tool for conservation biologists to gain information on reproductive status, adrenal health, and gender of individual animals to evaluate the overall health and fecundity of a wild population to improve conservation management and decisions.

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Gas chromatography mass spectrometry (GCMS): An alternative method to evaluating bioindicators in non-invasive samples from wildlife species

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Understanding the basics of reproductive endocrinology of animals is vital for their conservation and management. Non-invasive analyses of hormone metabolites in urine or faeces represent reliable methods for monitoring endocrine activities. Alternatively, semiochemicals carrying information for conspecifics, such as estrus signalling substances for example, could be used as indicators to detect estrus. Immunoassays (EIA) relying on antibodies against individual hormones are widely used for hormone metabolite profiling. An alternative analytical technique is gas chromatography-mass spectrometry (GC-MS). Contrary to EIAs, GCMS analyses allows the quantification of numerous compounds in a single run. As solitary living individuals, giant pandas (*Ailuropoda melanoleuca*) use olfactory cues (i.e. in urine) to mediate mating-related social interactions. In *ex-situ* panda breeding, urinary steroids serve as estrous indicators. Using GCMS we analysed urinary steroid profiles as well as urinary volatiles that adsorb on polydimethyl-siloxane (PDMS) tubes. When profiling urinary steroid metabolites, peak levels of estrone-sulfate were confirmed on the day prior to ovulation. Major gestagen metabolites found were 5a/b-pregnane-3a-ol-20-one and pregnanediol. Both metabolites are products of deviating metabolic routes; however, no difference in progestagen composition was found between pregnant and pseudopregnant pandas. Analyses of PDMS adsorbed urinary volatiles revealed an abrupt increase of fatty acids to peak levels 6 days prior to ovulation that had been used for an early ovulation prognosis in one panda. Moreover, we recommend the PDMS technique e.g. to compare odour profiles from scent gland secretions between individuals

of different social status as basis for semiochemical-based environmental enrichment to enhance animal welfare in captive populations

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Considerations and options for the statistical analysis of wildlife endocrinology data

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Non-invasive hormone monitoring can offer valuable insights about reproductive status and well-being of animals, both in captivity and in the wild. One of the unique aspects of this methodology compared to traditional endocrine techniques is that it is much easier to collect repeated samples and establish longitudinal patterns of hormone fluctuations. This is valuable because the biological activity of hormones is often determined by relative changes in hormone levels, rather than absolute values. However, it can also be challenging to figure out how to analyse these large longitudinal datasets. Furthermore, excreted hormone levels can fluctuate for several reasons, thereby creating quite a bit of noise in the dataset and making it harder to separate signal from noise. This part of the workshop will focus on how to make sense of your data. We will discuss different graphing approaches and things to look for, useful summary statistics, and strategies for identifying peaks and meaningful patterns in your data. We will also highlight some confounding factors that should be taken into account during data analysis. Actual examples from the literature will be used to illustrate different data analysis approaches and some of the pros and cons of different techniques.

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Discordance between mitochondrial and nuclear DNA complicates evolutionary history of north-west Australian rock-wallabies, *Petrogale*

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The four endemic species of rock-wallabies (*P. brachyotis, P. burbidgei, P. concinna, P. wilkinsi*) from north-west Australia represent a monophyletic lineage within *Petrogale* that diverged early in the evolution of the genus. Preliminary mitochondrial DNA (mtDNA) studies have revealed high levels of divergence and/or a lack of monophyly within most species. However, improved resolution was impeded by a lack of high quality genetic samples from key areas and taxa, as well as the examination of small numbers of loci. This study used next generation sequencing methods (targeted exon capture) to sample > 1,000 loci from across the genome of the 4 species of rock-wallabies from north-western Australia, and enabled museum skins to be utilised as a source of DNA. Analysis of the nDNA data reveals more divergent, well supported monophyletic lineages than the 4 currently recognised species in this group, indicating that additional taxonomic revision is required. The mtDNA reveals a complex and discordant pattern of relationships that appears the result of ancient hybridisation and introgression

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Population structuring and connectivity of Queensland dugongs (*Dugong dugon*): Implications for dugong management in the Great Barrier Reef region

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The dugong (*Dugong dugon*) is a marine herbivore that inhabits shallow tropical and sub-tropical coastal waters extending from east Africa to Vanuatu, with Australia considered a stronghold of the species. Within Australia, recent mitochondrial DNA analysis identified one lineage that is widespread across the Australian dugong range and one lineage predominately restricted to the east coast of Queensland. In contrast, nuclear data showed fine-scale population sub-structuring within south-east Queensland. This study aimed to examine the degree of population structuring and connectivity of dugongs along the Queensland coast. Analysis using nuclear markers (24 microsatellite loci, n = 168 skin samples) identified two genetic clusters within the Queensland population, with an abrupt break over a short geographic distance identified in the Whitsunday Islands region. This genetic break was not apparent in the mitochondrial data (partial control region sequences, n = 208 skin samples), which found agreement with the lineages described in the Australia-wide mtDNA study. The cause of the restricted gene flow in the Whitsundays region will be discussed. The outcomes of this study can be used to inform better management of dugongs in the central Queensland/Great Barrier Reef region.

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Phylogeography of the European red deer (Cervus elaphus): A synthesis based on mitochondrial sequences, nuclear microsatellites and ancient DNA

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The red deer (*Cervus elaphus*) is one of the most widespread and most iconic large mammal species in Europe. As both an ecological keystone species and an important game animal its genetic structure has been analysed in considerable detail over the last decade or so. Phylogeographic studies based on mitochondrial DNA have revealed three major lineages (A: western, C: eastern, B: Sardinian/North-African), interpreted as signatures of glacial refugia and postglacial recolonization routes. Until recently, however, no continent-wide nuclear genetic data were available to round off the biogeographic picture. Here, we present data from more than 600 red deer genotyped at 13 nuclear microsatellite loci and discuss them in the framework of known mtDNA phylogeography and intraspecific taxonomy (“subspecies”). We found that the nuclear genome carries a phylogeographic signal concordant with the three mitochondrial lineages, that the threatened subspecies from the Tyrrhenian islands (Sardinia, Corsica) and Mesola (Italy) are both genetically distinct and impoverished, and also present ancient DNA data from (sub-)fossil red deer remains found on the Tyrrhenian islands and the Italian mainland. The latter include the first genetic data from the extinct original Corsican population and have yielded information that the today geographically restricted B lineage once had a much wider distribution and represents an Italian refugial lineage, confirming once again that the Italian peninsula is a hotspot of unique intraspecific diversity in Europe.

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Using genotype-by-sequencing to investigate genomic variation and phylogeographic patterns in a widespread carnivore, the red fox (*Vulpes vulpes*), in Europe

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The advent of next-generation sequencing techniques has the potential to revolutionise our understanding of phylogeographic processes in mammals at a continental scale. Studies of mitochondrial DNA variation have revealed little structure in many carnivore species in Europe, despite their presence in different glacial refugia during the Last Glacial Maximum. To determine if next-generation sequencing techniques could uncover further levels of genomic structure in European carnivores, a total of 524 red foxes (*Vulpes vulpes*) stretching from Ireland in the west to Siberia in the east were genotyped using genotype-by-sequencing (GBS). Just over 15,000 ‘neutral’ SNPs were retained after various filtering steps and tests for outlier loci. We have identified seven clusters using individual-based Bayesian methods (fastSTRUCTURE), and six using a Discriminant Analysis of Principal Components (DAPC) at the population-level. These clusters correspond to known refugia in the Mediterranean peninsulas, as well as Scandinavian, Russian and the island populations (Ireland and Great Britain). Levels of genomic diversity were similar among populations but were generally lower in the island populations and in the most northerly populations in Scandinavia. Ongoing work will incorporate the use of Approximate Bayesian Computation (ABC) to simulate different re-colonisation scenarios, with an additional focus on adaptive processes in this charismatic carnivore across Europe.

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The distribution history of the Chinese water deer in Shanghai area, China

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The Chinese water deer (*Hydropotes inermis*) was ranked as VU species in IUCN red list and under the second category of protected animals in China. It used to live in Shanghai area since the Neolithic Age, and the last records were in Qingpu and Fengxian (two counties in Shanghai) in the 1880s. This species was extirpated in the wild at the beginning of the twentieth century from Shanghai mainly because of poaching and habitat destruction. Since 2006, a reintroduction project for recovery of Chinese water deer was conducted in Shanghai area. Firstly, 21 deer were introduced for breeding; secondly, the strong offspring were selected for wild training; thirdly, they were set free in suitable locations. Until now, Chinese water deer were in 6 locations (Huaxia Park, Pinjiang Forest Park, Mingzhuhu Lake Park, Punan Woodland, Xinbang Woodland and Nanhui East Shoal) in Shanghai. The whole population is about 300 individuals in Shanghai area.

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Mammalian collections in the United States provide minimal temporal and spatial coverage: A call for a renewed investment in primary science and education infrastructure

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Natural history collections are tremendous assets for research (and teaching) in environmental and health sciences. Because these collections have been developed primarily for studies focused on biodiversity discovery, it remains unclear how this infrastructure will enable assessments of critical scientific questions related to environmental change. Recent specimen digitization efforts present an emerging opportunity to critically evaluate existing infrastructures and assess their temporal and spatial coverage. Using digitized records from VertNet of US mammal collections, we identify opportunities and limitations for investigating spatio-temporal changes in mammals and their communities. From these key resources, we emphasize the need for a comprehensive plan for increased sampling of mammalian diversity to maximize research into the future and foster an improved understanding of essential interactions among organisms and between them and their environments.

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On-site variables improve the accuracy of a GIS-based occupancy model for a Critically Endangered arboreal marsupial, Leadbeater's possum.

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Occupancy models are widely used to predict the occurrence of threatened species to inform conservation planning, but evaluating their accuracy is less common. We developed an occupancy model for the Critically Endangered Leadbeater's possum (an arboreal marsupial endemic to south-eastern Australia), to help identify population strongholds after extensive bushfires caused significant declines in range and abundance. Timber harvesting also threatens this species, with approximately one third of its potential habitat available for harvesting. Our model was developed from surveys at 180 sites, together with mapped environmental variables. Additional site-based habitat variables of known ecological importance (hollow-bearing trees, *Acacia* and mid-storey density) were collected at each survey site. These variables could not be included in the model used for spatial prediction, as they are not mapped across the species' range. The results from surveys at an additional 287 sites were used to evaluate the predictive accuracy of the GIS-based and on-site variable based models. The model based solely on mapped environmental data performed poorly, with Leadbeater's possum often detected at sites where they were not predicted to occur. The model incorporating on-site habitat data had much greater predictive accuracy. Our results illustrate the importance of good spatial understanding of critical habitat features to accurately predict the distribution of threatened species. Remotely-sensed data such as LiDAR and infrared imagery may provide spatial representations of critical habitat features for Leadbeater's possum allowing us to improve the predictive accuracy of our model, to better inform fire and timber harvesting management within the species' range.

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Magnetic alignment in the context of the concept of sensory alignment.

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Alignment means arranging into a line or adopting a non-random, predictable position with respect to a certain cue or signal. Sun basking, attentive listening, turning away from blending light or whipping wind, curious gazing on object of interest are associated with alignment. Alignment is advantageous: It helps to acquire information, reduce noise, avoid overstimulation, or to save energy. Study of alignment has a heuristic potential: It informs about motivation and sensory capacity of an animal. The hierarchy of senses, motivation, and actual requirement determine which kind of alignment may prevail (and mask other possible kinds of alignment). Magnetic alignment (= alignment with respect to magnetic field lines) is one type of sensory alignment with all the attributes mentioned above. For many animals the magnetic sense is an ordinary sense guided by similar principles as other senses. The selection pressure on the magnetic sense may be lower than in the case of most other senses. Accordingly, individual variability in its efficacy may be larger than in the case of other senses (cf. color blindness, tone deafness, or different types of anosmia in humans). Even in the context of spatial orientation it may be inferior to other senses. We point out misunderstandings of the concept of magnetic alignment and caveats of its study in the lab and in the field. We present examples of mammals displaying magnetic alignment in different behavioral contexts and discuss its putative meaning in the context of cognitive mapping, crossmodal integration, directional or slope indicator, and distance measuring.

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Species boundaries in the dasyurid marsupial genus *Pseudantechinus*: Is *Ps. roryi* a valid species?

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The dasyurid marsupial genus *Pseudantechinus* comprises five currently recognised species: *Ps. bilarni, macdonnellensis, mimulus, ningbing* and *woolleyae*. The status of another species (*Ps. roryi*) erected by Cooper *et al.* (2000) has been questioned by Westerman *et al*. (2008) on the basis of DNA sequence data. To resolve this question we have extended the molecular study to include animals from a greater part of the species' range as well as the holotypes of '*macdonnellensis*' and '*roryi*' *sensu* Cooper *et al*. (2000). We include DNA from both mitochondrial (mitDNA) and nuclear (nDNA) genes but can find no molecular evidence for the continued recognition of '*roryi*' as a separate species within *Pseudantechinus*. Patterns of genetic variability in other species of *Pseudantechinus* will be discussed.

Cooper, N.K., Adams, M and Aplin, K.P. (2000). A new species of false antechinus (Marsupialia: Dasyuromorphia: Dasyuridae) from the Pilbara region, Western Australia. *Records of the Western Australian Museum* **20**: 115-136.

Westerman, M., Young, J., and Krajewski, C. (2008). Molecular relationships of species of *Pseudantechinus, Parantechinus* and *Dasykaluta* (Marsupialia: Dasyuridae). *Australian Mammalogy* **29**: 201-212.

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Wild source, founding and inbreeding in South African pet sugar gliders

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Over the last 15 years, the Australopapuan marsupial sugar glider (Petauridae: *Petaurus breviceps*) has become popular throughout the world as an exotic pet species. Here we present an investigation of genetic diversity, based on multilocus microsatellite genotypes and DNA sequence data, in a sample of 80 pet sugar gliders from South Africa. Our objectives were to infer the source region of these gliders, to estimate the effective size of the South African pet population, as a proxy for the number of founders, and to ascertain the risk of inbreeding depression in this captive population. Phylogeographic analysis of sequences from mitochondrial (ND2 and ND4) and nuclear loci (Omega Globin) suggests that the founders contributing to this sample were obtained from at least two distinct wild populations. The estimated effective population size is close to our sample size, implying that many founder individuals were imported into South Africa. Diversity within the captive population is high relative to that recorded from wild populations in Australia, consistent with admixture of founders from diverse and divergent sources. Although relatedness and inbreeding coefficients vary substantially among groups, there is low risk of inbreeding depression if breeders avoid mating close relatives. We discuss these results in the context of global trade in sugar gliders and the sustainable management of recently established captive mammal populations.

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Rainfall and topography predict gene flow among populations of the declining northern quoll (*Dasyurus hallucatus*)

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Landscape attributes often shape the spatial genetic structure of species. As the maintenance of genetic connectivity is increasingly a conservation priority, the identification of landscape features that influence connectivity can inform targeted management strategies. The northern quoll (*Dasyurus hallucatus*) is a carnivorous marsupial that has experienced dramatic population declines in recent decades. To inform management of surviving *D. hallucatus* populations across north-western Australia we examined the genetic structure of populations, and identified landscape features that influence gene flow within the Kimberley region. We sampled 249 individuals from 28 populations in three regions of north-western Australia, including the Kimberley, Pilbara and Kakadu. Genetic structuring was evident between the three regions and to a lesser extent between the north and central Kimberley. Landscape genetic analysis of Kimberley populations suggest this structuring may be due in part to the indirect effects of differences in rainfall between these two areas. Also, *D. hallucatus* populations with large areas of open habitat between them tended to be more genetically similar. Managing threats such as the occurrence of intense and frequent fires, and the density of introduced herbivores, could support the persistence of *D. hallucatus* populations, particularly in areas with high rainfall and flat terrain, where greater genetic connectivity confers a better chance of long-term population survival.

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Factors affecting the diversity of terrestrial mammals in oil palm dominated landscapes in Colombia

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Colombia is the largest producer of oil palm in the Americas. However, the impacts of the expansion of this crop on native fauna remain unclear. Using camera trap records, we evaluated the effect of oil palm and other landscape and local factors on richness and composition of mammals in the Eastern plains or Llanos Orientales of Colombia. We detected 26 species in total (plus 3 with direct observation) of which 17 species were shared between both land use/cover. Oil palm richness was on average 47% lower than forest, and species composition varied greatly between sites and species. Apart from jaguarundis and foxes that were more abundant in oil palm, and giant ant eaters that displayed similar (high) abundances in both forest and oil palm, other species had significantly lower abundances in oil palm plantations compared to native forest. The most important driver for richness and composition at the landscape scale was land use/cover, for which oil palm had a strong negative relation. Cattle and undergrowth vegetation had an important negative and positive influence, respectively, for richness and composition inside oil palm plantations, whereas no vegetation covariates inside forests emerged as important drivers for diversity. Oil palm plantations are expected to expand in this region of Colombia, and our results suggest that improvement of habitat complexity inside the plantations as well as maintenance and restoration of secondary forest is important in maintaining the diversity of mammalian species enhancing the conservation value of this human-dominated landscape.

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Mammal diversifications followed the Triassic-Jurassic and Cretaceous-Paleogene mass extinction events

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Recent molecular divergence estimates for placental mammals recapitulate their explosive interordinal diversification inferred from the Paleocene fossil record, but place this event some 10-20 million years earlier than apparently observed in the fossil record. We show that current models of molecular evolution do not adequately account for parallel rate changes, and result in dramatic divergence underestimates for large, long-lived mammals such as whales and hominids. Calibrating among these taxa has shifted the rate model errors deeper in the tree, inflating interordinal divergence estimates. We employ simulations to understand how such rate errors interact with fossil calibration strategies. We find that focusing on calibrations for taxa that retain “primitive” life-history characteristics substantially improves molecular dating accuracy. Applying this strategy to the empirical data favours the traditional palaeontological interpretation – a few Cretaceous placental lineages gave rise to an explosive diversification following the 66 Ma Cretaceous-Paleogene boundary mass extinction. This scenario closely aligns with a growing consensus for a similar model for bird evolution. Looking further back at the origin of mammals, we combine morphological and molecular data to merge fossils into the modern mammal tree. As a remarkable forerunner to the later placental diversification, we find that monotremes and therian mammals originated during a rapid adaptive radiation associated with the Triassic-Jurassic mass extinction event. Ancestral state reconstruction and lineage survival patterns suggest strong selection for traits enhancing endothermy around this origin of crown mammals.

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The role of climate in shaping mammalian body size distributions over the Cenozoic

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Understanding how ecological communities are organised and how they change through time is critical to predicting the effects of climate change. Studies on modern communities find that the shapes of body size distributions are weakly related to climatic variables and more strongly to habitat type, with flat distributions common in temperate habitats and peaked distributions common in tropical ones. In essence, increased habitat structure and productivity lead to more peaked body size distributions presumably because a greater number of ‘medium’ sized mammals can be supported. Because there have been major changes in mammalian community composition, body size, and global climate over the last 65 Ma, we ask how these patterns play out over geologic time. Using a database of Cenozoic mammal communities collected from the literature that spans multiple continents and habitat types, we analysed the shapes of community body size distributions and their relationships to habitat type and global climate. We find that 1) local body size distributions of Cenozoic mammals are weakly correlated with climate and more strongly with habitat type, 2) archaic and modern mammals show similar patterns in their body size distributions, and 3) maximum body size observed in local communities increases as mammals evolve larger body sizes and is correlated with climate change. The remarkable similarity in these patterns over the last 65 million years suggest a fundamental role of body size in community assembly, and that modern and archaic mammal faunas respond in similar ways to the environmental template.

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After the mammoths: Changes in the structure and function of mammal communities after the terminal Pleistocene megafauna extinction

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Globally, the majority of large-bodied wild mammals are at risk. The modern biodiversity crisis is a major conservation concern because the loss of these animals also means the loss of their ecological roles within communities. Growing evidence suggests mega-mammals have a disproportionate influence on the function of modern ecosystems, although a comprehensive understanding of their role remains elusive. Here, we use the late Pleistocene megafauna extinction as a proxy to examine the changes in the structure and function of a local mammal community after the catastrophic loss of 80% of large-bodied taxa. Hall’s Cave, in the great plains of Texas, has an unparalleled 20 ka geologic record that allows us to characterise the community before and after the extinction event at 13 ka. We employ the null model program PAIRS to evaluate the strength and type of mammal associations over time. The number and strength of interactions yields insights about the cohesion and resilience of ancient and modern ecosystems. We find that ancient ecosystems were more tightly structured than modern ones. Not only did extinct species form significantly more species associations than today, but the average interaction strength was also significantly stronger. Moreover, unlike modern communities, both positive (e.g. predatory-prey) and negative (e.g. competition) interactions were important before the extinction. In particular, extinct carnivores were much more tightly associated with their prey base than modern species. Our results suggest many fundamental aspects of mammalian communities changed with the loss of megafauna at the terminal Pleistocene.

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Fossilised birth-death priors on phylogenies given rate heterogeneity in the fossil record of carnivoran mammals

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Estimates of origination, extinction and sampling rates allow us to put prior probabilities on the divergence times of clades within phylogenies. Although these are easy to estimate given homogenous rates over time, origination, extinction and sampling all vary from one time interval to the next. Moreover, these rates can vary within the same clades on different continents. Additionally, sampling rates vary among taxa within clades simply because most species occupy relatively few areas whereas some occupy many areas. “Fossilized birth-death” models can be modified to accommodate these variations over time, space and taxa. I present an example here with North American and Eurasian Carnivora. Carnivora are one of the few known examples of a clade in which turnover rates differ between North America and Eurasia as well as over time. Carnivoran sampling rates also have been shown to vary over time, and to typically show lognormal distributions among species. Phylogenies are ideally suited for accommodating geographic variation in rates because phylogenies simultaneously allow us to estimate probabilities of unsampled lineages being present in different areas. Thus, the prior probability of a branch given Eurasian or North American rates can be weighted by the probability that the lineage was present in either area. Notably, the greatest effect on divergence priors comes from rate heterogeneity over time; however, there are small effects of biogeographic and taxonomic heterogeneities, and the ability to accommodate them should provide added confidence in the final results.

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Integrating modern and fossil museum collections to resolve taxonomic problems: The journey of a Churchill Fellow

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Museum collections often house some hidden treasures. New species are sometimes found amongst specimens of another, unnoticed for decades. However, specimens can often be scattered across several museums, in different states or countries, making it difficult and expensive to access and study them properly. The Churchill Fellowship, supported by the Churchill Trust, gives a unique opportunity to travel to multiple museums in multiple countries, to undertake such study. This journey will aim to study closely all museum specimens in the order Peramelemorphia (bandicoots and bilbies), to review type specimens, historical specimens (collected in the 1800s), and even fossil specimens (as old as later Oligocene in age), to uncover new species, revise current species, and uncover the evolutionary history of this group. The results of this journey, undertaken in April and May 2017, will be presented, providing a unique insight and highlight future research that can help continue broadening our understanding of this order of mammals.

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Coyote use of the urban core: Variation in movements, activity, diet, and conflict implications

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Coyotes (*Canis latrans*) have recently become top predators in most metropolitan areas across North America. Despite their ubiquity, the full extent to which they exploit urban landscapes is still poorly understood, especially within the urban core or the most heavily developed parts of the metro area. Our overall objective was to provide a more detailed analysis of coyote use of a heavily urbanised landscape, including the urban core, compared to suburban or natural areas. As part of a long-term monitoring project, since 2000 we have captured and marked over 1,070 coyotes from the Chicago, Illinois, USA, metropolitan area, an area that includes a population density of over 9 million people. We used the full sample for demographic analyses, which revealed largely consistent survival rates across years and across the landscape, including highly urban territories. We used a subset of intensively-monitored GPS-collared coyotes for analyses of space use for resident animals. Urban core territories (MCP) were relatively large owing to dispersed habitat patches, but more refined models (LoCoH) revealed similar-sized use areas across landscape classes. Diet profiles obtained from stable isotope analysis revealed substantial individual variation in diet, ranging from exclusive natural prey to exclusive anthropogenic foods, even for those residing within the urban core. Coyotes are now exploiting nearly all areas of the Chicago landscape, including the urban core; nevertheless, the frequency of nuisance coyotes has remained low across years regardless of location or length of time near people.

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Identifying space use and resource utilisation to understand drivers of human-wildlife conflict: Dingoes (*Canis dingo*) on Fraser Island (K'gari)

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Patterns of conflict in a number of carnivorous species have demonstrated that human-wildlife conflicts may be predictable. However, minimisation of human-wildlife conflict depends on the ability to anticipate the behaviour of each party involved, as well as the timing and location of conflicts. Conflict mitigation requires knowledge of the drivers of these conflicts, including patterns of landscape utilisation of the wildlife species involved. This information is lacking for the dingoes (*Canis dingo*) on Fraser Island, Queensland. We investigated home range, resource selection and landscape utilisation by Fraser Island dingoes by evaluating for the effects of habitat type and distance to landscape features and areas of high human usage. We used resource utilisation functions (RUFs) to compare resource utilisation at the dingo population level, as well as individuals grouped by sex and age class. Significant differences were found in home range between sexes and day phase, so resource selection analyses were stratified according to these groupings. We show how resource utilisation is influenced by geographic factors (i.e. variation in habitat), temporal influences (i.e. day phase) and population dynamics (i.e. sexes and age). These findings have direct management implications for reducing conflict between people and the dingoes of Fraser Island, and demonstrate the importance of knowledge of landscape utilisation patterns in strategies to minimise human-wildlife conflict.

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Mining for trouble: The population, behaviour and management of dingoes living within a remote Australian mining operation

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A change in resource availability and the provision of human-related sources of food and water to wildlife has a direct impact on the ecology, behaviour, and abundance of predators. In Australia, mining operations established in remote arid zones offer an attractive haven for wildlife, particularly dingoes (*Canis dingo*). Regular interaction between dingoes and humans at these locations increases the risk of ongoing human-wildlife conflict (incidents) that range from theft and property damage, to direct attack. The presence of large numbers of dingoes represents a significant challenge for management authorities charged with minimising risk to human safety, while also trying to conserve the local wildlife. I present a case study of a large mining operation in Western Australia (Great Sandy Desert), with the aim of understanding the impacts such environments have on dingo biology and behaviour, as well as determining the nature of the human-dingo interactions. This includes a comprehensive summary of the dingo population and population dynamics (including den site activity, and territorial boundaries), diet, attitudes towards dingoes and dingo management, and the nature of negative human-dingo incidents. I conclude by discussing the challenges of managing dingoes in a way that fosters co-existence.

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Co-occurrence of meso-carnivores in a human dominated landscape in Mahrashtra, India.

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Identifying factors influencing the distributions and interactions within the carnivore communities is particularly important in human dominated landscapes. In India, few ecological studies of wildlife have been conducted in such areas despite the increasing recognition of their conservation value. Nevertheless, recent research has revealed a rich faunal diversity in areas of high human population density. Within the carnivore guild, species differ in their ability to adapt to human influence depending on their degree of specialisation in habitat use and feeding habits. In our study, we investigated determinant factors for the occurrence and coexistence of meso-carnivores in an agricultural landscape in Maharashtra, India. We used camera traps to record the activity of Indian foxes, jungle cats and jackals during their most active hours (i.e. from sunset to sunrise). We recorded 115 events of the target species during ca. 280 trapping nights from 40 camera traps located within an area of ca. 270 km^2. Using co-occurrence occupancy models in a Bayesian framework, we investigated the relative influence of vegetation composition, agricultural crop types, domestic dog activity and distances to human settlements. We found that the activity of domestic dogs is an important factor influencing occurrence, and recorded differences among the species in the flexibility in their habitat use and responses to human influence. Future management actions in these landscapes should take into account the intra- and interguild interactions of the local carnivore communities, and be directed towards the conservation of native habitats embedded in human dominated land.

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Human-carnivore coexistence: Arabian wolves spatially favor but temporally avoid humans in an extremely arid landscape

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Global increases in anthropogenic activity have had considerable effects on the abundance and persistence of many species. Because of direct interactions and livestock depredation, large carnivores have a disproportionally high risk of conflict with humans. Current evidence suggests that the survival, abundance, and persistence of these species are negatively affected by human activity. Thus, large carnivores are predicted to spatially avoid human-dominated areas. Yet, as the global human footprint grows, it is crucial to understand the circumstances when large carnivores can persist in human proximity. Using GPS location data, we quantified the space use and movement of protected Arabian wolves (*Canis lupus arabs)* in the arid Negev desert (Israel). Contrary to the spatial avoidance prediction, wolves spent a large proportion of their time in proximity of human infrastructure, suggesting a strong spatial association with human activity. Wolves showed temporal avoidance of human activity by increasing activity and movement during the night. In addition, during night, wolves used space in proximity of human infrastructure in proportion to its availability. Combined with recent diet analyses, our findings suggest that wolves nutritionally rely on human subsidies such as garbage and agricultural produce. Given the scarcity of ungulate prey resources in the surrounding landscape, wolves appeared to fine-tune their movement and space use to persist in the vicinity of humans. We conclude that legal protection and tolerance by humans can promote close spatial coexistence with large carnivore populations. Our findings may also provide a glimpse into the process of dog domestication.

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History, successes, constraints of mammal re-introductions to fenced 'mainland islands' in Australia: The experience of Australian Wildlife Conservancy

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Small- to medium-sized native mammals have vanished from most of southern and arid Australia, primarily due to predation by feral cats and foxes. These species were often very abundant prior to European settlement and participated in a number of important ecological processes, including the dispersal of seeds and fungal spores, herbivory, predation and soil engineering. The loss of these species has likely had profound consequences for Australian ecosystems. The reintroduction of threatened mammals to feral predator-free islands and fenced ‘mainland islands’ has been an important tool in conservation in Australia for several decades. Australian Wildlife Conservancy (AWC), a not-for-profit organisation, is a leading exponent of this approach in Australia. Currently, AWC operates one island and four ‘mainland island’ reintroduction projects, ranging in size from 275 ha to 8,000 ha. These projects support populations of 11 threatened mammal species, including 90% of the global population of bridled nailtail wallaby, 30% of numbat and 10% of greater bilby populations. AWC is currently planning another four ‘mainland island’ reintroduction projects, ranging in size from 2,000 ha to 60,000 ha. When complete, AWC’s network of reintroduction projects aim to support secure populations of 19 threatened mammal species, substantially increasing global population sizes of many of these species. In this talk, I review the contribution of reintroduction projects to the conservation of Australian mammals and the restoration of Australian ecosystems. I consider three key issues: the value of reintroduction projects for conservation, the lessons learnt from existing projects and future directions for reintroductions.

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Fences and their foibles: Matuwa, a case study.

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The arid and rangeland areas of Australia have suffered a high rate of loss and decline of mammal fauna in the past 200 years. Fauna reconstruction is one of the ecologically integrated components of the Rangelands Restoration Project, which aims to restore natural ecosystem function and biodiversity at a landscape scale. The project is being undertaken on the Matuwa Kurarra Kurarra Indigenous Protected Area (formerly Lorna Glen and Earaheedy pastoral leases), on Martu traditional lands, in the northern Goldfields region of Western Australia. Direct wild translocations of several threatened mammal species to Matuwa in 2007-2009 had mixed success, with some heavily impacted by introduced predators such as feral cats and wild dogs. Following this outcome, a 1,100 ha feral predator proof fenced exclosure was constructed in 2010. Its aim was to create a protected area in which species’ could acclimatise to the environment before being wild released, and where secure populations of more predator sensitive species’ could persist for extended time periods, until improved environmental conditions and translocation techniques might allow successful wild release. In this presentation, we describe the outcome of translocations into the exclosure, outlining the benefits and challenges experienced at Matuwa, and discuss the pros and cons of fenced ‘mainland islands’ generally, their unique management requirements, and their place as one tool in a larger fauna reconstruction context in Australia.

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Phillip Island Ark: Integrated invasive predator management and translocations for conservation of rare and threatened species

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Creating predator-free islands is a cost-effective strategy in the long-term to reduce their impact on island fauna. Large, inhabited islands are frontiers for eradication programs as these pose logistical as well as socio-political challenges, but offer great potential benefits. A long-term program to eradicate red foxes (*Vulpes vulpes*) was initiated on Phillip Island, Victoria, Australia, to eliminate their impact on ground-nesting birds, particularly little penguins (*Eudyptula minor*). The fox population on this 100 km^2 permanently inhabited island has been reduced to undetectable levels. A Bayesian catch-effort model has been developed to assess fox population size, the effectiveness of the multiple detection methods that have been deployed, and the probability of eradication. With the success of the fox control program, a threatened species translocation program has been initiated: Phillip Island Ark. This program has begun with a successful trial introduction on Churchill Island, near Phillip Island, of the eastern barred bandicoot (*Perameles gunnii*), a species listed in Victoria as ‘extinct in the wild’. Future translocations are being planned to return other species that have either been lost on Phillip Island or are threatened species that cannot persist in the presence of invasive predators such as red foxes. Translocation programs such as this capitalise on our ability to effectively manage invasive predators on large inhabited islands. We present common management principles and lessons learned that can guide other pest eradication attempts and ultimately save threatened species from extinction.

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The challenges of managing confined populations: Dealing with issues of overabundance and species with naturally extreme population fluctuations

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Some Australian mammals are so vulnerable to predation by introduced predators that they cannot yet survive outside of predator-free islands or exclosures. Populations of these animals are confined either by water or by fences, with no means for dispersal. For species with high reproductive potential, this confinement, even within large areas, can lead to overabundance and impacts to the animals themselves, to other vulnerable species and to the resources they all rely on. We outline the case of the burrowing bettong (*Bettongia l. lesueur*) introduced into the Arid Recovery Reserve in South Australia. Arid Recovery is a 123 km^2 predator-proof fenced reserve from which cats, foxes and rabbits are excluded from 60 km^2. Bettongs have increased exponentially from 30 founding animals in 1999/2000. The bettong population now has a measurable impact on vegetation within the reserve, with likely impacts to other reintroduced species such as greater stick-nest rats (*Leporillus conditor*) that compete for the same resources. We are researching methods to address overabundance within an adaptive framework. Options we are testing include introduction of a native predator (western quoll *Dasyurus geoffroii*), one-way gates to allow dispersal, and fertility control. Preliminary data are presented. In establishing confined populations, managers of reintroduction programs have a responsibility for good stewardship of populations in their care. In planning re-introductions, it is sensible to be conscious of the potential for overabundance, and to build management triggers into monitoring programs that initiate adaptive management to address the issue before there are adverse effects that become insurmountable.

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Maintaining genetic and adaptive diversity in island and exclosure populations

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Islands and exclosures are being increasingly considered in the conservation of many mammal species exposed to threats across their broader historic range. However, the area available on islands and exclosures will often constrain the size of any mammal population. This has implications from a genetic perspective, particularly if founder size is small, growth rates are slow or there are large fluctuations in population size. Stochastic effects are likely to predominate in these situations resulting in chance matings between close relatives (inbreeding) and genetic drift playing a greater part in the evolution of these populations, as has been seen in many island-endemic species. Often, this will lead to a loss of fitness, reduced ability to evolve, and ultimately, an increased chance of extinction. Simple genetic translocation strategies can, however, be used to limit these effects and promote the maintenance of genetic diversity in island or exclosure populations. Importantly, a network of populations on islands or exclosures creates an opportunity to not only conserve genetic diversity, but also promote adaptive divergence in populations through time, which could ultimately flow on to an increased reintroduction success elsewhere. Here I will outline different genetic strategies aimed at maintaining genetic and adaptive diversity in islands and exclosures using examples from Australian threatened species, and highlight a key future priority for their use in mammal conservation genetics.

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Vegetation dynamics at refuge sites of the plains mouse (*Pseudomys australis*) in the western Simpson Desert, Australia

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A diversity of rodents and dasyurid marsupials in arid Australia occupy refuges; discrete areas of the landscape in which populations persist during periods of low resource availability ('busts'). Refuges are assumed to provide shelter from predators, suitable microclimate for thermoregulation and food resources during the low phase of population cycles. During bust periods, refuge-using small mammal populations occur at high density in refuges and individuals are in a body condition that is comparable to that of individuals during population irruptions. Reproduction is also ongoing. These findings imply that refuge populations of small mammals have access to a reliable and high-quality food supply. We examine this issue by quantifying the vegetation dynamics at refuges of the plains mouse (*Pseudomys australis*) on cracking clay and gibber plains in the western Simpson Desert. In particular we focus on changes in richness and abundance of plants across the population cycle of refuge populations of *P. australis*. Refuges typically occur in areas of microrelief within the landscape. Vegetation responses in these areas are driven by rainfall. Shallow-rooted, short-lived grasses and forbs dominate the flora. These plants have the capacity to respond to small rainfall events that occur during dry periods. Among these are important food plants of *P. australis* including *Dactyloctenium radulans*, *Chloris pectinata* and *Panicum* sp.. Thus, the location of *P. australis* refuges in areas of microrelief is likely to ensure access to suitable food plants even during dry years with some food available in some patches at most times.

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Continental patterns in the diet of an apex predator: Australia's dingo

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Restoration of large carnivore populations, such as dingoes, is controversial as these animals can prey on livestock and threatened species. Developing an in-depth understanding of dingo dietary preferences across Australia's bioclimatic zones may assist restoration proposals, especially if this helps to predict the types of impacts dingoes could exert on prey species and ecological processes such as bioturbation, herbivory and predation. Using 73 published and unpublished data sets, we examined bioclimatic variation in dingo diet across Australia, and focus here on the arid interior and temperate south-east of the continent. Dingoes consume at least 188, mostly mammalian, vertebrate species. Consumption of arthropods, birds and reptiles was highest in the arid and semi-arid regions, and lowest in the temperate south-east. Consumption of introduced rabbits was highest in the arid zone, and consumption of medium-sized mammals (0.5–6.9 kg) was highest in the temperate south-east. Dietary diversity was higher in the arid zone than in the temperate south-east. We use our results to describe dingo dietary patterns at the continental scale and discuss conservation and management implications.

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Northern quoll in the Pilbara: Diet, space use and population dynamics of a marsupial carnivore

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Good knowledge of species ecology is critical for effective management and conservation decision-making. The remote and spatially isolated Pilbara population of northern quolls (*Dasyurus hallucatus*) had not been well studied, but the presence of this endangered species in rocky areas targeted by the mining industry requires careful management actions. Toxic cane toads (*Rhinella marina*) threatening northern quolls elsewhere have not yet invaded the Pilbara, where northern quolls suffer a different suite of threatening processes including habitat loss via mining and associated infrastructure, inappropriate fire regimes, as well as introduced predators (especially feral cats, *Felis catus*). Pilbara northern quolls were prioritised for ecological and demographic research according to key knowledge gaps. We present an enhanced dataset of northern quoll distribution, population analysis via genetics, and temporal and spatial differences throughout the region. To better understand their habitat requirements, we analysed 498 scats collected across ~100,000 km^2, and calculated dietary composition for 10 study landscapes. This small marsupial was found to be highly omnivorous, consuming at least 23 species of vertebrates (mammals, birds, reptiles, frogs), as well as arthropods, molluscs, fruit, and carrion. There were not strong differences between sites within the Pilbara, but the species was shown to be highly opportunistic with dietary strategies of carnivory, herbivory and scavenging. A better understanding of this endangered species will assist in effective protection of the Pilbara population as future threats emerge.

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Who killed the wolf spider? Intraguild predation among taxonomically disparate micro-carnivores

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Successful foraging is important for animals to fulfil their specific energy and nutrient requirements. However, as these resources are generally limited, competition often arises. Intraguild predation (IGP) is a distinctive form of interference competition where a dominant predator selectively kills subordinate species and thereby gains increased access to resources. This asymmetrical interaction has been documented primarily among carnivores, with few examples from different taxonomic levels. We present such an example here. The lesser hairy-footed dunnart (*Sminthopsis youngsoni*) is a common generalist insectivore in arid Australia that has been shown to consume wolf spiders (Family Lycosidae) disproportionately often relative to their availability. In this study, we tested three hypotheses to uncover the underlying mechanisms driving this selective predation. Lycosids were not found to contain more energy, water or nutrients than other available arthropod prey, discrediting the hypothesis that *S. youngsoni* forages to optimise nutritional or caloric intake. However, we found a high degree of spatial and temporal overlap in resources (diet and microhabitat), providing support for the hypothesis of competition. This latter hypothesis, and the operation of IGP, was further supported by the results of cafeteria-style trials showing that *S. youngsoni* selectively targets lycosids when alternative prey types are equally available. This study is the first to uncover IGP between such taxonomically disparate groups, and its consequences extend beyond simple predator-prey relationships to suggest that IGP can have substantial impacts on community structure and ecosystem processes.

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Using accelerometers to determine the behaviour of wild dingoes

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The recent application of accelerometers for remotely classifying animal behaviours has improved our understanding of the ecology and physiology of many taxa. Statistical models are employed by researchers to predict specific behaviours using incremental changes in an animal's acceleration. However, model construction is not standardised with covariates often selected and modified arbitrarily. The aims of this study were twofold: 1) To produce a rigorously tested and repeatable statistical method for accurate classification of ecologically important behaviours from low-frequency (1Hz) acceleration recordings, 2) Apply this method to determine the behaviour of a wild population of Australia's largest terrestrial predator, the dingo (*Canis dingo*). We categorised six behaviours using video footage of captive dingoes fitted with accelerometers and manually annotated them to the raw acceleration data. The predictive ability of five widely employed classification models was compared by systematically testing different combinations of covariates followed by cross-validation. We then applied our best model to accelerometer data recorded from wild dingoes at Kalamurina, South Australia. Our best model predicted walking, running, trotting, foraging, standing, and lying down with >85% accuracy. Our study is the first to quantitatively measure behaviours in free-ranging dingoes, revealing a proclivity for lying down and no significant relationship between dingo activity and time of day. Interestingly, dingoes foraged in a temporally cyclical pattern, specific to individuals. The ability to classify ecologically important behaviours using such low-frequency data enables months of per-second behavioural information, which when integrated with GPS data will catapult our understanding of how animals interact with living systems.

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Underground rivers and the mammals that use them on Mexico's Yucatán Peninsula.

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Vast underground rivers flow through the limestone karst beneath the jungle on Mexico's Yucatán Peninsula. Mostly unseen, these rivers are accessible at cave entrances or 'cenotes' wherever the limestone cavern has collapsed. Because of the absence of flowing water above ground, cenotes are vitally important to the mammals of the Yucatán, providing a reliable source of freshwater and a favorable thermal environment to retreat from the heat of the jungle. However, development is happening apace on the Yucatán, and threatens the water quality in the cenotes. In addition, massive growth in tourism is turning many of these cave entrances into a busy tourist attractions with an unknown effect on wildlife attempting to share this limited and unique environment. We placed heat-in-motion camera traps at or inside the entrances of cenotes at a complex of cenotes near Akumal on the Yucatán Peninsula. Cameras recorded 1-minute-long videos of mammals using the cenotes, and often allowed us to determine activity of animals visiting cenotes. Our preliminary work has revealed a diversity of mammals regularly using cenotes as watering, denning, hunting, resting and mating sites. Notable mammals recorded in cenotes include jaguar (*Panthera onca*), puma (*Puma concolor*), northern tamandua (*Tamandua mexicana*), gray fox (*Urocyon cinereoargenteus*), tayra (*Eira barbara*), and white-nosed coati, (*Nasua narica*). Future work aimed at describing the biophysical features of cenotes, and linking these to mammal occupancy, will be discussed.

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Advances in camera-trapping network of Sino Bon-Mammals

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Recently launched by the Chinese Academy of Sciences, the Mammal Diversity Monitoring Network of Sino Bon (Sino Bon-Mammal) is one key member of the Biodiversity Monitoring Networks of Sino Bon for the monitoring and inventory of terrestrial mammal resources in China. My talk reviews some major advances in terrestrial wildlife observation using camera trapping in China. During the past decades, camera trapping has been used worldwide for species inventory and monitoring of terrestrial vertebrates such as medium- and large-sized mammals and birds. Since 2011, Sino Bon-Mammal launched a camera-trapping network for long-term monitoring of terrestrial vertebrates across China. We developed long-term camera-trapping monitoring protocols, and established CameraData (http://cameradata.ioz.ac.cn) as public database for data management, sharing, collaboration and information services. In addition, Sino Bon-Mammal also organized regular training courses and conferences, and published three special issues about camera trapping data from more than thirty protected areas such as natural reserves. This overview will be helpful for the development of a global observation program of wildlife diversity.

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Research on snow leopards using camera-trapping in Wolong Nature Reserve, China

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Snow leopards (*Panthera uncia*) are mainly distributed in the high mountainous or plateau areas of the middle Asia including 13 countries or regions. It is an endangered species with a wild population of 4,510–7,350 individuals. It has been reported that Wolong Nature Reserve (WNR) has the snow leopard, however, very few studies have been implemented on it in WNR. Our purpose is to monitor this species in WNR using infrared cameras. Between November 2013 and March 2016, twenty Ltl-6210MC infrared cameras were installed to monitor snow leopards. A total of 7,056 camera-days of data were collected including approximately 120,000 photos and video clips. The effective number of snow leopard samples collected by the cameras was 43, and the relative abundance index for this species was 6.09. During the 28 months of continuous data collection, records of snow leopards demonstrated that WNR is a relatively hospitable environment for this species. The analytical results indicated that the annual activity of snow leopards peaked in January, and the daily activity peaked between 18:00–20:00. The leopards' daily activity patterns showed seasonal variation. The preferred habitat is the alpine scree where snow leopards appeared most in the ridge areas. The preferred reference temperature was between –10℃ and –3℃. It was found that the snow leopard is fairly active at night, and the lunar-phase has a significant impact on its level of nocturnal activity ($P < 0.01$). This study provided primary sources for further protection and research on snow leopards.

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A picture tells a thousand words - the hidden benefits of camera trapping

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As a private land manager the Tasmanian Land Conservancy needs long term data to better understand the natural variability of mammal populations over time, and to track their response to on-ground management. This is especially important for short-lived, wide-ranging carnivores like Tasmanian devil and spotted-tailed quoll, both now threatened with extinction. In 2014 the TLC commenced an annual mammal monitoring program across its 11,000 ha Five Rivers Reserve using camera traps at 44 sites. In four years we have established basal relative abundance and occupancy data for 15 terrestrial mammal species, and we have learned so much more. We have mapped the distribution of feral cats, tracked the spread of invasive fallow deer, confirmed the status of Tasmanian devil facial tumour disease and monitored the health of common wombats susceptible to sarcoptic mange. Our analysis has been aided by a citizen science program 'Wildlife Spotter' crowdsourcing hundreds of on-line volunteers from around the globe to remotely classify over 12,000 fauna images via a web-based interface. The simplicity of this monitoring program and the capacity for broader community involvement has translated into a significant conservation benefit for us, for others and for nature. This collaboration will help sustain our monitoring program into the future, and that's what simple but effective ecological monitoring is all about.

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The scientific consequences of stolen camera traps

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The theft of scientific equipment from the field has long been the bane of a scientist's life. Often the theft of such equipment is fruitless because most thieves can't use the equipment they steal. However, with the rise in use of camera traps globally, such a general piece of technology has wide appeal to thieves and criminals because they are perceived as a threat to illegal activities, or be potentially valuable to them through on-sale or anti-social personal use. Despite going to some extraordinary lengths to prevent and reduce theft of camera traps, our research team has suffered some serious financial and data losses over the last 7 years. In 2016-17, we conducted a survey to quantify the significance of camera trap theft globally. In this paper, we will provide an overview of the survey results from >300 practitioners, the financial losses, methods used to avoid theft and importantly the effect of theft on the deployment of camera traps and data collection. Moreover, we will outline the potential effects of theft on experimental design and propose some options to address this impact on wildlife surveys.

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Kalahari aardvarks on the edge: drought-induced resource deficiency may compromise aardvark survival under climate change

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Aardvarks (*Orycteropus afer*) are keystone African mammals, with multiple species dependent on their burrows as shelter, including from temperature extremes. Thermal refuges may buffer impacts of climate change for these commensal species, yet the aardvark itself may be compromised; a recent summer drought in the Kalahari semi-desert resulted in high aardvark mortality. For two years we studied vegetation productivity, prey availability, diet, body condition, body temperature, and activity patterns of free-living aardvarks in the Kalahari. Termites were the principal prey item, comprising ~75 % of aardvark diet and providing ~90 % of dietary energy and water. Termite abundance was linked directly to grass availability, which was dictated by rainfall. Under non-drought conditions, aardvarks met their energetic needs, tightly controlled their 24-h body temperature rhythm (36-37 °C) and were active nocturnally. A drought-induced vegetation decline likely caused local termite population crashes. Concomitantly we recorded a marked deterioration of aardvark body condition and a shift to diurnal activity, including midday foraging and basking. Nutritionally-stressed aardvarks exhibited high 24-h body temperature variability around a mean of ~35 °C, with 24-h minimum body temperature as low as 26 °C. Drought-induced vegetation decline that reduces termite populations likely will occur more frequently under climate change in Africa, and threaten the survival of aardvarks. We have shown that measurement of body temperature and activity patterns provided direct indicators of physiological well-being of aardvarks and, combined with vegetation indices reflecting resource availability, could predict future aardvark survival.

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Coat colour change pattern in Alpine mountain hares (*Lepus timidus varronis*) along an altitudinal gradient in Grisons, Switzerland

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Alpine mountain hares are a glacial relict species in the Alps and can be found between 700 and 3800 m a.s.l. They show a coat colour change from brownish in summer to white in winter. The white fur provides camouflage and a better insulation, likely increasing winter survival. We hypothesise that the seasonal phenological timing of the coat colour pattern is under high selection pressure as observed in the related snowshoe hares and that the pattern is adapted to the environmental differences along an altitudinal gradient characterised with increasing snow cover duration. To test our hypothesis, we used data from regular hunting in the Canton Grisons, where about 1000 mountain hares are harvested every year. Hunters were asked to report the day and altitude of their hunting bag and to provide a photograph of the shot individual. Photographs were used to estimate coat colour (in % white). We collected datasets of 235 shot hares between 2012 and 2016 during the hunting season in autumn (October-November). The altitudinal range was between 1250 and 2960 m a.s.l. Coat colour was analysed in relation to calendar week, altitudinal class and bio-geographical region. Our results reveal strong relationship of coat colour moult pattern and altitude, with earlier change into white fur at higher altitudes. The results are discussed in the light of global warming with shorter snow cover

duration, genetic diversity and adaptability in highly fragmented populations and additional threats by European hares (*L. europaeus*) moving to higher elevations and heavy winter tourism.

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Mismatched environments and maternal effects: Gestational experience influences stress responses when environments change

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The environment that a mother experiences during her own gestation can have long lasting physiological and behavioural implications for her offspring, mediated via maternal effects. Although these maternal effects act at the level of the individual they influence population and ecological dynamics, through offspring traits such as dispersal and reproduction. Glucocorticoids are transferred from mother to offspring *in utero* and can result in maternal effects that persist into adulthood, including both physiological and behavioural alterations linked to offspring success in different environments. We manipulated the maternal hormone environment during late gestation in mice and tested how a low-stress prenatal environment influenced offspring behaviour as adults both in a novel environment and in response to a stressor. We found that exploration was not influenced by maternal stress levels, except when mice were exposed to a stressor. Offspring from low-stress mothers exhibited less exploratory behaviour and more fearful behaviour in novel environments and after exposure to an acute stressor. These results demonstrate a hormonally-mediated maternal effect that persists into adulthood, with strongest effects when environments change. We discuss the implications for an individual’s ability to respond to environmental challenges, and the implications for population dynamics.

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Climate-mediated variability in predator-prey dynamics: Impacts of climate change on snowshoe hares

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Predicting the impacts of climate change on community structure remains challenging due to the complexities in understanding how climate disruption will alter predator-prey dynamics. Predator species may be increasingly favoured if consumption rates are increased under climate change through improvements in variables such as capture efficiency. In multi-predator systems, changes in risk may result in either additive or compensatory mortality on the prey species depending on whether climate change leads to similar or inverse relationships in the consumption rate of each predator. These intricacies of climate change remain largely unexplored, mainly because of the difficulties of monitoring detailed changes in climate conditions coupled with cause-specific survival of the target species. Snowshoe hares (*Lepus americanus*) are a keystone prey species of the boreal forest, and the numerical response of several predator species are associated with their fluctuating abundance. Hares have a lower foot load relative to other species, providing them with an advantage in soft, deep snow over their predators. Increased temperatures and the frequency of freeze-thaw events may increase susceptibility of hares to predation throughout their range by reducing snow depths and increasing snow hardness. Cause-specific survival of snowshoe hares in the Yukon, Canada was monitored for three winters along with daily climate conditions such as temperature, snow depth and hardiness. We demonstrate complexities of climatic drivers on hare mortality risk from their two main predators, Canada lynx (*Lynx canadensis*) and coyote (*Canis latrans*) and discuss the potential importance of these findings on hare population dynamics over time.

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Tissue isotope ratios of California vole museum specimens indicate physiological responses to historical drought and land use patterns

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California has experienced increased drought frequency and intensity in addition to anthropogenic shifts in land use over the past 120 years. We used stable isotope analysis of California voles (*Microtus californicus*) from museum collections to assess relationships between isotopic composition of vole tissues and known patterns of drought and agricultural intensification. By associating δ^{15}N values of dated hair tissue with monthly statewide drought metrics, we observed a direct relationship between δ^{15}N values and drought intensity. Geospatial patterns of δ^{34}S values of hair tissue reflects baseline isotopic enrichment of coastal habitats with marine-derived sulfate inputs. However, comparably enriched δ^{34}S values in the southern-most inland localities appear to reflect anthropogenic effects on sulfur cycling via sulfur fertilization of croplands and subsequent sulfur transfer offsite in dissolved oxidized and isotopically enriched forms. Stable isotope analysis of museum specimens can thereby provide a climate record based on physiological performance of a study species in a region affected intensely by anthropogenic activities. To follow up such findings, a fine scale analysis of isotopic changes in modern populations over time and over varied climatic conditions is desirable.

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Are hibernators toast?

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The environmental changes caused by global warming will affect many organisms worldwide (Huey et al. (2010) Science 328:832-833). At first glance ‘heterothermic’ species, which are those that enter daily torpor or hibernation (multiday torpor), may appear to be most threatened because torpor is characterised by pronounced reductions of metabolism and body temperatures and therefore requires low temperatures to maximise energy savings. Seasonally hibernating species are potentially vulnerable because many have a well-defined winter dormancy that is closely synchronised with historical phenological patterns and may be unable to appropriately adjust their behaviour and physiology to the altered environment. Moreover, a change of climate may increase the energetic costs of hibernation and lead to the extinction, especially of species restricted to ‘sky islands’ with limited mountain habitats. In contrast, many other heterothermic species express torpor opportunistically and effectively at any time of the year including in summer. Opportunistic torpor can also be used to deal with environmental disasters such as cyclones and fires predicted to increase with climate change. As use of torpor reduces foraging requirements and therefore exposure to predators, which often invade areas after adverse events, and because heterothermic mammals generally have longer lifespans than related homeotherms (cannot use torpor), heterotherms will have an increased chance to cope with adverse periods. Consequently, those heterothermic species with plastic energetic requirements may also stand a better chance of survival than do homeotherms in a world with changing environmental conditions and greater climatic extremes.

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Persistence, entertainment and function of biological rhythms in a changing Arctic: Investigations of a free living arctic hibernator.

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Climate warming is predicted to lengthen the growing season, particularly at high latitudes, which provides increased foraging opportunities, although biological interactions can also be disrupted due to intra- and inter-specific variability in the response to climate forcing. Using patterns of body temperature in free-living arctic ground squirrels we can precisely determine the timing of key seasonal events including hibernation, mating and parturition, and immergence and emergence from the hibernacula. Long-term data collected from two arctic ground squirrel populations living 20 km apart that differ in timing and duration of snow-cover indicate that individuals can adjust their seasonal timing. Additionally, it has been hypothesised that a seasonal absence of circadian rhythms is common to all vertebrate residents of polar regions. While free-living arctic ground squirrels do not express circadian rhythms during the heterothermic and pre-emergent euthermic intervals of hibernation, they display entrained daily rhythms of body temperature throughout their active season which includes six weeks of constant sun. In winter, ground squirrels are arrhythmic and regulate core body temperatures to within +/-0.2 ºC for up to 18 days during steady-state torpor. In spring, after use of torpor ends, male but not female ground squirrels, resume euthermic levels of T_b in their dark burrows but remain arrhythmic for up to 27 days. However, once activity on the surface begins, both sexes exhibit robust 24-h cycles of body temperature. We suggest that persistence of daily rhythms through the polar summer enables ground squirrels to minimise thermoregulatory costs.

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The effects of epidermal fatty acid profiles, triacyl- and monoacylglycerols, and wax esters on the susceptibility of hibernating bats to infection with *P. destructans*

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White nose syndrome (WNS) is a cutaneous infection caused by the psychrophilic fungus *Pseudogymnoascus destructans (Pd)*. WNS has caused extensive mortality in hibernating North American bats, particularly *Myotis lucifugus, M. septentrionalis, M. sodalis*, and *Perimyotis subflavus*. The epidermis of *M. lucifugus* contains free fatty acids (FFAs) that have been shown to inhibit the growth of *Pd* in laboratory experiments – they are 14:0, 16:1, 18:1, and 18:2. However, the effects of other cutaneous lipids which contain these fatty acids on the growth of *Pd* has not been tested. In addition, the relationship between FFA depletion during hibernation and WNS susceptibility is also unclear. We thus hypothesised that 1) the FFA profile of *M. lucifugus* during mid-hibernation cannot inhibit the growth of *Pd* as well as at the onset of hibernation, 2) epidermal monoacyl- and triacylglycerols containing inhibitory FFAs may also reduce *Pd* growth, and 3) epidermal wax esters containing inhibitory FFAs reduce *Pd* growth. We conducted laboratory culture experiments with *Pd* maintained on media varying in lipid composition to test our hypotheses. We found that the early hibernation FFA profiles more effectively inhibited the growth of *Pd* than mid-hibernation profiles. We also discovered that triacylglycerols have no effect on *Pd* growth, but 1-oleoglycerol greatly reduced *Pd* growth. Finally, we found that wax esters containing 18:1, 16:1, and 18:2 can also inhibit the growth of *Pd*. These findings suggest that multiple epidermal lipids contribute to the susceptibility of bats to infection with *Pd* during hibernation.

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Exploring the phenological response of a wild hibernator to climate variation through experimental translocation.

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Phenologies represent the annual timing of life cycle events, and are the ecological traits most affected by climate change. Hibernation phenologies, however, have received considerably less attention than analogous traits (e.g., migration). As a result, we have a relatively limited understanding of natural causes of variation and, therefore, equally limited ability to forecast how wild populations of hibernators will respond to climate change. We have shown in a wild population of Columbian ground squirrels (*Urocitellus columbianus*) that natural variation in hibernation emergence date is both heritable and phenotypically plastic. We have also learned that population growth rates are lower in years of later average emergence. In total, these results suggest that emergence date is a fitness relevant trait and is likely to respond to climate change. However, the pace and magnitude of a future responses will depend fundamentally on the relative roles of phenotypic plasticity and microevolution. To further explore the capacity for these two processes in Columbian ground squirrels, we completed a reciprocal translocation experiment. Individuals were relocated across two populations varying in elevation (and consequently, emergence date) in the Rocky Mountains of Alberta, Canada. Our results confirm that Columbian ground squirrels display considerable phenotypic plasticity, but responses across the two translocations were asymmetric (individuals relocated from low to high elevation responded more effectively than those in the reverse). Responses to future climate change in this wild hibernator may thus be complex and spatially variable.

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Cold and alone? Seasonal roost choice and torpor expression differ between populations of New Zealand bats (*Mystacina tuberculata)*

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Variations in weather impact the energy budgets of endotherms depending on specific ecophysiology. While much focus has been on the thermal physiology of species that experience cold temperate winters, less is known about responses by species that experience subtle changes in seasonal weather patterns. We monitored summer skin temperatures (T_{sk}) of individuals from a North (Pureora) and South Island (Eglinton) population of New Zealand lesser short-tailed bats (*Mystacina tuberculata),* and winter T_{sk} patterns of individuals from Pureora and an offshore island (Hauturu) population using temperature telemetry. Summer T_a was only <2°C lower for the Eglinton population relative to Pureora yet Eglinton individuals used torpor on 36% of days compared to 11% for Pureora bats. Roosts housing solitary bats were warmer than those shared, and temperatures within them fluctuated less than T_a. Solitary roosts were occupied more often by Eglinton individuals (38%) than Pureora individuals (17%), with individuals from both populations occupying solitary roosts exclusively for torpor. During winter, despite a >6°C difference in mean T_a, neither torpor bout duration, nor minimum T_{sk} differed for individuals between sites. However, bats on Hauturu used short torpor (<24 hours) more frequently (51%) than in Pureora (33%). Hauturu bats preferred thermally unstable roosts and preferentially roosted inside dead punga (*Cyathea dealbata*). Site-specific roost choice and torpor patterns are apparent between *M. tuberculata* populations demonstrating T_a may differentially impact populations across a latitudinal gradient. Our results provide evidence that site and climate specific adaptations appear to be employed that affect roost choice and torpor patterns.

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Glacial allopatry vs. postglacial parapatry and peripatry: The case of hedgehogs

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Hedgehogs from genus *Erinaceus* went through the typical retractions of area of distribution during the Quaternary climate oscillations. After the last ice age, European hedgehogs (*Erinaceus europaeus*) and northern white-breasted hedgehogs (*Erinaceus roumanicus*) expanded from their Mediterranean refugia and created broad zone of sympatry within Central Europe. Although hedgehogs are well-known examples of postglacial recolonisation, the specific processes that shape their population structures have not been examined by detailed sampling and genome-wide markers. In this study, we combine information gained from classical population genetics (D-loop sequences and microsatellites) with the methods of genomics (SNPs via RADSeq). The most pronounced pattern of population structure of the northern white-breasted hedgehogs involved differentiation of the insular populations in the Mediterranean Sea and population within the secondary contact zone. Rate of recent inter-species hybridization was confirmed to be very low in this area. Recent population in post-refugial area related to Balkan Peninsula shows a complex pattern with pronounced subpopulations located mainly in the Pannonian Basin and at the Adriatic and Pontic coasts. Detailed analyses indicate that parapatry and peripatry may not be the only factors that limit range expansion, but also strong microevolutionary forces that may change the genetic structure of the species. Population differentiation at Balkan Peninsula and adjacent regions could be ascribed to diversification in steppe/forest biomes and complicated geomorphology, including pronounced geographic barriers as Carpathians.

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Genetic and morphological differentiation in rakali, the Australo-Papuan water rat (*Hydromys chrysogaster)* with implications for its taxonomic and conservation status.

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Rakali or the Australo-Papuan water rat (*Hydromys chrysogaster* Geoffroy 1804), is a large, carnivorous, semi-aquatic rodent distributed in Australia and New Guinea. Despite being the first native rodent described it remains relatively poorly researched. This study aims to clarify the species' taxonomy and conservation status through examining: 1) spatial patterns of polymorphism 2) phylogenetic relationships by partial sequencing of the cytochrome *b* gene of mitochondrial DNA) and 3) genetic structure using six microsatellite markers.There was male-bias body size sexual dimorphism, correlation between body weight and latitude, colour phenotypes and differences in tail tip albinism. Phylograms revealed presence of a separate Australian/New Guinean and New Guinean clade and reciprocal monophyly between distribution extremes, with support for subspecies differentiation in Australia. Two potential new species within New Guinea were paraphyletic with the waterside rat (*Parahydromys asper*). Nuclear DNA results indicated six major genetic clusters aligning with geographic region and isolation by distance (IBD) effect. Southwest WA and Barrow Island populations were insular and highly differentiated; remaining groups demonstrated contemporaneity of gene flow. These results reflect divergence arising from dispersal, radiations and temporal and geographic history of separation and warrant taxonomic revision of the species whilst providing guidance for conservation and management efforts.

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Between the Balkans and the Baltic: Phylogeography of a common vole lineage limited to central Europe.

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The common vole (*Microtus arvalis*) has been a model species of small mammal for studying end-glacial colonisation history. In the present study we expanded the sampling from central and eastern Europe to identify the role of a potential 'northern glacial refugium', i.e. a refugium at a higher latitude than the traditional Mediterranean refugia. Altogether we analyzed 786 cytochrome *b* (cyt*b*) sequences (representing mitochondrial DNA; mtDNA) from the whole of Europe, adding 177 new sequences from central and eastern Europe, adding data for 311 new specimens. Our new data fill gaps in the vicinity of the Carpathian Mountains, the potential northern refugium, such that there is now dense sampling from the Balkans to the Baltic Sea. Here we present evidence that the Eastern mtDNA lineage of the common vole was present in the vicinity of this Carpathian refugium during the Last Glacial Maximum and the Younger Dryas. The Eastern lineage expanded from this refugium to the Baltic and shows low cyt*b* nucleotide diversity in those most northerly parts of the distribution.

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SNP versus mtDNA: Genomic phylogeography of a widespread European species, the bank vole

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It is clear that the golden age of mitochondrial DNA (mtDNA) in phylogeography has passed, but data derived from this marker have made an enormous contribution to our understanding of the process of post-glacial colonisation and other aspects of population history in many species. However, it often remains unclear how well mtDNA findings truly represent genome-wide patterns. Despite the recent advent of population genomics, it is still uncommon to have high coverage genomic studies relating to phylogeography of non-model organisms. We have been able to apply a high-throughput genotyping-by-sequencing (GBS) approach to discover and genotype 10,000+ SNP loci for 300+ bank voles (*Clethrionomys glareolus*) from all over Europe with the aim to determine how well the genome-wide population structure matches with mtDNA phylogeography. The knowledge of the detailed genomic phylogeography is essential to the study of adaptive differences between bank vole populations and their role in post-glacial colonisation.

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Adaptive phylogeography of the bank vole (*Clethrionomys glareolus*): The role of functional divergence between populations in shaping current species distributions

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The bank vole (*Clethrionomys glareolus*) represents an important model species in studies of adaptive phylogeography aimed at elucidating the role of selection in postglacial recolonisation. Functional variation in haemoglobin (Hb) distinguishing two bank vole populations that successively colonized Great Britain from different glacial refugia presumably helped facilitate the population replacement. The two Hb variants are distinguished by a single amino acid substitution of serine by cysteine in the beta globin chain. The presence of extra cysteine in haemoglobin carried by the second colonising population demonstrably increases the antioxidant capacity of the red blood cells and it thus may have had a role in determining the adaptive advantage over the first colonists. Here, we found that both Hb variants are widely dispersed in continental Europe, showing a clear geographical pattern with each variant exhibiting association with a different phylogeographic lineage, as defined by mtDNA. This supports the functional differentiation of Hb between different refugial populations of the bank vole. The results from spatial analysis show that environmental conditions have a significant predictive value on Hb allele frequencies, which supports the hypothesis of the Hb divergence (and hence selection) being important in determining which glacial refugia were ultimately successful in populating the current bank vole distribution.

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Dealing with the uncertainties- research priorities for taxonomic work on SMSG species within Australasia and insular Southeast Asia

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In general, small mammals have received less research attention, funding, and conservation effort, compared to larger charismatic mammals. Consequently, we have significant issues that other mammal specialist groups are less likely to have. There are two areas of uncertainty that remain regarding the systematics of group, which need to be addressed through further research. Firstly, for many families within the SMSG there is not the data available to fully understand the systematics, and work is required to resolve cryptic species, therefore for many species we cannot accurately assess their conservation status. The important gaps in our scientific understanding of the taxonomy within the group for the regions of Australasia and insular Southeast Asia will be discussed, along with the developing role of molecular approaches in conservation, especially in revealing cryptic species groups.

The second of the uncertainties for the group is connected with areas that have received little or no survey effort. We have observed a number of huge developments in the understanding of the biodiversity of previously unexplored areas, such as in Sulawesi and in the Philippines, where since the 2008 Red List many new species, and in some instances new genera, have been discovered. We will discuss where in the focal regions there are still likely to be significant discoveries of new species to be made and how we might go about encouraging expeditions to these places.

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Conservation priorities for SMSG species within Australasia and insular Southeast Asia

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The group plans to use several programmes of work to increase research and conservation efforts for key species and areas. We will talk about high priority conservation areas, where there are particularly high densities of Globally Threatened species and the type of work we would like to conduct at these locations. One of the greatest challenges that the SMSG faces is how to address and reduce the large number of Data Deficient species, where there is inadequate basic ecological information to use a different Red List category. Here, we will provide some examples that show some of the challenges we face in addressing these, and how we can try to encourage organisations, research institutions, museums etc. to undertake activities such as expeditions that will target these specific places. The other main programme will be to identify key species using certain prioritisation systems and in this talk we will discuss potential candidate species. We will also explain how we intend to use species champions to support conservation actions on the ground for the nominated species.

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Introduction to the SMSG and the current knowledge of conservation status of SMSG species within Australasia and insular Southeast Asia

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The first talk will introduce the purpose of the workshop, the topics and schedule for the session, and set out what we want to achieve by the end of the workshop. There will be a brief outline of the Specialist Group's structure, aims, and an update on progress made by the group so far. This update will include an overview of the IUCN Red List reassessments for species within Australasia and insular Southeast Asia, using case studies within the regions to demonstrate some of the main changes to the conservation status of species and challenges faced in undertaking the reassessments. We will show detailed results of analysis based on the latest Red List data, and highlight particularly important areas containing high densities of Globally Threatened and Data Deficient species. Finally, we will explain the future plans of the group, which will set the scene for the following talks and structured discussions.

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Free-ranging domestic cats (*Felis catus*) on public lands: estimating density, activity, and diet in the Florida Keys

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Feral and free-ranging domestic cats (*Felis catus*) can have strong negative effects on wildlife such as small mammals and birds, particularly in island ecosystems. We deployed camera traps to study free-ranging cats in U.S. national wildlife refuges and state parks in the Florida Keys, and used spatial capture-recapture and kernel density models to estimate cat abundance/density, movement, and activities. We also used stable isotope analyses to examine cat diets captured on public lands. Top models separated cats based on differences in movement and detection with three and two latent groups on Big Pine Key and Key Largo, respectively. We hypothesize that these latent groups represent feral, semi-feral, and indoor/outdoor house cats based on the estimated movement parameters of each group. Estimated densities and activity varied between the two islands, with relatively high densities (~4 cat km^{-2}) exhibiting crepuscular diel patterns on Big Pine Key and lower densities (~1 cat km^{-2}) exhibiting nocturnal diel patterns on Key Largo. Stable carbon and nitrogen isotope ratios from hair samples of cats provided estimates of the proportion of wildlife and human-subsidized foods in cat diets. Cats on both islands consumed mostly human-provisioned foods (>50% of the diet), but some individuals were effective predators of wildlife (>50% of the diet). We provide evidence that cat groups within a population move different distances, exhibit different activity patterns, and that individuals can consume wildlife at different rates. We discuss the benefits of non-invasive sampling and robust statistical techniques to assess a variety of population vital rates.

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The estimation of different species of monkeys in the University of Cape Coast Forest Reserve, Ghana

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Climate change, habitat loss and illegal hunting have caused a significant reduction in the number of monkey populations in the University of Cape Coast (UCC) Forest Reserve. This work reports the results of a survey of the population of species of monkeys in the secondary rainforest vegetation of the University of Cape Coast. The 0.5 km^2 study area was demarcated into six (6) sections. The entire area was then surveyed for the presence of species of monkeys. Surveys resulted in the detection of two species of monkeys in the Reserve. These are *Cercopithecus petaurista* and *Cercopithecus cephus*. We recorded a total of fifty six (56) *Cercopithecus petaurista*. Of this number, thirteen (13) were juveniles while forty three (43) were adults. For *Cercopithecus cephus*, a total of seven (7) individuals was observed with only one (1) being a juvenile. *Cercopithecus petaurista* was friendly and least affected by the presence of unarmed persons, but *Cercopithecus cephus* seemed very timid, always on alert and therefore more difficult to be seen. Both species of monkeys were observed to move from different parts of the forest in search for food (foraging). Additional surveys are necessary in subsequent years to map annual fluctuations in the size and distribution of the monkey populations in the UCC Reserve.

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Landscape 2D and 3D metrics and mammals’ diversity in agricultural landscapes of Southeastern Brazil

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The relatively high abundance of small mammals appears tdo sustain a relatively high diversity of canids and felids in agricultural landscapes of southeastern Brazil. However, there is still little information on the possible causes of such abundance. In the present study, we surveyed medium to large mammals, respectively, by camera traps and small mammals by pitfall traps in 15 stations distributed over a sylvicultural landscape with *Eucalyptus* plantations as the matrix and native vegetation (a transition zone between Cerrado and Atlantic Forest) and abandoned pasture (five sampling units each) as conservation areas. The sampling design was based on a grid adapted from the Biodiversity Research Program (PPBio), where sampling units are 1 km distant from each other. The functional diversity of medium to large mammals has been affected by the landscape shape index, whereas taxonomic and phylogenetic diversity of small mammals have been predominantly determined by the percentage of native vegetation, both 2D landscape metrics as they are basically related with area. However, their abundance has been determined by an indirect estimate of the native vegetation biomass (i.e. NDVI), which can be considered a 3D landscape metric as it is related to volume. Such patterns suggest land sharing and native vegetation recovery as best strategies to increase conservation value of agricultural landscapes. In addition, the present results support the use of native vegetation biomass as a proxy of small mammals’ abundance in agricultural landscapes.

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Estimating red fox (*Vulpes vulpes*) abundance with spatial mark-resight models and camera traps: the effects of tagging, observer and individual recognition

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Abundance estimation is paramount for the conservation and management of mammalian carnivores. The use of camera-traps for the study of carnivores has exponentially increased in the last decades, mostly for density estimation of species with individual natural coat patterns. Since canid species are not easily individually recognized from their pelage design, their population density is rarely estimated from camera-trap data. We assessed camera-trap data to estimate red fox (*Vulpes vulpes*) abundance in two areas of SW Europe with contrasting densities. We compared estimates from spatial mark-resight (SMR) models in a Bayesian approach, and assessed the effect of individual identifications by different observers, using as reference the density estimate including as identified exclusively those tagged individuals (unequivocally recognized). We also assessed whether individual identification with ear-tags and GPS-collar movement data improved the precision of estimates. Our results show a high variability among observers in the number of individuals identified and, consequently, in the density estimates, ranging between 1.05 and 1.58 foxes km^{-2} in the high-density area, and between 0.19 and 0.44 foxes km^{-2} in the low-density area. The density estimates obtained from spotlight-counts and distance sampling methodology are close to estimates from SMR models. Selected SMR models included a sex-effect, consistent with radio-tracking data indicating that males moved over larger ranges than females. The effects of behavior response and different detection due to lure/bait were also included in the models. We discuss the consequences and applications of these results for monitoring, conserving and managing canids with cryptic pelage patterns.

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Monitoring a cryptic burrowing marsupial using DNA extracted from scats: greater bilby populations in the Pilbara region of north-western Australia.

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The greater bilby (*Macrotis lagotis*) is a burrowing marsupial that was once found across most of arid and semi-arid Australia; however, since European colonisation, bilbies have disappeared from at least 80% of their former range. The lesser bilby (*Macrotis leucura*), a closely-related species, has become extinct. Introduction of the cat (*Felis catus*) and fox (*Vulpes vulpes*), changed fire regimes, the degradation of bilby habitat through pastoralism, introduced herbivores, and clearing, have all contributed to the range contraction. Bilbies are cryptic and not easily observed or trapped, they are distributed across large areas, and populations can move across the landscape. Therefore, detection has relied on observation of sign, such as tracks, scats, diggings and burrows. No reliable technique for monitoring abundance within populations was available. We developed a technique using DNA extracted from faecal pellets to obtain a measure of abundance at populations remaining in the Pilbara region in the north-west of Australia. After three years of monitoring, two populations were lost to large scale wildfires. We found that populations in the Pilbara are small and isolated geographically, which may make them particularly vulnerable to the threats described above.

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The critical importance of palaeontological data in efforts to optimise conservation of endangered mammals: an Australian focus

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Australia has lost 24 mammals since 1788. Failure to understand how this continent's unique lineages and species have been changing through time, whether they are declining, increasing or stable, has sometimes led to incorrect, even fatal misconstructions about their conservation status. The fossil record provides important information about changes in diversity, distribution, habitat and abundance through time. As we come to understand more about these factors which can indicate greater environmental adaptability than current distributions suggest, it becomes possible to envisage a wider range of options for translocations in a world where sustainability of habitats is under increasing threat. As an example, the alpine Mountain Pygmy-possum, *Burramys parvus*, is already threatened by climate change. Using conventional biological/ecological wisdom, there would be no viable strategy for stopping this iconic marsupial from becoming extinct. The fossil record, however, has inspired an innovative strategy for saving this species. For the last 25 million years this lineage has always been represented by a single species in cool, temperate, species-rich lowland forest communities spanning what is now the Simpson Desert (24 mya) to northwestern Queensland (24-15 mya) and northwestern Victoria (4 mya). This palaeontological understanding has led to the now-supported 'paleoconservation' proposal to construct a lowland breeding facility in Secret Creek Sanctuary, NSW, with the goal of introducing this critically endangered mammal back into the traditional core habitat for the lineage. If this project succeeds, and all indications are that it will, similar projects should be considered for other climate-change-threatened mammals in and beyond Australia.

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Using subfossils to create a baseline: A pre-European small mammal assemblage of the north western Flinders Ranges, South Australia

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Reconstructing Australia's pre-European mammal communities is challenging as many species became extinct, or were severely impacted on, prior to intensive scientific interest. Critical baseline data as a result, is almost non-existent, and alternative sources of information must be used, such as from Holocene fossil deposits. Cave-roosting owls are well known contributors of small mammal remains to Holocene deposits. To determine the original small mammals of the north western Flinders Ranges in South Australia, we examined well-preserved subfossil barn owl pellets and disarticulated pellet remains from the rock pile and sediment floor of a small cave in Aroona Dam near Leigh Creek. The sheltered depositional environment of the cave provided a unique sample of intact pellets that acted as a time capsule for the original small mammals of the area and effectively sealed off from any modern additions. The pellets were radiocarbon dated to between 678 and 1547 yrs BP. A total of 22 mammal species were identified from the assemblage. Over 34% of these species are now completely extinct, with over 21% locally extinct from the surrounding area. When data from our study is combined with existing Holocene records for the north western Flinders Ranges, it is evident there has been an overall drop in small mammal species diversity of around 56% since European settlement. Subfossil deposits in caves are useful indicators of the original mammal assemblages in Australia and provide critical data that are relevant to conservation of vulnerable species.

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Dietary ecology and consequences of drought events on extant macropods: Implications for conservation and palaeoecological reconstructions

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As Australia is projected to experience more extreme droughts and ~0.8 to 2.8ºC temperature increases by 2050, it is critical to assess the effects of climate change on extant marsupials. Furthermore, our understanding of extant marsupials can help clarify the palaeoecology of extinct taxa, elucidating the consequences of climate change over longer time periods than are accessible to neontologists. Dental microwear texture analysis (DMTA), the analysis of tooth wear surfaces in three-dimensions, records the dietary textures of consumed foods over the last few days to weeks of an animal's life - an effective tool for assessing diets just prior to the death of organisms, both today and in the past. We developed a DMTA baseline of extant macropods, including *Dorcopsulus vanheurni*, *Macropus fuliginosus*, *Macropus giganteus*, *Notamacropus rufogriseus*, *Osphranter robustus*, *Osphranter rufus*, *Petrogale lateralis*, *Setonix brachyurus*, and *Wallabia bicolor*. Results demonstrate the ability of DMTA variables (e.g. anisotropy and complexity) to differentiate between tough and hard food consumers, i.e. extant grazers and woody browsers, respectively. Further, when comparing *M. giganteus* and *M. fuliginosus* individuals that were killed during "normal" conditions to those killed during extreme droughts, DMTA reveals dramatic dietary shifts in both taxa to include more woody material, as inferred from significantly greater complexity, during periods of extreme aridity. These data reveal that mammalian dietary niches are not static, but change in response to extreme droughts, and DMTA is useful for identifying dietary ecology of extant and extinct macropods shortly before their death.

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Congruus sp. nov. a semi-arboreal kangaroo (Marsupialia: Macropodidae) from the Pleistocene Nullarbor Plain of south central Australia

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The biology of Pleistocene kangaroos of the genus *Congruus* is poorly known. Two new specimens with associated postcranial remains from the Thylacoleo Caves, Nullarbor Plain, Western Australia have provided an opportunity to elucidate a more complete picture of the ecology of these animals. The skeletons of the two individuals differ in the robustness and relative development of muscle scars on the humerus and femur, and especially the size of the hands. These features are known to differ between male and female conspecifics in many species of kangaroos and wallabies, and thus likely illustrate sexual dimorphism in this new species. The remarkable preservation of almost the complete postcranial skeleton of these individuals has enabled an ecomorphological analysis of this species. Unexpectedly, the morphology of the postcranial skeleton demonstrates many adaptations for a semi-arboreal lifestyle, particularly in the mobility of the gleno-humeral joint, the development of muscle attachment sites for strong adduction and mobility of the forelimb, and large, robust manual and pedal digits with strongly recurved distal phalanges. These features distinguish *Congruus* from terrestrial macropodines, but are to some extent convergent with adaptations in tree-kangaroos (*Dendrolagus*). This discovery, in addition of the two previously described species of *Bohra* from this area, further highlights the deficiencies in our understanding of the Pleistocene environments of southern Western Australia.

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The cottontail rabbits (Lagomorpha: Leporidae: *Sylvilagus*) of Costa Rica: a novel taxonomic and systematic perspective.

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Costa Rica, despite its size (51,060 km^2 or 0.03% of the world's land area), contains an almost unparalleled mammalian biodiversity; some 250 species (ca. 4% of the World's total) inhabit the country. Among the cottontails, *Sylvilagus*, that diversity is manifested in the presence of one likely endemic, *S. dicei*, and two widespread species, *S. gabbi* and *S. floridanus*. Or is it? Detailed cranio-dental inspection of the holotypes of *S. f. floridanus* and *S. f. costaricensis*, while confirming a degree of phylogenetic affinity, also point to clear and distinct species–level differences. A similar situation may exist in *S. gabbi*, currently considered a polytypic species distributed from the Mexican state of Veracruz to the Colombian Chocó. Detailed examination of holotypes, together with the recent description of a neotype for *S. brasiliensis*, are enabling us to begin to appreciate the taxonomic diversity formerly obscured within the morphologically conservative *Sylvilagus*. In addition to excising *S. costaricensis*

Harris, 1933 from synonymy with *S. floridanus*, we demonstrate the existence of extensive, undocumented variation in Costa Rica's cottontails, from both lowland and highland areas. We hypothesize that the marked topographic relief of Costa Rica results in remarkable plant biodiversity, architecture, and function, in turn leading to the establishment of fine scale allopatric populations distributed both altitudinally as well as within ecologically allopatric redoubts in the apparently homogeneous lowlands. This concept of the ecological milieu may result in the presence of many more species than have heretofore been appreciated.

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The adaptive significance of fluctuations in populations of arvicoline rodents: Habitat reach

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Population "cycles" and other fluctuations of arvicoline rodents (Cricetidae) challenge concepts and hypotheses of "population regulation." Relevant studies have been undertaken since the emergence of ecology as a discipline, but largely with respect to the "mechanics" of cycles. Longitudinal study of montane grassland species [24 y, montane voles (*Microtus montanus*, 18 sites) and longtail voles (*M. longicaudus*, 3 sites)] and of Laurentian forest species [34 y, 19-22 sites, Boreal redback voles (*Myodes gapperi*), rock voles (*Microtus chrotorrhinus*,), southern bog lemmings (*Synaptomys cooperi*)] suggest that large populations are adaptive, not epiphenomenal. They allow 1) the annual expansion of populations in spring into contiguous seasonally flooded land, 2) the dispersion of individuals into segments of the metapopulation (*sensu stricto*), 3) the expansion of the species into appropriate peripheral and isolated habitat patches (*e.g.*, isolated boulder fields), and 4) the expansion of the species into novel habitats (*e.g.*, from bog and fen to the upland ericaceous shrub community). This paradigm is discussed in the context of reproductive plasticity and should lead to more investigations of reproductive physiology and genetics.

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Evaporative water loss of subterranean rodents: a South America-Africa comparison

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Salt and water balance is essential for life but is challenging, especially for those organisms that require special water regulatory mechanisms because of their life in extreme habitats. In endotherms, a significant avenue of water loss is evaporation. Evaporative water loss (EWL) is inevitable, but individuals can limit such loss and use it for cooling, as metabolically-produced heat is dissipated by evaporating body water. One of the most important challenges for mammals living in an underground environment is the need to dig new burrows through a dense substrate in an almost water saturated atmosphere. The heat produced during digging in such an environment could cause overheating, especially at ambient temperatures (T_a) within and above the thermoneutral zone (TNZ). The aim of this study was to evaluate the effect of T_a on EWL and energy metabolism of subterranean species from different rodent families, African mole-rats (Bathyergidae), and South American coruros (Octodontidae) and tuco-tucos (Ctenomiydae). Individuals of all species follow a typical endotherm pattern, maintaining relatively stable EWL below and within TNZ and increasing evaporation above TNZ. However, they show difference in the total EWL, especially above TNZ. We relate ecological pattern to the underlying physiological mechanisms aiming to understand the evaporative water and heat loss in subterranean rodents. We analyzed both social and solitary species, so we focus, also, on the effect of sociality on EWL. Finally, by comparing different unrelated species of subterranean mammals, we gain insights into the factors that influence the broad scale pattern of EWL in these mammals.

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The spiny mouse (*Acomys cahirinus*) – a menstruating rodent

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Menstruation, is the cyclical shedding of the decidualised endometrium in the absence of pregnancy. Menstruation is limited to 78 higher-order primates (human beings and Old World monkeys), 4 species of bat, and the elephant shrew. This represents only ~1.5% of the known ~5502 mammalian species. We recently made the unexpected discovery of menstruation in a rodent, the spiny mouse (*Acomys cahirinus*), a desert-adapted rodent native to the Middle East. Virgin female spiny mice aged 12-16 weeks were studied for 2 consecutive reproductive cycles. Mean menstrual cycle length was 8.7 ± 0.4 days with red blood cells observed in the vaginal lavage fluid over 3.0 ± 0.2 days. Cyclic endometrial shedding and blood in the vaginal canal after each infertile cycle was confirmed in all virgin females. The endometrium was thickest during the luteal phase, when plasma progesterone peaked and the optical density for prolactin immunoreactivity was strongest. The spiny mouse undergoes spontaneous decidualization, demonstrating for the first-time natural menstruation in a rodent (Bellofiore, 2017, AJOG). The unprecedented discovery of menstruation in a rodent species suggests that this reproductive feature was overlooked by previous investigators because of the dogma that rodents are not menstruating mammals. There is a need to consider the possibility of other menstruating species. The peripheral position of *Acomyinae* in most rodent phylogenies suggests a need to broaden phylogenetic analysis of this and related genera.

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Genetic management of fauna reintroductions

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Managing genetic diversity in fauna reintroduction programs is important to retain species' evolutionary potential. While it is critical to source genetically-diverse founders for reintroduction, constraints on population growth and longer term population size can lead to erosion of genetic diversity with time and create additional management challenges. This is of particular relevance for island and mainland exclosures where hard boundaries act to limit population sizes and create effectively isolated populations. Here we present genetic assessment of the translocation of golden bandicoots (*Isoodon auratus*) from a large source population on Barrow Island off the north-west coast of Western Australia to two other island sites and a mainland fenced enclosure. We assessed the genetic diversity of animals translocated to each site and their wild-born progeny, and whether wild-born animals showed evidence of genetic bottlenecks or genetic drift from the source population. Population viability modeling predicts that each of the translocated populations is susceptible to loss of genetic diversity over time, given constraints on long-term population size. We discuss these genetic management issues in light of the proposed fauna reconstruction program on Dirk Hartog Island. This ambitious project aims to reconstruct the island's fauna assemblage by reintroducing 10 species of native mammal and one species of bird, and introducing two other threatened mammal species for conservation reasons, over a 12 year period, and will be the largest ecological restoration project undertaken in the southern hemisphere.

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Beyond the fence: Are we any closer to re-establishing Australia's threatened mammals in open landscapes?

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Australia has an unenviable record of recent extinctions due to the post-European impacts of habitat clearance, introduction of feral cats and foxes and grazing by exotic herbivores. Many of our native mammals now survive only on offshore islands or in fenced mainland sanctuaries. Efforts to re-establish these species in open landscapes on Australia's mainland usually fail, most often due to predation by introduced cats and foxes. Despite a litany of failed re-introductions, some progress is being made towards re-establishing threatened species outside of islands and fenced reserves. We now understand more about the sensitivity of each native species to introduced predators and which species make suitable candidates for reintroduction trials. A significant body of re-introduction research has been conducted which has improved our knowledge of the timing, causes and patterns of post-release predation. Many similarities have emerged including rogue predators, poor habitat quality and prey naivety. Most significantly, this research has led to the development of a range of new tools and technologies to address these issues and the impacts of cats and foxes. Whilst most of these tools are still under development or field testing, initial results are encouraging and suggest that future re-introductions are likely to have a greater chance of success. Examples will be presented including baiting, grooming traps, in situ predator training and toxic implants as well as positive reintroduction outcomes from recent releases outside of fenced reserves.

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Predicting biosecurity risk for islands using Bayesian belief networks: Mammalian threats and threatened mammals

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In the Pilbara region of Western Australia there are approximately 600 islands spread out over 30,000 km^2 of ocean. Many of the islands are refuges for threatened and endemic species. Notably, foxes (*Vulpes vulpes*) probably extirpated black-flanked rock-wallabies (*Petrogale lateralis lateralis*) from Depuch Island. Foxes and black rats (*Rattus rattus*) are present on other islands that host the endangered northern quoll (*Dasyurus hallucatus*), and vulnerable bandicoots (*Isoodon auratus*). Feral cats (*Felis catus*) are a frequently appearing, but rarely establishing, threat. With such widely dispersed publically accessible islands effective quarantine is infeasible. Surveillance programs become cost-prohibitive unless we limit surveys to high-risk islands. We designed Bayesian belief networks (BBNs) that estimate the risk of threats arriving and establishing on each island via five dispersal pathways: recreational boats, industrial transport, tidal land-bridges, swimming and floods. BBNs are particularly useful for modelling complex systems where data are incomplete or uncertain. The BBNs were based on data derived from literature or expert elicitation. The probability of animals entering a natural dispersal pathway proved to be the most sensitive and uncertain variable. Relative arrival and establishment rates identify the high-risk islands and high-risk threats. Assuming threats were not already present: 11 islands have > 5% chance of rodents establishing a new population within one year; 7 are at similar risk from cats and 3 have > 2% chance of a new fox population. Dolphin Island hosts northern quolls and all three threats despite on-going aerial fox baiting, and has a 2.8% chance of fox re-invasion.

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Confounding considerations of fencing for conservation

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Fencing for conservation has become an important weapon in the conservation arsenal, and has led to real conservation success stories from mainland islands like Scotia Sanctuary (Australia) and Zealandia (New Zealand) to the reduced extinction risk of lions inside conservation fences. However, there are several issues that need to be addressed before conservation fencing becomes mainstream. Firstly, mainland islands are viewed dimly by conservation purists often from philosophical and economic terms but given the dearth of the original fauna at many of these sites this attitude may need to change. Secondly, mainland islands are inherently isolated and so strategies, like metapopulation management, to ensure gene flow are necessary, but not universally practised. Thirdly, this isolation has ramifications for human access, and this can limit the use of conservation fencing in some countries (notably the UK where the Countryside Right of Way Act may prohibit the use of fences if they block human access). Fourthly, fencing is really only an appropriate conservation action for a limited number of threatening processes – particularly introduced species and human persecution. Expecting conservation fences to address threats they are not designed to mitigate will not improve conservation outcomes, and nor will confusing fences designed for conservation with those designed for other purposes. With these considerations in mind, conservation fencing can continue to yield genuine conservation benefits – at least until the scale of threat amelioration expands beyond that which can be fenced (e.g. Pest-free New Zealand).

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Age- and sex-related changes in the social environment of wild giraffes

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Giraffes (*Giraffa camelopardalis*) are one of Africa's most iconic species and their decline in the wild has received extensive media attention with their new IUCN listing as Vulnerable, however their behaviour and social structure in natural environments are surprisingly poorly understood. Social structure results from the patterns of interactions among individuals and influences individuals' fitness as well as disease transmission, population genetics and dispersal. Understanding changes in individuals' social relationships through time is essential to inform conservation action plans, as social relationships can affect survival and breeding potential. The social system of giraffes is characterised by high levels of fission-fusion dynamics, where social groups change regularly in size and composition, but non-random connections exist between individuals. Here, we use a unique dataset from Namibia's Etosha National Park spanning 12 years on 160 individuals with known ages to describe the dynamic nature of giraffes' social networks. We test the hypothesis that giraffes' social connections vary with sex and age. We predict that different changes occur between the social environments of males and females as they move from adolescence to sexual maturity. We also expect differences in the longevity of males' and females' dyadic relationships. In particular, we predict that females maintain long-term social relationships with others of their age cohort while males' relationships decrease in strength as they adopt a roaming strategy to find potential mates. This long-term analysis will add to the understanding of social dynamics for the management of giraffes and other long-lived species with fission-fusion social systems.

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Differences in reproductive tract morphology and behaviour between two arid zone old endemic Australian rodents: Possible causes and consequences

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Arid zone old endemic Australian rodents include the spinifex hopping mouse (*Notomys alexis*) and the plains mouse (*Pseudomys australis*) both of which undergo "boom" and "bust" population cycles. How similar is their reproductive biology? Laboratory studies have shown that, compared to most murine rodents, both species have low reproductive rates with pregnancy length in non-suckling females being 30-36 days, litter size around 3.5, and maturation at 50-60 days. Dramatic differences are nevertheless apparent in their male reproductive tract morphology and mating behaviour. Mature plains mice have a large relative testes mass (RTM) of 2-4% body mass (mean body mass 55-60 g; testes mass ca. 2,000 mg), large epididymides with number of stored sperm ca. 500×10^6, and very large seminal vesicles and coagulation glands. By contrast, sexually mature hopping mice have maximum RTM of only ca. 0.15% (mean body mass 30-37 g, testes mass ca. 40 mg), very small epididymides with only ca. 1×10^6 sperm, minute seminal vesicles and coagulation glands but larger ventral prostates. Mating behaviour in hopping mice, but not plains mice, involves locking for up to several minutes. Related to this male hopping mice have a penis with much larger spines but narrower shaft and smaller baculum, and females a more muscular vagina with narrower lumen and much less fibrous, smaller, cervix. The huge differences in RTM suggest marked interspecific differences in mating system with hopping mice exhibiting monogamy and plains mice polyandry/promiscuity. Preliminary laboratory data support this conclusion; field observations are now required to test this hypothesis.

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The sensory world of a large-eared canid.

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The bat-eared fox (*Otocyon megalotis*) is a medium-sized meso-predator common to arid and semi-arid zones in southern and eastern Africa. Although anecdotal evidence suggests that their primary sensory organs are their eponymous, large ears, no researchers have investigated these foxes' sensory *umwelt*. We performed field experiments and conducted 24 months of behavioural observations to ascertain which sensory modality is favoured by these myrmecophageous mammals. Furthermore, we assessed how environmental factors would impact on foxes' foraging as well as anti-predator behaviour, considering the importance of different sensory systems. A series of choice experiments in the Kalahari Desert indicated that foxes rely primarily on auditory cues when hunting for invertebrate prey. Olfactory information appeared to be of secondary importance, while vision was the least reliable indicator of success in these experiments. In line with the hypothesis that bat-eared foxes' vision was a less prominent sensory modality, foxes' risk-taking behaviour was not impacted by vegetation height or density. Observations of natural foraging behaviour, however, indicated that wind noise – decreasing the availability of acoustic information – did not reduce foraging success, suggesting that bat-eared foxes are able to exploit an alternative source of information during unfavourable conditions. These data represent one of the most comprehensive investigations of carnivore sensory ecology, highlighting several novel approaches that may be applied to research on other mammals living in the arid zones of the world.

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The diversity of carnivorous marsupials (Dasyuridae) in the Australian arid zone

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Arid Australia supports a high diversity of carnivorous marsupials (Dasyuridae) with about half of the Australian species living entirely or partially in the arid zone. This environment is dominated by long periods with low resource availability and daily extremes in temperature. Here we examine patterns of occurrence and mechanisms of persistence of dasyurids with a particular focus on a 10-year study in the western Simpson Desert. The study area supported an assemblage of 10 species. Population dynamics varied across species, but two species showed a pattern of capture that is analogous to population irruptions of sympatric rodents. These two species, the kultarr (*Antechinomys laniger*) and fat-tailed dunnart (*Sminthopsis crassicaudata*) had within-site capture rates as high as 31% (31 animals per 100 trap-nights) during peaks of abundance. All dasyurids used torpor. A detailed study of torpor patterns in the two larger species, brush-tailed mulgara (*Dasycercus blythi*) and crest-tailed mulgara (*D. cristicauda*) showed that torpor use was frequent and bouts of torpor were long during winter. However, torpor did not seem to be employed as an immediate response to energy shortage, rather it was tied to reproduction. Both mulgara species captured a broad prey base that included vertebrates, invertebrates and plants. Diets were dominated by invertebrates less than 2 g in body mass. These findings indicate that torpor ensures reproductive success and ongoing persistence in arid carnivorous marsupials and it enables species inhabiting environments with high resource variation (e.g. gibber plain) to exploit peaks in prey availability.

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Estimating population size of rural and urban hedgehogs (*Erinaceus europaeus)* using camera trapping and citizen science without the need for individual recognition.

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The European hedgehog (*Erinaceus europaeus*) is considered common and abundant throughout its European wide range and therefore considered globally to be of Least Concern. However, in several west European countries its distribution and populations appear to have declined markedly since the 1950s. Current methods used to monitor hedgehog populations are associated with factors which either limit their use for long-term monitoring and not all can be applied easily in all habitats, or are unable to yield population density estimates. This study aims to (1) assess the suitability of the Random Encounter Model (REM), a method that has been previously used to estimate population densities of species without natural markings; and (2) validate the REM results by comparing them to capture-mark-recapture. The study took place in 2016 in one rural and three urban locations across England, where 120 cameras were deployed following a randomised sampling design. In urban areas the cameras were located in private gardens with a very positive citizen involvement. 2016 results indicated REM was suitable for estimating population density of hedgehogs, providing a technique with clear animal welfare advantages. REM was time-consuming, as animal and camera parameters needed to be obtained specifically to each study are to avoid unbiased estimates. In 2017 another rural and two/three urban areas will be surveyed to further standardise the required parameters and improve the time required by researchers to implement the method, allowing the application of the REM to monitor long-term population changes.

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Habitat selection by mammals based on radiotelemetry

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Advances in biotelemetry have greatly increased the spatial and temporal resolution of data that can be obtained from wild mammals. These data have afforded opportunity to examine movement and associated distribution, dispersal and habitat selection. Most applications employ a use/available design using the logistic discriminant derived by G. A. F. Seber—I will explain how this is distinct from logistic regression analysis. Scale is a continuing challenge in habitat selection studies because of data constraints but also because mammals can select at a variety of spatial and temporal scales. We have proposed a new method for habitat selection, integrated step-selection analysis, that explicitly uses movement to constrain the available resource units focusing scale to the behavioural selection process. I will review case studies for ecology and conservation of elk (*Cervus elaphus*), cougars (*Puma concolor*), grizzly bears (*Ursus arctos*), and wolverines (*Gulo gulo*). Individual variability in habitat selection can be high for each of these species sometimes warranting the characterisation of a functional response shaped by learning.

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Wildlife wearables: Advances in remote wildlife surveillance, from real-time GPS to wearable video cameras in kangaroo case studies

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Ecologists have long been interested in the factors that drive wild animal movement patterns, social behaviour and foraging strategies. Understanding these processes is becoming increasingly important, as we try to predict the ways in which animal populations will respond to rapidly changing environments. Recent advances in remote sensing technologies, such as miniaturisation of GPS units, batteries and cameras, combined with a decrease in the cost of these technologies, means that there is now a plethora of technological approaches for remotely studying wild animal behaviour. We will present results from a series of studies incorporating remote sensing technology into ecological investigations of eastern grey kangaroos. We will demonstrate the capacity of animal-borne video cameras, combined with GPS continuous data-loggers, to provide an “animal’s eye-view” of fine-scale foraging behaviour in field conditions. From six successful deployments in kangaroos, we analysed simultaneous GPS tracks and up to 120 hours of video footage to reveal foraging performance and choice. These results demonstrate the enormous potential of this technology to enhance our understanding of foraging patterns and habitat preferences of wild mammals. We will also report on the use of miniaturised GPS and solar battery technology to record and remotely download the location data of eight kangaroos in a periurban environment, compared with traditional store-on-board and off-the-shelf GPS trackers. These combined case-studies highlight the need to consider the costs and benefits of different technologies relative to the specific ecological and management questions in mammalogy to ensure that the technology is fit for purpose.

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Remote data collection on very small mammals using Raspberry Pi and other technology in a bait station

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Live-trapping of very small mammals, such as pygmy shrews, is challenging due to high BMR, FMR, and energy expenditures of these species. Sherman and Longworth traps require vigilant monitoring; yet even with careful methods, escape and mortality may lead to unsatisfactory data. We developed a bait station, designed with Tinker Cad software and printed on a 3-D printer, that allows us to weigh, measure, and photograph trap visitors while allowing mammals to enter and exit at will. The station was designed to obviate the need for 1-2 hr/day trap checking or handling of small, often fragile mammals. Data is collected using a combination of mini-DV camera, small force plate, and Raspberry Pi 3 computer. Photographs are taken as the force plate is touched, while the force plate records a voltage that is translated to weight in grams. We will describe our testing of the prototype station in the laboratory, followed by our field setup and success rate. We will also give an overview of new challenges, such as protection of the credit card-sized computer from condensation and determining accurate weight ranges, and identifying individuals. This bait station alternatively uses a LoRa (long-range, *ca.* 19 km radius) radio with a built-in microprocessor that can submit data directly to a laptop or phone for efficient field-monitoring. The hope is that this station will be applicable to studies by other researchers and students for eutherians and metatherians at the low end of the mammalian size spectrum.

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Aquatic giants with tiny voices: Exploring the drivers of acoustic communication in mammals

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Acoustic communication plays an important role in the ongoing success and survival of mammals in a rapidly changing world. Anthropogenic activity is increasing and spreading at a steady rate and it is important to understand how this activity has the potential to impact mammals' ability to communicate. The first step is to have a strong knowledge of the acoustic communication abilities of as many species of mammals as possible. We compared the acoustic signal design (vocalisation) and reception (hearing) thresholds of over 190 species of mammals to examine which life history traits are responsible for driving their diversity. We found that the same two drivers, environment and body size, were responsible for the majority of variation in mammals' acoustic communication thresholds. As had been found in early smaller studies on terrestrial mammals, we found that larger mammals produce and receive lower frequencies than smaller mammals. However we also found the surprising result that aquatic species produce and receive signals at higher frequencies than their terrestrial counterparts. Aquatic species had previously been largely underrepresented in previous comparative studies, and including them uncovered some interesting and unexpected results. While we expect a large mammal to have a deep booming voice, we found that large aquatic mammals are capable of producing high frequency clicks and whistles as high as a mouse. Our results provide a bigger picture for mammal acoustic communication and can hopefully be useful in easily determining which species may be affected by increasing levels of anthropogenic change in the environment.

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Foraging decisions of North American beaver (*Castor canadensis*) are shaped by energy constraints and predation risk

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Foraging herbivores have to trade-off between energy requirements and predator avoidance. We aimed to study the relative roles of these factors in beavers (*Castor canadensis*) when foraging on land. We hypothesized that beavers were able to assess the risk of predation by using two main cues, the distance from water, and the presence or absence of predator odors. First, we studied the food selection of beavers in relation to distance from the water in natural settings. Transects were made at beaver ponds and the diameter, species, and distance from the shore of intact and beaver cut trees were recorded. Secondly, we placed rows of aspen sticks (*Populus tremula*) perpendicular to the shore around beaver ponds, and treated each row with a neutral, alien, or wolf odor. We found that aspen, downy birch (*Betula pubescens*) and speckled alder (*Alnus incana*) were preferred tree species. More of these species were cut close to the shore and cut trees were smaller further away from the shore, except in the case of aspen. In the experiment, most of the aspen sticks were taken close to the shore. As predicted, beavers took less aspen sticks in rows treated with wolf odor than water. As the predator odor did not affect the foraging distance from the shore, it is likely that our observation that foraging was the most intense close to shore, is due to energetic constraints. However, predation risk probably affects the decision whether to forage on the land in the first place.

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What defines phenotypic variation in sexually dimorphic marsupials of South America? Assessing skull shape variation in *Didelphis albiventris*, *D. aurita* and *D. marsupialis* (Mammalia: Didelphidae).

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Ecogeography and sexual dimorphism represent a significant source of phenotypic variation within mammalian species. The skull is a key trait to investigate such issues, especially in mammals, since its size and shape relate to feeding and other functional adaptations. We explored skull variation in three wide-ranging South American marsupial species to determine the impact of sexual and ecogeographical selection. We selected members of the genus *Didelphis* that are phylogenetically and morphologically very similar: the generalist *Didelphis albiventris*, the Atlantic forest dweller *D. aurita* and the Amazonian forest dweller *D. marsupialis*. By employing geometric morphometrics, we quantified skull shape and size in a sample of 425 wild-caught adult specimens. Species skull shape responds differently to each explanatory variable: skull size, environment and spatial filters (generated by principal coordinates of neighbour spatial matrices). There is a general pattern between sexes with males exhibiting a larger allometric effect on shape than females. Larger individuals are capable of producing higher bite forces, with a relatively wider zygomatic arch. Male opossums fight each other for mating competition, thus explaining the stronger influence of allometry on their skull shape. Where geographical variation is concerned, we noted higher spatial autocorrelation in the skull shape variation of females. Indeed, in all *Didelphis* species, females are more sedentary while males tend to be more active, moving across longer distances. The environment alone explains 1% or none of skull shape variation in *Didelphis* species, although it has a greater role when interacting with size and the spatial filters.

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Merycism in western grey (*Macropus fuliginosus*) and red (*Macropus rufus*) kangaroos

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Kangaroos occasionally regurgitate and re-chew digesta. This so-called 'merycism' is distinct from rumination, being non-essential for digestive activity, significantly varying in frequency, and causing seeming discomfort. Triggering mechanisms and benefits remain unknown. Although often reported, detailed descriptions are lacking. We performed a systematic evaluation of 17 anecdotal observations of six kangaroos (*M. fuliginosus, M. rufus*) in captive feeding situations (14 videos with lucerne pellets and 3 with chopped lucerne hay feeding, covering 4.38 h with more than 55 regurgitation events). A characteristic merycism sequence consisted of retreat from feeding trough, pumping abdominal contractions, slurping, re-chewing and re-swallowing. In some individuals variations occurred, e.g. instead of re-swallowing digesta, it was spilled (35 % of cases). We hypothesize that the purpose of merycism is grinding of non-sufficiently chewed food particles that trigger contractions of the forestomach beyond voluntary control. The numerically higher frequency of this behaviour during pellet compared to hay feeding supports this hypothesis, as pellets were often gobbled hastily. In accord with observations in the literature, we hypothesize that merycism happens more frequently in captivity, as the type of food, fixed feeding times and limited feeding spots make gobbling of food more likely.

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Tooth outline shape analysis of the Ryukyu wild boar and the Japanese wild boar by geometric morphometrics

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Investigating morphological characteristics of archaeological remains of *Sus scrofa* among the Ryukyu Islands, south west of the Japanese archipelago, is necessary to understand the origin and dispersal process of the modern Ryukyu wild boar (*S. s. riukiuanus*). For this purpose, we examined whether the shape of teeth, which are often well preserved at archaeological sites, is useful to distinguish morphological variation of *S. scrofa*. We photographed the occlusal outline of the lower teeth of five modern populations of the Ryukyu wild boar and two populations of the Japanese wild boar (*S. s. leucomystax*). The outlines of each tooth were digitized into landmark coordinates and statistically compared. The difference in shape among the populations was evaluated by calculating the distance of homologous coordinates among them. Our results suggested that tooth outline shape is significantly different between the two subspecies. In addition, correct assignment rates of the populations based on their tooth shape was the highest for the fourth deciduous premolar, which showed that this tooth is the most useful for distinguishing variation of *S. scrofa*. The tooth outline shapes of geographically adjacent populations tend to be similar. Therefore, we concluded that the tooth outline shape is a powerful tool for distinguishing subspecies of *S. scrofa* as well as their geographical variation. This method is especially useful for archaeological remains, because of its applicability for isolated teeth, and has potential to increase our understanding about the history of migration and introduction of *S. scrofa* into the Ryukyu Islands.

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Community change during ecological restoration: small mammals as indicators

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Ecological restoration projects have been initiated world-wide with the goal of recovering damaged or degraded ecological systems, increasing the resilience of biodiversity, and providing ecosystem services. Assessment of such projects is essential for improving their implementation and justifying their costs, but comprehensive monitoring and evaluation have rarely been incorporated into projects. We developed a cost-effective monitoring program for lands managed by five Native American tribes in northeastern Washington and adjacent Idaho. Key ecological objectives of restoration are that the restored area (1) has an assemblage of species characteristic of a reference ecosystem that provides appropriate community structure, and (2) consists largely of indigenous species. We established 24 reference points representing the best extant representatives of 8 habitat types, and 83 sampling points on 39 management units where restoration was initiated. Composition and structure of vegetation, and composition and relative abundance of small mammals, birds, and larval amphibians were monitored over 3 years for reference points and at 5-year intervals on restoration sites. Similarity indices that incorporate relative abundance (Chao-Jaccard) were calculated to compare managed lands to the reference for each habitat. Non-metric multidimensional scaling was used to visualize the relationships of restoration to reference sites for each habitat type. Small-mammals appear to be appropriate indicators of change for habitats such as shrub-steppe where there are clear linkages with herbaceous vegetation, and for structurally simple habitats.

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Top-down or bottom-up? Drivers of density and distribution of northern quolls

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The endangered northern quoll (*Dasyurus hallucatus*) is a carnivorous marsupial that inhabits the northern third of Australia. It has experienced severe range contraction into rocky habitats and away from lowland habitats. The introduced cane toad (*Rhinella marina*) is considered a major threat. Being currently free of cane toads, the semi-arid Pilbara region of Western Australia offers a unique opportunity to explore other aspects that may be contributing to the decline of northern quolls. Thus, the main goal of this study was to assess the ecology of northern quolls and investigate drivers of its density and distribution in the Pilbara. We examined top-down and bottom-up processes including predation risk, potential for competition with native species, demography of quolls, habitat structure, den availability, vegetation cover, and prey availability. Our results suggest that prey availability fails to explain range contraction of northern quolls into rocky habitats. Conversely, we found evidence that feral cats (*Felis catus*) occupy open habitats, excluding quolls form these habitats. Den availability was higher in rocky habitats, offering added protection from introduced predators. The combination of den and prey availability, along with severe droughts, may be limiting factors to quoll density within rocky habitats.

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Scats of a mammalian bioturbator increase the diversity of rhizosphere fungi associated with seedlings of a key forest tree

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Mammals provide many ecosystem functions that help maintain the health of their habitat. In Australia, where soils are nutrient-poor, the tripartite interaction between mammals, fungi and plants are particularly vital. Mycorrhizal fungi form mutualistic symbioses with plants, facilitating water and nutrient uptake. Consequently, plant health is often tied to the mycorrhizal fungi community present in soil. The presence of mycophagous animals can alter or maintain rates of mycorrhizal colonisation by the dispersal of spores in their scats. While not obligately mycophagous, scat analyses of quenda (*Isoodon obesulus fuscivente*r) have shown they feed opportunistically on fungi, including many mycorrhizal species. To investigate the viability of quenda as a fungal vector, wild-collected quenda scat was used as a mycorrhizal inoculant to grow a keystone forest tree, *Eucalyptus gomphocephala,* from seeds under glasshouse conditions. Autoclaved scats were used as a negative-control and sporocarp tissue from known mycorrhizal species as a positive-control inoculant. Seedlings were harvested at ten weeks to assess plant growth, and early mycorrhizal colonisation of roots was determined using Next Generation Sequencing. Seedlings grown in scat inoculant had significantly more diverse assemblages of mycorrhizal fungi compared to negative- and positive-sporocarp controls. However, no difference in shoot or root mass in these young seedlings could be attributed to root fungi assemblages at this early growth stage. Mycorrhizal spores from quenda scat successfully germinated and colonised *E. gomphocephala* seedling roots. In addition to their bioturbator role, quenda can improve biological activity for forest health by dispersing viable mycorrhizal spores across the landscape.

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House mice and wood mice as historical proxies: Phylogeography of mice transported by the Vikings

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The use of genetic markers to track colonisation history of mammal species is largely applied to natural colonisations, such as the end glacial colonisations of previously ice-covered areas in northern latitudes. However, it is also possible to use genetic markers to track colonisations of mammal species inadvertently transported as stowaways on boats, such as house mice (*Mus musculus*). Those mammalian colonisations obviously reflect historical movements of people. Therefore, if comparisons of mice from possible source areas are made with mice from places colonised, any similarity reflects historical movement of people between those two areas. Vikings transported foodstuffs and livestock around the periphery of Europe and mice were able to exploit those resources. There is a remarkable correspondence between mitochondrial lineages of house mice and areas of occupation by Vikings, with differentiation between mice in the Danish Viking area and mice in Norwegian Viking area. Evidently Vikings were important in the foundation of house mouse populations in the northwestern periphery of Europe, and we can see this because particular mitochondrial types became associated (by chance) with particular types of Viking – being transported by them wherever they went. The colonisation of Iceland by mice and people is particularly interesting. The history of human colonisation of Iceland is well-described in the sagas, and two species of mice: house mice and field mice (*Apodemus sylvaticus*) were taken there, and they occur throughout Iceland. These features create opportunities of using mice as fine-scale proxies of human history.

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Phylogeography, demographic history and genetic connectivity of Asian elephants (*Elephas maximus*) in the Tenasserim Range, Thailand

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Due to habitat fragmentation and conflicts with humans, distribution and abundance of Asian elephant have declined throughout mainland Southeast Asia (Indochina), however the impacts of this fragmentation on the genetic diversity and connectivity of important regional populations is unknown. First, we assessed the demographic history of Indochinese elephants using 600-bp mtDNA sequences to test the prediction of long-term stability of this population dating back 600 KYA. Second, in the current timeframe, we used 10 microsatellite loci from 167 dung samples to test whether there were genetic structures between the Western Forest Complex (WEFCOM) and Kaeng Krachan Forest Complex (KKFC), two large protected areas which were formerly connected as part of the Tenasserim Range along the Thailand-Myanmar border. From 39 mtDNA variable sites, we identified 13 haplotypes: 6 α and 7 β haplotypes. The presence of two highly divergent clades splitting approximately 2.149 MYA suggests the Tenasserim is a zone of secondary contact of individuals previously isolated in at least two refugia. Four α and 1 β haplotypes were unique to the Tenasserim. A Bayesian skyline plot of the a haplotypes indicated a large, stable effective size of females (N_{ef} =13,000) in Indochina since 600 KYA. However, the estimated low current gene flow (within five generations or 100 years) across landscape was insufficient to prevent genetic differentiation (R_{ST}=0.03, K=2) between WEFCOM and KKFC based on our spatially explicit model. Landscape planning that restores dispersal between these populations is needed to ensure viability of elephant populations in the Tenasserim landscape.

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Temporal variation in the genetic composition of a newly established population of dibblers (*Parantechinus apicalis*) reflects translocation history

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Loss of genetic variation and increased population differentiation from source populations are common problems for translocations that use captive animals or a small number of founders to establish a new population. This study evaluated the genetic changes occurring in captive and translocated populations of the dibbler (*Parantechinus apicalis*) that were established from multiple source populations over a ten year period. While the levels of genetic variation within the captive and translocated populations were relatively stable and did not differ significantly from the source populations, their effective population size reduced 10–16 fold over the duration of this study. Evidence of genetic bottlenecks was detected only after the translocated population was established. There were also marked changes in the genetic composition of both populations that were strongly associated with the origins of individuals introduced to the populations. Interbreeding between individuals from different source populations lowered genetic relatedness among offspring, but this was short-lived. These results highlight the importance of the origins and the timing of release of founding individuals in determining the genetic composition of a newly established population.

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Limited dispersal in an ectoparasitic mite, *Laelaps giganteus*, contributes to significant phylogeographic congruence with the rodent host, *Rhabdomys*

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Exploring how biogeography, parasite life history and host vagility influences evolutionary codivergence, we followed a comparative phylogeography approach using a host-specific non-permanent mite, *Laelaps giganteus*, that occurs on four rodent species within the genus *Rhabdomys*. A mtDNA COI haplotype network derived for 278 parasite specimens showed marked phylogeographic congruence with host distributions. Analysis of the less variable nuclear intron Tropomyosin was partially consistent with these results. Although distance-based cophylogenetic analyses in AXPARAFIT failed to support significant mtDNA codivergences ($P \geq 0.02$), event-based analyses revealed significant cophylogeny between sampling localities of *Rhabdomys* and *Laelaps* using CORE-PA ($P = 0.046$) and JANE ($P = 0.026$; $P = 0.00$). These findings, in conjunction with the weak congruence previously reported among the permanent ectoparasitic lice *Polyplax* and *Rhabdomys*, suggest that host–parasite intimacy is not the most important driver of significant codivergence in our study system. Instead, the more restricted dispersal ability of *L. giganteus*, when compared to *Polyplax*, resulted in stronger spatial structuring and this could have resulted in significant codivergence. Host switching occurred predominantly on the edges of host distributions and was probably facilitated by climate-induced range shifts. When host ranges shift, the phylogeographic structure of *L. giganteus* is not reflecting the host movements as most of the nest bound parasites do not disperse with the host (they miss the boat) and the genetic contribution of the few dispersing mite individuals is often overwhelmed by the large number of individuals already present in nests within the new environment (causing them to drown on arrival).

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Monitoring koala density and habitat condition to trigger management intervention in an overabundant population in south-eastern Australia

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Some koala (*Phascolarctos cinereus*) populations in south-eastern Australia occur at high density, resulting in over-browsing of preferred food trees. The koala population on French Island, Victoria, has high fecundity and low mortality, resulting in over-abundance in many areas of preferred habitat. This issue is currently managed by Parks Victoria and the Department of Environment, Land, Water and Planning (State Government) via contraception and translocation. Preservation of habitat is the primary management goal, as this will achieve better overall biodiversity maintenance. Effective management, which requires setting priority areas for management within budget constraints, is an ongoing challenge. This long-term study is examining koala density along permanent transects, and correlating this with food tree condition. In prime habitat, koala density was up to 24 ha^{-1}, vastly greater than the recommended 1 ha^{-1} for suitable Victorian koala habitat. At these densities there is significant defoliation of the more preferred food tress, which places them at serious risk. Data on the percentage of contracepted females across sites is also being collected, to examine how long it takes for population density to decline under the current management regime. This study will provide data on optimal population density for maintaining habitat in good condition, which will allow Parks Victoria and DELWP to prioritize their management efforts. Ultimately assessment of habitat condition will become the major data source for driving localised management intervention, as this is a more rapid, and therefore cheaper, method for determining when management intervention is required.

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Now you see me: How thermal imaging increases detection of cryptic nocturnal mammals in tropical regions

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Accurate measures of species abundance and distribution underpin effective wildlife management and conservation strategies. Obtaining these data is very challenging when researching the cryptic nocturnal arboreal mammals of in the dense forest of the Wet Tropics. Our research shows that using a hand-held thermal imager significantly increases the detection rate of all mid-sized arboreal mammals when compared to the most commonly used method of spotlighting. We determine the optimal environmental and mechanical parameters for thermal imaging, and we investigate 'cost-versus-result' of hand-held imaging devices currently available on the market. We suggest that hand-held thermal imaging is a great emerging technology for cryptic arboreal mammal detection across tropical forested regions and beyond.

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Population dynamics of the near-threatened Cabrera vole in Mediterranean farmland as assessed from non-invasive genetic sampling

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Non-invasive genetic sampling has been increasingly used to obtain demographic data for rare or elusive species, though its application to small mammals is still tenuous. Here, we explored the utility of non-invasive genetic sampling to provide insights on population dynamics of the near-threatened Cabrera vole, *Microtus cabrerae*, in a relatively large (250 ha) and highly dynamic Mediterranean farmland area from SW Portugal. During one year, we conducted intensive sampling of fresh scats on four occasions (late Autumn, Winter, Spring, and early Autumn). After identifying genotypes, we used capture-mark-recapture modelling techniques to estimate variations in population size and individual survival, while controlling for heterogeneous recapture probabilities. We found that population variations were in general agreement with previous studies based on life-trapping, peaking from Winter to Spring, and being lower in both Autumn surveys. However, density estimates were notably lower than those reported in less intensive farming systems. Recapture rates were negatively affected by genotyping success, and were higher for males. After controlling for these effects, we found that survival estimates were positively (albeit weakly) affected by population size, and were relatively higher for males. Reasons for such male-biased survival are uncertain, but may be related to possible female-biased dispersal, as predicted by the resource competition model for monogamous species. Overall, our study provides evidence that non-invasive genetic sampling yields useful insights into the ecology and population dynamics of rare and elusive small mammals, such as the Cabrera vole, which may be valuable for guiding management and conservation planning.

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Competition, courtship and control: Breeding strategies of female platypuses (*Ornithorhynchus anatinus*) in captivity

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Courtship behaviour is important in sexual selection by allowing animals to select or reject mates based on mate “quality”. Opportunities to study these behaviours are often limited and they have never been studied in wild platypuses (*Ornithorhynchus anatinus*) due to their cryptic nature. We studied breeding pairs and trios of platypuses over seven years in a successful captive breeding program at Healesville Sanctuary, Victoria, to describe and quantify breeding interactions, to determine which sex controlled courtship behaviours and to investigate whether females used evasive strategies to avoid mating. Behaviour, including non-contact and contact courtship, mating and avoidance, was recorded daily with infrared cameras and footage analysed for these activities. Breeding behaviours occurred over 41.0 ± 6.6 days, with females behaviourally receptive for 29.6 ± 5.1 days. Females demonstrated evasiveness and controlled the duration of breeding behaviour in 79% of encounters. We also describe a new, antecedent courtship behaviour, with females reducing or changing their activity in the pre-breeding phase while they were non-receptive to minimise contact with males, most likely to avoid injury from coercion, as males are often quite aggressive. We obtained the first record of two females competing for access to a male and also to nesting material. Time invested in courtship behaviour and mating was not an indication of breeding success, with failures to breed more likely during fertilization, nest building or incubation. We have shown evasiveness and control of breeding behaviours by female platypuses and the importance of these behaviours in captivity for successful breeding.

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The applicability of a Bayesian state-space model for evaluating the effects of localised culling on subsequent density changes: Sika deer as a case study

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At the landscape scale, localised culling is often conducted to achieve various deer management aims. However, few studies have assessed the effects of localised culling on deer population dynamics due to the spatially and temporally insufficient datasets of deer abundance that are derived from limited survey efforts. Here, we estimated the population dynamics of a sika deer (*Cervus nippon*) population in the Tanzawa Mountains, Japan, using Bayesian state-space modeling employing spatially and temporally insufficient abundance indices; we evaluated the effects of localised culling on subsequent density changes in 56 units. The responses of deer density to unit-specific culls differed greatly among units. Further, there was no correlation between the intensities of unit-specific culls and the reduction in density. Deer populations in some units tended to resist density decreases despite high culling pressure, whereas those in other units exhibited decreases in density with little to no culling pressure. Because the spatial scales of each unit were relatively small (the average size is 13.6 km^2), annual density changes in each unit were largely influenced by deer migration in this estimation. The obscured effects of unit-specific culls, which were probably derived from deer migration in this case study, re-emphasize that deer migration should be incorporated into the planning of localised culling, and that management should be coordinated over a wide area transcending landscape components and land ownerships. We thus demonstrate that Bayesian state-space modeling is valuable for practical deer management programs over a large spatial scale even if different abundance indices are used.

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International cooperation to improve frontline wildlife forensics, using the illegal rhino horn trade as a case study.

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Wildlife crime is a trans-national business worth upwards of USD 23 billion dollars a year. The primary demand for many of these wildlife products comes from Asian countries such as Vietnam and China for use in traditional medicines or as trophies seen as symbols of status and wealth. Appropriate action by law enforcement and successful prosecution is often hindered in these countries by the lack of appropriate forensic infrastructure, preventing comprehensive intelligence collection. While the magnitude of trade in Australia is relatively lower than some of its neighbouring Asian countries. Australia does have established and accredited wildlife forensics facilities and the resources to provide both efficient forensic case work, as well as research, development and validation of new testing schemes. Given the common nature of many of the trade items that wildlife forensic labs across the globe are asked to identify (i.e. rhino horn, elephant ivory etc), laboratories like ours, The Australian Centre for Wildlife Genomics (ACWG) at the Australian Museum Research Institute, Sydney Australia, are well positioned to provide capacity building and training opportunities throughout the region. This talk will outline joint projects by the ACWG, civil society organisations such as TRACE Wildlife Forensics Network and TRAFFIC and participating European and Asian wildlife forensic laboratories to develop and implement improved and standardised testing across the globe, using the illegal rhino horn trade and the development of appropriate forensic tools as a case study.

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Wolf-dogs, “wild dogs”, and beefalos: What do we do with hybrids and why is policy falling short?

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Hybridisation and introgression affect a range of species globally, challenging the biological species concept. Animals that blur our definitions complicate species management as there are limited policies and guidelines to shape our decisions for dealing with such animals. This is particularly important for threatened species affected by hybridisation by either wild species or their domesticated relatives, where, especially for the latter, management may result in lethal control of hybrid animals. We investigate the degree of threat by hybridisation to threatened vertebrates globally, by analysing the key threats for species listed on the IUCN Red List. We then analyse mammalian species threatened by hybridisation in particular, to identify to what extent policies have been developed to address the issue. Using case studies, we discuss how lack of appropriate policies can lead to inaction in conservation management, and where human-wildlife conflict occurs, ambiguity allows affected stakeholders to interpret policy to suit their purpose, such as livestock producers culling wild canid-dog hybrids. We argue that research is needed to determine the biological role of hybrids which should inform policy on a species-by-species basis.

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Thermal physiology concepts revisited: Misconceptions in predicting mammalian responses to climate change

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Because anthropogenic land fragmentation will prevent large terrestrial mammals from dispersing, the future welfare of these mammals will depend on their abilities to cope with changing climates in their existing habitats, and the capacity of phenotypic plasticity to extend those abilities. Correlative and mechanistic models have been constructed to predict the welfare of mammals under climate change. Mechanistic models, currently preferred, require an appreciation of thermal physiology, sometimes wanting. For example, some mechanistic models assume that any conditions outside the thermoneutral zone (TNZ) will be deleterious, but there is no evidence that TNZ has any relevance to mammalian ability to cope with climate change. Desert antelope live and reproduce at air temperatures well above their TNZ. TNZ usually is defined by air temperature and the heat loads experienced by mammals depend on much more than air temperature, with direct, reflected and reradiated solar radiation often forming the major component of the load. Some models, whether based on TNZ or not, ignore radiation. Some mammalian models inappropriately import concepts from ectothermy. The concept of temperature-dependent optimal performance may provide insight into ecology of ectotherms, but is less relevant to mammals. Homeothermy is not a requirement for sustained existence in mammals. Large mammals under heat load maintain homeothermy if they are resourced well, but relax homeothermy if water or food become limited. Their temperatures are unpredictable without knowledge of their nutrition and hydration. Large mammals give priority to water regulation over thermoregulation. If water is available, large mammals, including elephants that neither sweat nor pant, use evaporative cooling to support homeothermy. The use of evaporative cooling is not an unsustainable state, as is assumed by models that employ upper limits of TNZs to predict lethal limits. Another concept imported inappropriately from ectotherm thermal physiology is the assumption that skin temperature is equal to air temperature. Our measurements, including infrared thermography, have confirmed that the skin temperature of free-living large mammals may be far from air temperature. The mechanistic models also tend to ignore the wealth of information available from humans. For example, studies of human acclimation show that acclimatization to heat lowers body core temperature; some models assume that mammalian core temperature is insensitive to environment. Contrary to some models that predict the opposite, we have shown that core temperature decreases with increasing body mass in large mammals. A widely-acknowledged limitation of both correlative and mechanistic models is that they tend to address the welfare of species independently of their biotic environments. We and others have shown that the future welfare of large mammals will depend not only on their abilities but also on the resilience of their plant and animal food under climate change. Finally, all models suffer from uncertainty about how mammals will respond physiologically to climate change. Better predictions will require long-term studies, requiring biologging, of the thermal physiology of large mammals living free in their natural habitats and unstressed by human observers, studies that we have begun.

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Integrated foraging ecology and the magnetism of food patches

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Foraging ecology seeks to understand the drivers behind where animals go and what they eat in a spatiotemporal context. To date, much of the theory is about why animals quit patches: the extrinsic and intrinsic factors animals incorporate in rules governing decisions of when to leave. But patch quitting is only part of the foraging story. An equally important question is – why visit in the first place? Deciding which patches to visit involves perception, attention, learning, cognition, and detection of cues in reasonably short timeframes; overlaid by factors acting on a longer timeframe and associated with background risks, nutritional status, experience and memory of the foraging landscape. So an integrated foraging theory should incorporate the question of "why visit?" as well as the question "why quit?" We explore these questions with a focus on mammalian herbivores. We introduce a conceptual model of food patches as a landscape of magnets that attract and repel; and consider the rules animals use to manoeuvre through this magnetic landscape at small temporal scales associated with visiting and quitting patches. We argue that characteristics of food patches that attract animals, i.e. the cues or signals they emit, should be considered an important axis of patch quality. By adding this axis we can integrate sensory and movement ecology with classic foraging models such as optimal, Bayesian, and risk sensitive foraging.

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Plant odour and visual cues as proximate attractors to food patches

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Key foraging decisions herbivores make are where to go and what to eat. Yet, we know very little about the cues herbivores use to make these decisions, nor the scale at which these cues are used. By detecting high quality food from afar, herbivores could forage more efficiently. To explore this, we tested the use of plant cues by two generalist browsers, African elephants and (Australian) swamp wallabies. Semi-domesticated elephants were able to locate preferred plants within feeding stations, and between patches using only olfactory cues. Elephants could also detect and select tiny food rewards through odour alone despite background odour from unpreferred plants. In the absence of visual cues, free ranging swamp wallabies relied on odour to locate high quality *Eucalyptus* seedlings. Moreover, time to discovery was related to odour cue size (i.e. number of leaves). When leaf odour was suppressed in whole seedlings yet visual cues intact, seedling detection at night was severely compromised. Though, suppression of visual cues with odour intact had a smaller impact, delaying discovery compared to whole intact seedlings, but not restricting nocturnal detection by wallabies. We conclude that leaf odour plays a critical role in the foraging efficiency of these mammalian herbivores. Moreover, the use of cues to detect plants may provide insight into food quality. As such, we suggest that these cues, in particular the role of leaf odour, should be explored in other plant-mammalian herbivore systems.

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Australia: extreme post-European mammalian extinction; extreme dependence upon remains for knowledge of many native mammal species

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Immediately before European settlement, the Australian mainland fauna included about 320 species of land mammals comprising 3 monotremes, 174 marsupials, 75 bats, 67 native rodents and the dingo. Extinction has been uneven among the groups. While the bats have suffered no extinctions, many non-volant species in a critical weight range (CWR) between 35 and 5,500 grams adult body weight have either become extinct or are endangered. CWR insectivorous marsupials have generally survived better. Native rodents, except for members of the genus *Rattus*, have been particularly badly affected. The extinction was very rapid, and continues because the main threatening processes (feral cats and foxes) remain. A consequence of the speed of extinction was that the majority of populations of susceptible species disappeared before they were sampled by collectors, and several originally widespread extinct species are only known from very few live-caught specimens. At least 7 species with restricted ranges were never collected alive at all. Sites containing late Holocene mammal remains are abundant in Australia, with >740 in the western two-thirds; most are caves in karst limestone or desert mesas and ranges, but also sand dunes and tree hollows. The main accumulators were owls. Mammalian predators also contributed. Remains reveal that many now extinct or endangered species originally had vast geographic ranges. Understanding of the ecology of many Australian native mammals, and the communities of which they were members, can only be achieved by studying their remains using multivariate analyses incorporating correlations with surviving species with known ecological requirements.

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Fossil insights into the peri-European diversity and decline of terrestrial mammals from Australia's Murray Darling Depression.

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Faunal baselines are fundamental for understanding and abating biodiversity declines. However, these can be highly reliant on historical records derived from already disturbed ecosystems. In the Murray–Darling Depression bioregion of Australia, European settlement and associated ecosystem changes elicited rapid declines and losses of native species. These losses occurred prior to systematic documentation of the region's fauna, thus masking their extent. We describe a dated vertebrate fossil assemblage from Light's Roost, lower Murray Mallee region of South Australia, and combine our findings with other local fossil assemblages and historical records to reconstruct the region's pre-European mammal fauna (excluding bats). Our revised faunal baseline shows that the region's original mammal fauna was more diverse than formerly known and underwent substantial reduction after Europeans colonised the area. Half of the Murray–Darling Depression's mammals that were present when Europeans arrived have been lost since this time. Lost species include the mulgara (*Dasycercus blythi/cristicauda*), placing the taxon within 40 km of the hitherto-disputed type locality for *D. cristicauda* at Lake Alexandrina. Nearly half of the Murray Mallee fauna is known principally from fossils and over three-quarters of the fauna were represented in the fossil record. Our findings show that baselines for species distributions taken from historical records and modern faunal surveys can be improved by inclusion of fossil remains, particularly for smaller and more cryptic species. Deficiencies in regional records can conceal the scale of mammal declines resulting from European colonisation and associated land-management practices, and thus their vulnerability to anthropogenic disturbance.

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It's time to hit the road; temporal overlap of species using tracks

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Linear clearings, such as roads and tracks, are often the only obvious anthropogenic feature in many remote environments where infrastructure is sparse. When multiple species use such clearings for movement, their spatial and temporal patterns of use of these features can potentially influence the species interactions. Here, we used a paired camera trap array to investigate temporal patterns in the use of cleared seismic lines at four time points post clearing (1 mo, 3 mo, 7 mo, 48 mo) by five mammal species; bilbies (*Macrotis lagotis*), feral cats (*Felis catus*), dingoes (*Canis lupus dingo*), agile wallabies (*Macropus agilis*) and cattle (*Bos indicus*). Temporal overlap between bilbies and cats was 0.68 on seismic lines, and 0.55 in control areas. A similar relationship was seen between bilbies and dingoes (0.66 on seismic lines, and 0.33 in control areas). Temporal overlap between cats and dingoes was not different between treatments (0.73 on seismic lines and 0.68 in control areas). Feral cats, dingoes, and cattle used seismic lines at different times from control areas, whereas bilbies and agile wallabies showed similar activity times both on and off seismic lines. Our results indicate that linear clearings can significantly alter the activity of some species, which may in turn affect predator-prey, or predator-mesopredator relationships.

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Spatiotemporal relationship between guanaco (*Lama guanicoe*) and hare (*Lepus europaeus*) and their role as prey for the endangered mountain lion (*Puma concolor*) in the Andean Mountains of Central Chile (34º 27´ S, 70º 27´W).

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The demise of the guanaco in the Andes of central Chile after hunting and livestock competition peaked 50-70 years ago in the Mediterranean ecosystems of Chile. Hares became the predominant wild herbivores besides domestic livestock in this mountain range. The Río Cipreses Natural Reserve was established to protect a small population of guanacos in 1984. Cattle were removed and guanacos recovered from the brink of extinction. We studied how hares and guanacos overlapped in space and time (Co-occur and overlap packages in R) and determined their ecological role for puma subsistence. A camera trap study (n=5,008 trap-nights) between 2013-2015 and puma scat collection since 2012 (n=107 scats) showed that hare-puma and hare-guanaco co-occurred spatially and time overlap was only significant between puma-hare. Hares' percentage of occurrence in the diet was 71% and hares accounted for 85% of the relative biomass consumed by pumas. Our results indicate that the hare continues to be the most important prey item in the diet of the puma, despite guanacos 1,000% increased population to about 250 animals in the study area (8,372 ha). We discuss the ecological role of hares as exotic prey for the survival of pumas.

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Free ranging body temperature of mammals: Are there still phylogenetic effects?

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It is well documented that resting body temperature (T_b) of mammals, measured under standard laboratory conditions, differs for the three major clades, with average T_b lowest for monotremes (30.9°C), intermediate for marsupials (35.5°C), and highest for placentals (36.6°C). It is not clear whether these phylogenetic differences remain for mammals when active in the field, but the increasing use of small implantable temperature loggers enables this question to be addressed for resting, active and maximum T_bs. Monotremes in the field have a lower maximum active T_b (about 35.3°C) than both marsupials and placentals, which do not differ (about 39.3 and 39.9°C respectively). Similarly, active T_b is lower for monotremes in the field (about 33.1°C) than both marsupials and placentals, which do not differ (about 37.5 and 37.8°C respectively. Resting field T_b is different for monotremes (about 31.2°C), marsupials (about 33.9°C), and placentals (about 35.5°C). The similarity of maximum active and active T_bs for marsupials and placentals in the field suggests that T_b-dependent physiological differences between the two clades when resting in the laboratory (such as metabolic rate and evaporative water loss) will be reduced but probably not eliminated during activity in the field.

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What body temperature patterns reveal about the functioning of large free-living mammals

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Although the temperature-regulating system usually acts to maintain mammalian body core temperature high and within narrow daily limits, conspicuous and predictable perturbations to body temperature are evident in large free-living mammals under different physiological states. Through the use of biologging to record body temperatures continuously in large (greater than 5kg) mammals in their natural habitat, we have shown that restriction of food energy or water leads to a trade-off that relaxes thermal regulation and results in heterothermy. Maintaining homeothermy requires a mammal to use energy and water. Dehydrated mammals exhibit higher than normal maximum daily body temperatures, while insufficient energy leads to lower minimum daily body temperatures. This relaxation of body temperature does not appear to be regulated and moves a mammal closer to its thermal limits of performance. Regulated changes in body temperature are evident in fever and during reproduction. Spontaneous fevers in free-living mammals are characterised by an upward shift in body temperature, without changes to the daily rhythm, which may last from days to weeks. In contrast, a progressive reduction in body temperature is evident in female mammals throughout gestation, with parturition characterised by an immediate return to normal body temperature. Body temperature patterns therefore provide a measure of reproductive phenology, infectious illness, malnutrition and dehydration in large free-living mammals. Long-term biologging of body core temperature therefore provides a tool for us to investigate how large mammals work in the natural environment, and how their functioning may be altered when confronting environmental change.

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‘Scoop a Poop’- Citizen Scientists tackle antibiotic resistance in the wild

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Combating antibiotic resistance requires a multimodal approach, spanning community, basic science, medical and veterinary practice. Public awareness is central for dealing with the problem of antibiotic resistance and its global effects on populations. We aim to use wildlife as a vehicle for conveying issues of antibiotic resistance to the public by involving citizens in fundamental science that addresses dissemination of resistance. Under the banner ‘Scoop a Poop’, citizens will learn about resistance, how to identify and collect wildlife scat samples, and become familiar with the science used to investigate resistance. Participants (school students) will collect possum scats from urban backyards using a specially designed kit. They will also have the opportunity to attend university for a day to learn the DNA methods used to test samples for resistance genes. We will leverage the increased sampling intensity afforded by citizen participants to assess the ecology and transmission of antibiotic resistance in a widespread species, the brushtail possum. Possums thrive in rural and remote areas, but have also adapted well to urban environments. They are therfore exposed to varying levels of contact with antibiotic resistance genes carried by humans and domesticated animals. Consequently, possums are a potential sentinel species for understanding dissemination of antibiotic resistance in the Australian environment. Addressing this issue at the ecosystem level will help direct decisions on where national efforts should be placed in combatting transmission of resistance between environmental compartments.

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Subtle dietary differences are associated with significant shifts in the composition, diversity and functional capacity of the gut microbiome of a true dietary specialist, the koala.

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As an obligate dietary specialist feeding almost exclusively on the foliage of a single plant genus, *Eucalyptus*, the koala (*Phascolarctos cinereus*) is a rarity amongst mammals. The koala has a particularly large hindgut and slow gut passage rate, accommodating a gastrointestinal microbiome that assists in digestion of this diet, which is physically tough, nutritionally poor, high in fibre and defended by digestibility-reducing tannins and numerous toxins. Using 16S amplicon sequencing followed by a gene-centric analysis of whole-community shotgun sequencing data, we characterized the gastrointestinal microbiomes of 20 koalas from a single geographic location but with two contrasting diets: *Eucalyptus viminalis*, a highly-preferred species that supports unsustainable rates of koala population growth, and *Eucalyptus obliqua*, a less-preferred species with low koala densities. *E. viminalis* has more protein and digestible protein than *E. obliqua* and lower tannin and fibre concentrations, and a different suite of defence compounds. Of the two diets, *E. viminalis* produced microbiomes with fewer bacterial species and less diversity which were dominated by the bacterial genera *Parabacteroides* and *Bacteroides* (Phyum Bacteroidetes) rather than by genera from the family Ruminococcacea (Phylum Firmicutes). We highlight likely microbiome functional differences identified from catalytic and carbohydrate-binding enzyme abundances associated with oligo- and polysaccharide degradation from the CAZy database, and potentially active metabolic pathways identified from the KEGG database. These differences highlight the close association between the koala, its diet and its symbiotic gut microbes and raise the question, can specialized microbial communities further narrow the nutritional niche of their dietary specialist hosts?

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Status and distribution of two otter species in coastal areas of southern Thailand

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The smooth-coated otter (SMO) and small-clawed otter (ASCO) are both globally threatened species important for the stability of riverine ecosystems. However, their current distribution status in southeast Asia is still unclear and thus difficult for conservation management planning. This project aims to (1) assess their current distribution status in coastal areas of southern Thailand, (2) evaluate distribution change and the factors influencing the changes, and (3) identify hotspot areas for otter conservation. We conducted surveys using both local fishermen interviews and field surveys (direct sighting, track and sign, camera-trap). During the first six months (July-December 2016), surveys covered 29 grids (725 km^2). Each grid contained at least 10% mangrove forest. In total, 125 line-transects were surveyed and 123 camera-traps were set (2,165 trap-nights). Based on interview (n = 50), most (50%) local fishermen believe that the populations of both otter species have declined during the past 30 years due to hunting, persecution, being kept as pets and prey depletion, respectively. Combining all survey methods, SMO appears to occupy two times larger area than ASCO (21 vs 9 grids). From camera-trap data, SMO has occupancy estimate at 72% (95%CI = 33-93%), with detection probability at 25% (95%CI = 14-40%). Camera-trapping is the most suitable method for confirming species presence in these habitats. Persecution and opportunistic hunting remain a threat, and thus require more attention.

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The cost of conservation, conflict and welfare in a commensal baboon population, South Africa

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Primate populations are threatened by habitat loss and fragmentation yet behavioural and dietary flexibility in baboons (Papio sp.) have enabled them to thrive in select anthropogenic landscapes through access to nutritious food and the elimination of natural predators. On the Cape peninsula, South Africa, the baboon population (*Papio ursinus*) is geographically isolated and persists within a fragmented matrix of housing, agriculture and natural land. Chronic levels of conflict exist between baboons and people and between people on how best to manage them. Concerns about the viability of the population led to legislation to protect the baboons and the implementation of an intensive management program using field rangers and pain aversion to minimise the overlap of baboons and people, thus reducing conflict. In this study we review the development of baboon management and conservation strategies by analysing long-term demographic data for the population, including injuries and mortality. Our results reveal steady growth in the overall population but with marked regional variation linked to both land use and socioeconomic factors. Human-induced injuries and death have both declined substantially which together with facilitated dispersal is improving the welfare and conservation status of the population. Reduced human-caused mortality of baboons in the absence of natural predators is predicted to stimulate rapid population growth in an expanding city. Management will need to consider alternate options including contraception, removal of individuals or groups and intensive efforts to reduce access to anthropogenic food sources. The Peninsula baboon population exemplifies how omnivorous, generalist mammals can adapt to anthropogenic environments.

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Evolution and development of functional change, increase, decrease, and loss of teeth in mammals: examples of Carnivora and platypus

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Evolution of dental morphology and dental formulae is an important topic in mammalogy. Carnivora is a successful taxon in terms of dietary divergence. The molar row of Carnivora is separated into two parts: in the lower molars, the anterior part of the first molar possesses a shearing function that benefits a carnivorous diet, whereas the posterior part of the first molar and the remaining molars possess a grinding function that benefits an omnivorous diet. The shape of the first molar, relative size of molars, and the number of molars are important for dental function. According to the result of a comparative morphological analysis of museum specimens and gene-manipulated mice as well as molecular evolutionary analysis, all three factors can be changed by molecules that represent a developmental model, the inhibitory cascade model (such as BMP7). The model can also explain the increase and decrease of molar number in Carnivora. Among all mammals, the modern platypus is a unique mammal, which has lost teeth but still masticates using horny pads. However, their direct ancestor *Obdurodon* possessed teeth. Comparative cranial morphological analysis revealed that *Obdurodon* had a larger infraorbital foramen than the modern platypus, indicating that *Obdurodon* possessed a less-developed maxillary nerve that passes sensory information from the bill to the brain. Additionally, the modern platypus has a thin maxilla that is unable to house a tooth root because of a well-developed infraorbital canal. These results indicate that loss of teeth in the modern platypus is a resulted of amplification of electroreception.

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Gene expression, not local adaptation, sufficient for pikas to occupy vast Himalayan elevational gradient

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Species are shifting their ranges due to climate change, many moving to cooler and higher locations. However, with elevation increase comes oxygen decline, potentially limiting a species' ability to track its environment depending on what mechanisms it has available to compensate for hypoxic stress. Pikas (Family Ochotonidae), cold-specialist small mammal species, are already undergoing elevational range shifts. We collected RNA samples from one population of *Ochotona roylei* in the western Himalaya at three sites – 3,600, 4,000, and 5,000 meters – and found no evidence of significant population genetic structure, nor any loci under positive selection between sites. However, out of over 10,000 expressed transcripts, 26 were significantly up-regulated at the 5,000 m site and were significantly enriched for pathways consistent with physiological compensation for limited oxygen. These results suggest that differences in gene expression alone may enable hypoxia tolerance on this local scale, indicating elevational flexibility that may facilitate successful range shifts in response to climate change.

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Mind the gaps: Assessing continent-wide knowledge of small African carnivores

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Small African carnivores – here defined as African carnivorans with an adult body mass < 15 kg – represent about 35% of extant small carnivores worldwide. Eight of the world's 13 terrestrial carnivore families have representative species meeting this criteria in Africa (Canidae: 14% of small African carnivores; Eupleridae: 8%; Felidae: 9%; Herpestidae: 32%; Hyaenidae: 1%; Mustelidae: 12%; Nandiniidae: 1%; and Viverridae: 21%). In spite of this diversity, studies on larger species seem to dominate African carnivore research. To both quantify research bias and highlight knowledge gaps for small carnivores in Africa, we undertook a thorough literature review of all published works until April 2014 on African carnivores, both large and small. We identified 6,270 published records for all carnivore species. Sixty-three percent of all papers focused on at least one of the 10 large African carnivore species, while only 37% were focused on the remaining 81 small species. Utilising titles and abstracts we scored papers across 21 categories to identify particular areas of research lacking for individual species. For small African carnivores, a majority of research to date has focused on peripheral inclusion of species in broader studies (e.g. carnivoran phylogenies, morphological evolution), evolution of sociality in mongooses, and distributional records/observations. Little to no research exists on the fundamental ecology or conservation status of most small African carnivores. We therefore strongly encourage more research to increase our understanding of the ecological roles and, when relevant, better devise protection measures for this diverse and understudied group of small carnivores.

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Aspects of the ecology of a poorly-known conflict-prone mesocarnivore: The case of the caracal (*Caracal caracal*) on farmland in South Africa

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Livestock depredation by carnivores is on the rise worldwide and is one of the key conservation issues in arid landscapes with low abundance of wild prey. To mitigate such a conflict, understanding its drivers is the first step conservationists should undertake. In South Africa, extensive conflict between small-livestock farmers and caracals (*Caracal caracal*) is reported to impact adversely on biodiversity and to threaten human livelihoods and food security. However, we know very little about caracal ecology, especially on farmland and about farmers' management practices and attitudes towards this cryptic cat. We monitored 12 caracals using GPS radio-collars on farmland in the South African Central Karoo semi-desert and studied diet through GPS location clusters (> 100) and scat collected on farmlands (n = 102) and in a nearby protected area (n = 80). We conducted face-to-face interviews with 77 local farmers to assess their tolerance of caracals. Caracals diet determined through scat analysis on farmland consisted primarily of domestic ungulates (25%) and scrub hare (19%) while they mostly prey on micromammals (58%) in the reserve. At GPS clusters, we found 30 wild prey items (rock hyrax: 22%) and 16 domestic prey items (sheep: 32%). Questionnaires showed that retaliation by trapping and hunting is common in the region. Caracals were ranked second most damaging predators with 94.8% of the farmers wanting to reduce their number on their farms and 41.6% wishing to eradicate caracals completely. Our work is the first one to provide information on caracals' movement, diet choice and interactions with farmers in a landscape where they are heavily persecuted.

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Genome-wide SNP-based high-throughput DNA sequencing helps resolve long-standing issues in Australian bat taxonomy

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With unabated encroachment of human land uses on natural habitats, there is an increased imperative to catalogue biodiversity, produce accurate identifications and understand species distributions. Such knowledge helps to increase clarity and confidence in decision-making as part of environmental impact assessments. However, taxonomic ambiguities undermine this process, even in mammals that are often assumed to be adequately described. High through-put DNA sequencing technology has exceptional power to help resolve species boundaries and taxonomic issues that remain in numerous bat groups. It can be particularly helpful in speciose groups characterised by low morphological diversity, island forms and an abundance of poorly ‘anchored’ taxonomic names. We present two simpler but typical cases where high-throughput sequencing has helped overcome the technical limitations of preceding methods. Reduced representation sequencing was used to investigate reproductive isolation between two cryptic sister taxa of *Taphozous* over a 1000 km long zone of potential sympatry and hybridisation; and gene capture was used to evaluate the taxonomic status of the allopatric Pilbara and more northern populations of *Rhinonicteris aurantia*. Genome-scale reduced representation sequencing is also comparable in cost to Sanger sequencing, and can be an efficient and cost-effective addition to an integrative approach to taxonomy.

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Predicted climate change impacts on the phylogenetic diversity of bats across the Australian continent

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Conservation programmes that aim to protect and enhance Australia’s biodiversity have typically been focussed at the species level, but there has been a push to broaden the focus to incorporate genetic, functional, and phylogenetic diversity. Australia’s phylogenetic diversity needs protection because it contains a concentration of plant and animal lineages not found elsewhere, and is particularly vulnerable to climate change. Phylogenetic trees have become available for many organisms, but no such tree existed for Australia’s bat biota. We set out to a) construct the first comprehensive phylogeny for Australian bats and b) using this information, predict how climate-induced range shifts might impact the distribution of bat species and phylogenetic diversity by 2085. The mitochondrial cytochrome-*b* and nuclear RAG1 genes were sequenced for most of Australia’s bat species, and trees were reconstructed using maximum likelihood and Bayesian methods. Trees were then paired with MaxEnt species distribution models for 60 species for which adequate point location data were available for construction. The models were developed both for present-day and 2085 climatic conditions based on climate projections. Finally, present and future species and phylogenetic diversity—the summed length of the tree branches—was calculated for the entire Australian landscape. This study is the first in

Oceania and Asia to establish the locations of important centres of bat diversity and to predict how that diversity might change in the future, which is key information for conserving this group.

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European bison: A post-bottlenecked recovery, its consequences and current threats

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The European bison (*Bison bonasus*) is a flag example of a successful recovery of a big ungulate species. It went extinct in the wild nearly 100 years ago due to mass poaching during WWI in the Białowieża Forest. Thanks to immense international effort, single remnants of the species from zoos and collections enabled its recovery and also their re-introduction into the forest, years later. Since the recovery, the total number of the species has grown up to 6000 individuals, the majority of which are in free-living herds.

However, the bottleneck that European bison went through left a dramatic mark on its genetic diversity and thus on its evolutionary potential. European bison have one of the least favourable genetic parameters ever reported for wildlife and extremely high level of inbreeding. The latter is associated with a series of developmental and reproductive disorders. Six to eight percent of males every year are affected by an incurable and lethal genetically-conditioned disease of male reproductive organs (*posthitis*). High genetic homogeneity of a species is a serious potential threat in case of emerging a new risk factor. The substantial threat for the European bison is also, most generally speaking, inapropriate management of the population i.e. unreasonable culling, excessive winter feeding, inadequate locations for new herds, rapid animal movements and lack of genetic monitoring of the transported animals.

The experience of the European bison reintroduction could be a reliable reference of potential ups and downs for any other megafauna species recovery.

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Which life-history variables have the greatest potential contribution to population growth rate? A test with marsupials

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Life histories of mammals vary along a fast-slow continuum. Mammals with fast life histories mature early, have large litters, and short life spans relative to mammals with slow life histories. Differences in life history have been linked to differences in the pattern of potential contribution of survival and reproduction to population growth rate (PGR). The eutherian pattern asserts higher potential contribution of age at first reproduction and fertility to PGR in fast mammals and higher potential contribution of juvenile and adult survival in slow mammals. However, eutherians and metatherians diverged in several aspects of their biology and ecology over the last 160 Myr. These differences reflect on the life history of the group and we hypothesized that marsupials do not follow the eutherian pattern of potential contribution. We measured the potential contribution of five variables to PGR in 17 species (26 populations) of marsupials with contrasting range of body sizes and life histories. Marsupials do not follow the eutherian pattern of potential contribution. Fertility was not an important variable for marsupials and juvenile survival had a great potential contribution to PGR no matter the life-history strategy adopted. Differences probably rely on the mode of reproduction. Fast species raise large litters which are highly vulnerable during weaning and juvenile phases. The low survival reduces female net reproductive rate and the actual number of young entering the population is similar to litter size of slow species. Thus, survival of young through weaning and juvenile phases is critical for marsupials.

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Ecology of gaur (*Bos gaurus*) in highlands of Central India: A case study of Pench Tiger Reserve, Madhya Pradesh (India)

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Indian gaur (*Bos gaurus*) is one among the nine species of wild oxen found in the world. Gaur is listed as endangered in IUCN Red list. The gaur ranges from India to peninsular Malaysia and the population of gaur in India is between 5000-10,000 individuals. Despite gaur's vast range of distribution, they are listed as endangered species and kept in schedule-I of the Indian Wildlife Protection Act (1972), appendix-I on CITES (2003). Due to habitat loss and illegal killing of the species, the population is declining. In the present study efforts were made to understand abundance, group composition and feeding habits of gaur in Pench Tiger Reserve. Pench Tiger Reserve is the 19th Tiger reserve of India, situated in Seoni and Chhindwara district of M. P. India (21°41′35″N 79°14′54″E). Distance sampling and microhistological techniques were used. The density of gaur was 1.82 ± 0.28 km^{-2} for the winter season whereas during the summer season the estimated density was 1.54 ± 0.30 km^{-2}. Diet compositions of gaur were studied using micro-histological examination of 32 dung piles collected from 169 sampling plots of 10 m radius established at 200m distance intervals. A total of 88 permanent reference slides of available plants were prepared and used for plant fragment identification from the different dung piles. A total of 36 species (28 browse and 8 grass) were identified from different dung piles of gaur. The results show that gaur are primarily a grazer as its diet constitutes 62.09% grass and 37.90% browse items.

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Platypuses and land-use practices: Catchment-scale studies provide some insight into the effect of forestry and agriculture

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Information on the impact of land-use activities on semi-aquatic mammals is limited. Such keystone species are of global conservation concern. Two catchment scale studies of the platypus in Tasmania provide insights into the impact of land-use activities on populations of this species. A study of platypus population health in a river catchment with a long history of forestry and agriculture took a multidisciplinary approach. Platypuses were found throughout the catchment and were generally in good health. There were no differences in infectious agents between subcatchments and age/sex categories. Higher capture rates and body mass in stream reaches running through cleared agricultural land were attributed to the naturally more favourable habitat in such areas compared to subcatchments with high forest cover (native and forestry combined). A second study investigated the use of streams by platypuses in a forestry dominated catchment. Surveys in 2000 found that despite the long history of forestry disturbance (since 1934), platypuses were found throughout the catchment, with larger streams used more often than smaller headwaters. Individuals in the headwaters were mainly sub-adults and adults in poor condition and they avoided streams disturbed in the 80's by logging. However, a follow-up study in 2015 found a similar sized platypus population. Analysis of the combined data indicated that use of streams by platypus was influenced primarily by both local and catchment factors, and to a lesser extent forestry disturbance. Improved management practices and the resilience of this species to environmental change may explain the findings of these studies.

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To what extent do elephants use pre-ingestive cues and/or postingestive feedback when making diet choices?

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Plant quality varies dramatically both among and within species, creating a patchy foraging environment. Elephants, like all other herbivores, can use various sources of information to assess plant quality, make dietary choices, and move among patches. Both pre-ingestive cues (appearance, smell, or taste of a plant) and postingestive feedback measures (crude protein, digestibility, tannin content) can potentially contribute to their process of dietary selection. The role of these mechanisms in influencing foraging of elephants is poorly understood. Previous studies have focused on postingestive measures and have yielded mixed results regarding their importance. Because all plants emit odours composed of various volatile organic compounds (VOCs), elephants could obtain information about a plant prior to ingestion. However, the degree to which they use pre-ingestive odour cues when making foraging decisions is unknown. We assessed the importance of postingestive measures and/or pre-ingestive cues (specifically plant odours). Dietary choices of foraging African elephants were compared to attributes of the available plant species that provided pre-ingestive cues and postingestive measures. We found that avoided plant taxa contained both high levels and a wide diversity of plant secondary metabolite odour cues, particularly monoterpenes, known antiherbivore compounds. Our behavioural studies and laboratory analyses suggested that these volatile monoterpenes played a stronger role in elephant diet choice than phenolics (such as tannins). This is likely because monoterpenes are a pre-ingestive cue that incurs postingestive costs. Furthermore, analysis of elephant saliva indicated that elephants likely can cope with a certain amount of tannins via salivary tannin-binding proteins.

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Does personality affect habitat use by common brushtail possums on the urban fringe?

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Animals living on the urban fringe have a choice between two very different environments: Houses and gardens with many roads *versus* natural plant communities or farmland. These environments likely vary in the quality of food they provide and the risks involved in accessing it. For small arboreal animals, urban areas may provide higher quality food, but higher risk from dogs, cats and traffic. How animals perceive habitat quality, especially risk, should affect their choices. As animal personality defines an individual's perception of and response to the environment, personality should also affect habitat use. Here we test whether predictable personality traits affect habitat use by a nocturnal arboreal herbivore, the common brushtail possum (*Trichosurus vulpecula*) on the urban boundary with open eucalypt forest near Sydney, NSW. We tracked brushtail possums using GPS collars every 3 minutes nightly (7-26 days), and conducted personality tests for all animals. We calculated range size from the 95% isopleth of the Brownian bridge movement model (BBMM), and core area size from 50% BBMM. We found that the proportion of core area spent in urban habitats varied between 7% and 83%, and we related this to the three personality axes; exploration, boldness and activity. This is the first study to quantify habitat use as a function of personality in mammals. We suggest that animal personality provides an additional important axis needed to explain intra-specific variation in habitat use, with significant implications to how we define and conserve high quality habitat for free living animals.

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Bringing the landscape of fear back to conservation

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Variations in animal behavior can be studied to assess how animals perceive spatial variation of their landscape. An important example is 'the landscape of fear' (LOF) in which maps of behavior reveal the comparative danger perceived by a species in the various habitats of its landscape. LOFs have many uses but here we use them for conservation, their original purpose. In particular, we look at two free-ranging mammals in their native habitats, dunnarts (*Sminthopsis sp.*) in the Simpson Desert, central Australia, and collared peccaries (*Pecari tajacu*) on Tumamoc Hill, Tucson, Arizona. We measured the LOFs for both species in their native habitat using foraging patches. Dunnarts, small desert marsupials, which are preyed upon by invasive predators, found that artificial shelters as safe only in a particular habitat, a goldilocks zone of natural shelters and preferred elevation on the sand crests. The group of collared peccary that we studied lives in a nature reserve with heavy human traffic on a hard-surfaced road. We discovered that the peccaries, though not shy of humans, perceive proximity to the road as added risk — they did not forage near pedestrian trails at all. We raise the baton, to show the application of this method for conservation purposes and wildlife management.

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Food availability for ungulates: First step to population reinforcement in protected areas of Itaipu Binacional (Paraguay)

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The Itaipu Binacional Hydroelectric plant owns 8 protected areas within the Upper Parana Atlantic Forest on the Paraná River located between Paraguay and Brazil. As part of the *Mazama gouazoubira* (brown brocket deer) and *Pecari tajacu* (collared peccary) population reinforcement program, individuals of these species born in captivity will be readapted to the wild in enclosures built for that purpose in the Tati Yupi Nature Reserve. These Readaptation Enclosures measure approximately 4.5 hectares. Sampling of trees and shrubs was carried out with 7 transects of 150 m. long by 4 m. wide. The species were identified, and the DBH (diameter at breast height) was measured. Also, the contribution that these will represent to the diet was analyzed according to published scientific studies for these two species of ungulates. Results show that the diversity of species and the physiognomy of the forest corresponds to high forest in regeneration due to the history of use of the area. More than 41 species were found with 10 types of fruits. Of the species found, 15 (43% of the trees measured) and 11 species (24%) were cited as part of the diet of *P. tajacu* and *M. gouazoubira*, respectively. These data show that the animals will be in contact with a natural source of food and in an enclosure with characteristics similar to the habitat where they will be released in afterwards. During the project, the diet and movement of the animals will be monitored to test their re-adaptation to nature.

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Contrasting perspectives on the introduction of exotic rodents from archaeological and natural predator bone accumulations on Flores, eastern Indonesia.

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Palaeoecological reconstructions based on vertebrate faunal remains are often carried out from archaeological contexts, using human food remains or bones deposited into the same context by other predators, such as owls or mammalian carnivores. Taphonomic issues related to human occupation of these sites, including the effects of trampling, excavation of hearths and burial pits, and in some places, secondary foraging by scavengers, can result in considerable admixture of remains; in turn, this can limit the suitability of these contexts for providing fine-scale palaeoecological records. We contrast the palaeoecological records derived from two caves situated very close together on the island of Flores, Indonesia—one archaeological and the other a natural owl roost accumulation. Our focus is the timing of first appearance of introduced exotic rodents, members of the genera *Rattus* and *Mus*. The archaeological sequence appears to support the common assumption that the arrival of exotic rodents coincided with the transition among human populations to a 'Neolithic' lifestyle, involving sedentary living, crop production, and the keeping of domestic animals. The owl roost deposit spans only the past 2,500 years but with 13 C^{14} dates on charcoal in near-perfect stratigraphic order, it demonstrates convincingly that introduced rodents were absent locally prior to 500 years ago, and arrived sequentially, rather than as a single event, with the species identifications confirmed by DNA sequencing. Our results illustrate the importance of precise dating and identifications in palaeoecological studies, and the as yet underexploited potential of non-human bone accumulations for reconstruction of regional palaeoenvironments.

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Discovering lost (or not so) regional diversity: New Muridae detected in owl pellet assemblages from the poorly surveyed region of Wallacea, eastern Indonesia

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The Muridae are a highly successful family of small mammals that have colonised most continents and islands globally. Within Mammalia, they represent a uniquely important study group for their significant impacts on cultural, agricultural, biogeographic, and evolutionary fields. Their large number of offspring and high reproductive rates make them particularly successful island colonisers amongst mammals, and they display high levels of endemicity across many isolated regions. In Wallacea, the group of islands situated between the continental landmasses of Sunda (continental Southeast Asia) and Sahul (Australia and New Guinea), our knowledge of murid diversity is hampered by limited historical collecting or recent biological surveys, incredibly large numbers of islands, their isolation and difficulty of access, and for most islands, the degraded state of natural environments and contemporary occurrence of exotic rodents such as the black rat and house mouse. We describe the challenges of sampling efforts targeting owl roosts and conducted under the purview of archaeological investigations of human movements through the region. We present taxonomic and systematic information derived from both modern and fossil rodent remains recovered from the islands of Roti, Timor, Talaud, Pantar, and Kisar, all of which prove to have hosted endemic species of murine rodents, and discuss the possibility that some of these species might still persist as relict populations. Finally, we highlight the synergistic advantages of an interdisciplinary effort for understanding the biogeographical history of Wallacea, in particular the benefits of collaborations between archaeologists, palaeontologists, and geneticists.

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A key role for owl pellet accumulations in regional small mammal surveys and monitoring activities in Papua New Guinea.

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The mountainous, equatorial nation of Papua New Guinea (eastern half of the island of New Guinea; western half is Papua Province of Indonesia) supports a relatively low human population and retains large tracts of pristine or lightly modified natural habitats, from lowland swamp and rain forests to subalpine scrub and grasslands. All habitat types support diverse but incompletely documented mammal faunas, and many also host resource development projects in the mining, oil and gas, hydropower, forestry and agricultural sectors. While PNG environmental regulations and international lender regulations (e.g. IFC Performance Standards) demand a high standard of baseline documentation, impact mitigation, and monitoring, the primary taxonomic, distributional and ecological data needed to underpin rigorous assessments are often lacking. Field survey in remote and previously undocumented regions is challenging, and results obtained for mammals are often far less complete than for other survey target groups such as birds and amphibians. Analysis of owl pellet assemblages has multiple potential benefits in this context, including: 1) more complete species inventories than can be obtained by traditional methods; 2) detection of previously unknown mammal species; 3) detection of cryptic species through study of large series of specimens from single locations; 4) perspectives on relative abundance of species that are rarely encountered by conventional survey methods; and 5) evidence for locally reproducing populations through recovery of juvenile remains. Examples of each will be provided, and a case made for systematic use of owl pellet assemblages in biodiversity assessment and monitoring activities across wider Melanesia.

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An introduction to the contribution of mammal remains to conservation

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As previous authors in this session have explained, European colonisation of Australia has devastated its endemic mammals. Consequently, Holocene fossils provide more reliable records of Australia’s pre-European terrestrial fauna than historical records. But what does this mean for conservation? Recent fossil assemblages provide very useful conservation tools that can identify and fill gaps in knowledge, and contribute to the management and restoration of Australia’s degraded ecosystems. Owls are better at surveying biodiversity than humans, and Holocene owl accumulations can provide extremely accurate spatial and temporal data that describe the composition, heterogeneity, diversity, richness and evenness of pre-European mammal assemblages. Analysis of these parameters in stratified assemblages may also reveal the drivers behind faunal change. Holocene fossils can guard against baseline shift (where an arbitrary baseline is accepted and used to evaluate change with no consideration of prior human-induced ecological modification), reveal ‘hidden’ biodiversity (undescribed species or species complexes), species range contractions, community naturalness (where human vegetation modification encourages invasion by native species), inform perceptions of species’ environmental preferences and the calibration of predictive climate models. Fossils can also yield (ancient) DNA that can be used to identify taxa, distinguish between fragmented or diverging populations and help source appropriate genetic stock. Finally, reintroduction programmes should be structured so that environmental engineers such as bettongs and other ecological service providers are re-established first to enhance overall community resilience and the successful reintroduction of subsequent species.

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Reexamining the role of food in the snowshoe hare cycle

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Understanding the causes behind population cycles is a fundamental issue in ecology. The primary objective of this project is to examine the effects of food limitation on the survival and reproduction of snowshoe hares (*Lepus americanus*) which undergo 10-year cycles. We work in the southwest Yukon where previous studies supplemented food for hares on large study grids with the net result being high immigration and limited improvement in survival. We radio-collared hares at Kluane Lake, Yukon, Canada, and selected individuals were fed throughout the winter with known amounts of commercial rabbit chow administered from selective feeders. We monitored daily survival using VHF telemetry from the fall through spring. Females from both treatment and control groups were placed in maternity cages just prior to giving birth. Food supplemented individuals experienced increased survival and reproductive output over controls. Fed females gave birth to larger offspring and had larger litter sizes in comparison to control females. These results demonstrate a potentially strong effect of food limitation on the snowshoe hare cycle, given that demographic parameters linked to the decline (i.e. adult survival, reproductive output) were significantly affected by food addition. Our current understanding of the fundamental drivers of the cycle may need to be re-evaluated given these findings.

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Arctic foxes benefit their prey and subsidise wildlife through ecosystem engineering

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Predator-prey interactions have strong effects on population dynamics and community structure, yet predators can also affect organisms through mechanisms other than predation. By altering the distribution of nutrients on the landscape, predators can affect soil nutrient dynamics and vegetation productivity, which could affect the distribution of herbivores and other wildlife. We examined the use of Arctic fox dens by mammalian herbivores and scavengers in western Hudson Bay in Canada and explored some of the mechanisms that may attract other wildlife and the benefits to their prey despite the apparent increased predation risk. Winter nests of lemmings, the primary year-round prey of Arctic foxes, occurred on over two-thirds of the fox dens visited each year. Vegetation on dens was more abundant, taller, and more nutritious (higher nitrogen content) than on off-den sites. The thicker snow in winter trapped by this vegetation on dens generated warmer subnivean temperatures that enhanced lemming reproduction, reflected in the size distribution of faeces in winter nests, suggesting fox dens may act as refuges for declining lemming populations by improving winter habitat. Motion-sensor trail cameras recorded more visits by caribou and scavengers to dens than control sites in summer, and the numerical response of mammalian scavengers to fox prey remains suggested they were attracted to these carcasses. These positive effects of ecosystem engineering contrast the negative effects of predation, highlighting the importance of integrating these dual roles for a broader understanding of the impact of predators on community dynamics.

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Dingoes and trophic cascades in Australia - a red herring for ecological restoration

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Wolves have been widely documented as being influential in top down regulation of prey and trophic cascades in North America. Reintroduction plans for the dingo in south east Australia are currently proposed with emphasis on the positive effects of canid driven trophic cascades on biodiversity. The biophysical elements of North America shape that environment for trophic cascades but it is not clear that Australia provides a comparative context for the dingo. The wolf-elk-willow trophic cascade in Yellowstone National Park provides a case study to understand the broader system controls on trophic interactions and comparatively apply the knowledge to the south east Australian environment. Both ecosystems have a canid top predator and an arid environment, making their comparison highly relevant for dingo reintroduction plans in Australia. Climate stability has emerged as the critical influence underlying trophic cascades in Yellowstone National Park through the regularity of predictable resource supply which sustains strong trophic interactions. Conversely, the instability of the Australian climate which yields unpredictable resources is unlikely to produce trophic interactions of similar strength. Consequently, predator reintroduction experiments based on the conceptual framework of dingoes driving trophic cascades are likely to be constrained.

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Exposure to a novel predator induces visual predator recognition by naïve prey

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There is a natural asymmetry within predator-prey systems. The 'life-dinner principle' suggests that there is an evolutionary advantage for the species that has more to lose in an interaction. There is an advantage for prey to learn quickly, especially in response to novel, introduced predators. Here we test the 'learned recognition' hypothesis that posits that naïve prey species' ability to recognize and respond to introduced predators can be induced as a result of ontogenetic experience. We did this by quantifying the behavioral response of initially predator naïve burrowing bettongs (*Bettongia lesueur*) living in the presence and absence of an introduced predator (feral cats) to models of cats and European rabbits (a harmless herbivore), plastic buckets (novel objects) and no object (a procedural control). We expected that if bettongs recognized cats as a threat they would be more wary in the presence of cat models than either rabbit models or the procedural control. Bettongs living without predators approached all models (bucket, cat and rabbit) cautiously in comparison to the control treatment, suggesting that bettongs responded to the presence of an object and/or model, but did not discriminate between them. Bettongs living with cats spent significantly more time cautiously approaching the cat model compared to the rabbit, the bucket and the control. Our findings are consistent with the learned recognition hypothesis and show that a predator-naïve preys' ability to visually recognize predators is inducible through ontogenetic experience. It is also clear that these behavioral changes may be rapidly induced.

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Body temperature may indicate high costs of locomotor activity in an arboreal species, the edible dormouse (*Glis glis*)

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Measuring T_b during the active season can provide information about the timing of reproduction, the use of short bouts of torpor and may be used as a proxy for the locomotor activity of animals (i.e. maximum T_b). This kind of information is especially important to understand life-history strategies and energetic costs and demands of hibernating mammals. We investigated T_b throughout the active season in edible dormice (*Glis glis*), since they *i*) have an expensive arboreal life-style, *ii*) are known to show short bouts of torpor and *iii*) are adapted to pulsed resources (mast of beech trees). We show here for the first time that maximum T_bs in free-living active dormice (during the night) increase regularly and for up to 8 h above 40°C, which corresponds to slight hyperthermia, probably due to locomotor activity. The highest weekly mean maximum T_b was recorded one week prior to hibernation (40.45 ± 0.07°C). At the beginning of the active season and immediately prior to hibernation, the mean maximum T_bs were lower. The time dormice spent at T_b above 40°C varied between sexes, depending on mast conditions. The date of parturition could be determined by a sudden increase in mean T_b (plus 0.49 ± 0.04°C). The occurrence of short torpor bouts (< 24 h) was strongly affected by the mast situation with much higher torpor frequencies in mast failure years. Our data suggest that locomotor activity is strongly affected by environmental conditions, and that sexes respond differently to these changes.

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The daily rhythmicity of core body temperature provides an index of performance in free-living mammals

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Biologging allows us to record core body temperatures in mammals living free in their natural habitat, where they are subjected to complex stressors. In species that do not go into torpor, changes in the pattern of the daily rhythm of core body temperature can be quantified using cosinor analysis. Changes in energy intake and expenditure result in changes in the daily amplitude of the body temperature rhythm, and those changes are correlated with changes in animal performance, including growth and reproduction. Kangaroos displayed a gradual reduction in the minimum morning body temperature with little to no change in the nighttime (active) body temperature as spring progressed into the dry summer. Sheep restricted to 70% of their normal food intake exhibited increases in the daily amplitude, with decreases in the nighttime minimum, of body temperature. In free-living rabbits, the initial amplitude of the body temperature rhythm predicted the number of pregnancies that a female had during the subsequent seven months. In alpacas, shearing, during benign ambient conditions, induces a large increase in amplitude of the body temperature rhythm, and the individual monthly growth could be predicted by the amplitude of the daily body temperature rhythm. Homeothermy seems to be the default condition in well nourished and hydrated larger mammals, while disturbances to energy or water balance, associated with decreased individual performances, often lead to heterothermy. We suggest that the characteristic of the individual daily T_b rhythm provides a sensitive index of fitness.

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Body temperature and activity patterns reveal that free-living cheetahs are opportunistic hunters

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As one of the few felids that is predominantly diurnally-active, cheetahs *Acinonyx jubatus*, in their natural habitat, are exposed to high heat loads. Whether they are at risk of hyperthermia is not known, because long-term measurements of body temperature never have been reported for cheetahs. We measured body temperature and locomotor activity with implanted data loggers over seven months in five free-living cheetahs in Namibia. Air temperature ranged from -2ºC in winter to a maximum of 39ºC in summer. The cheetahs displayed higher maximum 24 h body temperatures (~0.4ºC), peaking later in the day (~1 h), with larger fluctuations in the amplitude of 24 h body temperature rhythm (~0.4ºC) during a hot-dry period than during a cool-dry period. When ambient temperatures were high cheetahs shifted from a diurnal to a crepuscular activity pattern, with reduced activity between 9:00 and 15:00 and increased nocturnal activity. Yet, when a hunting opportunity presented itself, cheetahs hunted in the midday heat (air temperature 33.6ºC), and in total darkness (new moon). Although cheetahs were proficient in total darkness, the nocturnal activity was higher on moonlit nights than dark nights. Overall hunting success rate (derived from body temperature and activity profiles characteristic of hunts) was 38 ± 15%, similar to that reported for cheetahs previously. Our cheetahs coped well under high heat loads. They were opportunistic in their hunting strategy, hunting when they encountered prey rather than selecting preferred conditions in which to hunt.

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Life in the warm: Comparative energetics of a nocturnal and a diurnal tropical small mammal

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The relationship between animals and their thermal environment has been gaining prominence in the fields of ecology and physiology with the increasing concern over climate change. Yet, despite a large body of knowledge on the thermoregulation of temperate and cold-climate endotherms, our functional knowledge of endotherms in warmer climates remains incredibly scarce. In particular, their use of facultative heterothermy, lowering or raising body temperatures to conserve energy and/or water, has been chronically understudied. As well as providing a general overview of some of the forms of heterothermy observed in warm climates, we review the results of field studies on a highly heterothermic nocturnal mammal (the greater hedgehog tenrec, *Setifer setosus*) and a homeothermic (yet thermally labile) diurnal mammal (the large treeshrew, *Tupaia tana*). We discuss the costs and benefits of the body temperature variability in warm climates and the evolution of homeothermy in mammals.

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Mammals in anthropogenic landscapes: Case studies from China

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We are in an era of Anthropocene; humans have modified the Earth's landscapes. Mammals have to cope with the new problems in the anthropogenic landscape. First, their habitat is often fragmented, migration routes are blocked and their population sizes are small; second, many larger mammals are hunted by humans because human are replacing the role of top mammal predators in many ecosystems or replacing the wild ungulates in grassland ecosystems with domestic animals; humans exploit wild ungulates, whales and dolphins as source of protein or fur; on the other hand, rodents become androphile species and thrive in an anthropogenic landscape. I will present the case of fates of mammals in China – a country with mega biodiversity and rich endemic fauna and flora. I will talk about how the once extinct Milu (*Elaphurus davidianus*, also called Père David’s deer) was reintroduced to China in the 1980s and revived with human assisted survival and dispersal in contrast to the example of unsuccessful reintroduction of saiga antelope (*Saiga tatarica*). I will explore the invasion and successfully establishment of the brown rat (*Rattus norvegicus*) as a typical case of mammal invasion facilitated by transportation development in western China and invasion of American mink (*Neovison vison*) in Mt. Altai region, Xinjiang, China, a place which is the most distant location to the ocean of anywhere on earth. Finally, I will summarise how humans can help mammals in peril while managing invasive, overabundant and androphile species.

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Bridging the gap for the western ringtail possum (*Pseudocheirus occidentalis*): Rope bridges provide safe passage across roads for a critically endangered marsupial

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The western ringtail possum (*Pseudocheirus occidentalis*) is a critically endangered arboreal marsupial endemic to the south west of Western Australia, the only biodiversity hotspot on mainland Australia, and one of its most rapidly growing regions. A population viability analysis on its last stronghold population living along Caves Road, between Busselton and Dunsborough, predicted a risk of extinction as high as 92% in the next 20 years. Mortality on the road was contributing to its rapid decline, with the removal of road mortality events from the model reducing the extinction risk to 32%. To address road mortality, a rope bridge was installed across Caves Road in 2013 and we monitored its use using motion sensor cameras and microchip readers to identify factors influencing the crossings. We analysed the crossing data using generalised linear models that included factors such as days since installation, breeding season, wind speed and temperature. Possums started investigating the bridge even before installation was completed and made the first complete crossing only 36 days after the installation, with crossing rate reaching to 8.9 ± 0.59 crossings per night. Mothers were observed crossing with young that continued to cross after they reached independence. Possums crossed the bridge less on windy nights and warm nights probably due to the risk of being blown away and heat stress on warmer days. Breeding season did not influence the crossings. Our results demonstrate that rope bridges have a potential as an effective mitigation measure against the negative impacts of roads on this species.

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Reintroduction of a native rodent in the presence of competition with an invasive rodent

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Competition between native and invasive species is an often overlooked mechanism that can contribute to species loss. Conversely it may also provide a novel opportunity to improve conservation outcomes for native fauna. Rodents with established territories in intact vegetation can potentially exclude invaders through direct aggressive interactions. A reintroduction of the native rodent *Rattus fuscipes* was facilitated by providing this species with a competitive advantage over invasive *Rattus rattus*. *Rattus fuscipes* was reintroduced in three stages between 2014 and 2016. *Rattus rattus* was strategically suppressed within localised release sites in an attempt to transfer residency status to the newly released animals. In less than three years the *Rattus fuscipes* population had expanded through the landscape and displayed successful recruitment across multiple generations. In contrast, suppression of *Rattus rattus* led to slow re-invasion and a shift in population ecology of the re-invaders. This conservation program demonstrates that native rodent populations with established territories in intact vegetation can potentially exclude invaders through direct aggressive interactions. This type of approach can provide opportunities to restore native fauna in habitats dominated by *Rattus rattus*.

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Geoffroy's cat in Brazil: Estimating density and behavioural patterns of the species in human-dominated landscapes

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Geoffroy's cat is the most abundant felid of the temperate Neotropics. We investigated which factors influence its persistence in one of the most threatened biomes in Brazil, the Pampas. Our study area was a mosaic of open-grassland with pasture, croplands and riparian vegetation. We recorded 516 camera-trap images of Geoffroy's cat and nine individuals were captured using box-traps. Of those, eight adults were radio-collared (5M and 3F), and monitored through VHF telemetry for a cumulative period of 16 months (434 locations). One male was killed by dogs and a female was poisoned, possibly a result of human conflict from preying on chickens. Despite these disturbances, density estimation using SECR ranged from 34.54 ± 13.51 (SE) to 41.78 ± 16.12 individuals $100km^{-2}$, reasonable in comparison to other areas. Even though considered an open area species, our study population selected significantly more riparian vegetation ($D = 0.45$, 95%Kernel; $D = 0.48$, 95%MCP, $P < 0.01$), and avoided open grassland ($D = -0.59$, 95%Kernel; $D = -0.51$, 95%MCP; $P < 0.01$). It is noteworthy that the protection of riparian vegetation is required by national law. Hence, this habitat may provide additional shelter for Geoffroy's cats. This population was nocturnally active ($Z = 8.03$, $P < 0.01$) and showed a slight difference between seasons ($\Delta_4 = 0.79$ *CI* 0.71-0.85), increasing nocturnal activity during spring-summer. In this study of Geoffroy's cat in Brazil, we have produced results that can contribute to the design of conservation management actions for the species in this threatened biome.

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Untangling the evolutionary history of the European bison (*Bison bonasus*)

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The evolutionary history of the European bison (*Bison bonasus*) has often been debated and remains cryptic despite recent ancient DNA and genomic studies. Nonetheless, bison are one of the few species to have survived the mass megafaunal extinction during the Pleistocene/Holocene transition (12-9 ky BP), and they can inform on the response of megafaunal populations to periods of rapid environmental change. Ancient DNA (aDNA) provides a unique opportunity to directly observe genetic evolution by investigating the changes in genetic structure of species and populations in real time. A previous study containing predominantly mitochondrial control region sequences as well as 13 complete mitochondrial genomes of bison samples from a restricted geographical range in Eastern Europe has revealed dynamic series of events through time correlated with environmental changes (Soubrier et al., 2016). Here we describe the evolutionary patterns observed in high-resolution mitochondrial sequencing data from over 60 ancient European bison samples across Eurasia, specifically delineating patterns of succession of various bison ecomorphs across a broad geographical and temporal range.

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The resource pulse game: Figuring out winners and losers in the Kluane Red Squirrel Project

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Resource pulses come in many forms, including mast seeding by conifers in northern systems. Masting is thought to be an adaptation by trees to increase seed escapement by swamping seed predators. Red squirrels are the dominant seed predator for spruce but they have developed their own adaptation whereby they are able to anticipate mast years. The anticipation by squirrels and changes in their density lead to some very interesting patterns of selection that lead to various life history traits and behaviours being favoured at different points in the masting cycle. The Kluane Red Squirrel Project has followed over 10,000 individual red squirrels over 25 years to try to sort out the winners and losers in this highly dynamic system. I will describe some of our findings and the results of a 10 year experimental evolution experiment designed to understand how resource pulses drive micro-evolution in this system.

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Deep time to conservation: Quantifying shape variation within the last four vombatiform species through 3D geometric morphometrics.

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The koala and three species of wombat are the only survivors of the diverse clade of Vombatiformes, including many gigantic, herbivorous megafauna species. They are also specialized herbivores, which makes them susceptible to environmental change. Understanding the relationship between wombat/koala cranial shape and feeding ecology allows an assessment of their adaptability to current environmental change, and a chance to extrapolate on the evolution of the giant herbivorous Vombatiforms. Here, we use 3D geometric morphometric analysis to assess intra-and inter-specific cranial shape diversity in all three wombat species and the koala (n=29-31/each species). Not unexpectedly, principal component analysis and 3D warp visualizations of PC space revealed a dichotomy between broad and blunt crania of wombats and narrow, pincer-like snouts in koalas. However, koalas showed far less shape disparity than wombats, possibly due to their more extreme specialization on eucalypt folivory. All wombat species showed substantial intra-specific cranial shape variation, which unexpectedly was neither explainable by allometry nor broad geographical categories. The closely-related Northern and Southern hairy-nosed wombats (NHNW/SHNW) do not overlap much in principal component space, with SHNWs showing some shape similarity (teardrop-shaped, more procumbent skulls) with common wombats. This is unexpected because SHNWS feed on harder vegetation and live in more arid habitats than NHNWs and common wombats. From the lack of clear diet-related shape differences, we conclude that either wombat crania are extremely susceptible to localized (dietary) environments, or is not selected for feeding efficiency; extended sampling of captive specimens might provide an avenue of testing these alternatives.

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A new method to find environmental mechanisms of life history evolution in insectivorous mammals

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Temporal variation in food availability shapes the life history strategies of female mammals. Females are assumed to gain fitness benefits from matching births with annual or seasonal peaks in food abundance, thereby increasing their ability to meet the maximum energetic demands of lactation. Selection for synchronised seasonal breeding results when young born outside the peak birth period face long-term disadvantage. Overall food abundance affects reproductive rate and other life history traits. In mammals, most studies on these topics have been on herbivorous species. We know little about food availability on a macroecological scale and its life history consequences for insectivorous mammals. We present a standardised method to record long-term but detailed food availability for insectivorous mammals. We used horizontally-set, programmable time-lapse camera traps with a close focal distance and white led flash. We have deployed cameras at sites throughout Australia (and 2 in PNG) since 2013. These are revealing how arthropod seasonality and abundance are related to latitude, mean and variation in rainfall and temperature, substrate and vegetation; helping to increase understanding of the underlying environmental mechanisms of life history evolution in female dasyurid marsupials at a macro-ecological scale.

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Use of GPS telemetry to study the spatial ecology of common genets (*Genetta genetta*) in central Kenya

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The advent and continued development of global positioning system (GPS) tracking devices for use in studying wild animals has revolutionised our ability to study animal ecology. For carnivores however, most of the benefits realised from these technologies have occurred in larger species. For small carnivores (< 15 kg), use of GPS telemetry remains less explored. In particular, applications of these technologies to African species remains quite limited. This study reports findings from the first attempt to elucidate the spatial ecology of the common genet (*Genetta genetta*) using GPS telemetry. Between January and March 2015, we successfully fitted 22 common genets with GPS collars (eObs tags, Germany) on two properties in Kenya's Laikipia County, a private conservancy (Mpala Ranch) and an adjacent community group ranch (Il Motiok). GPS tags were set to record fixes every 60 min and accelerometer data every 15 min throughout the night and were intended to be deployed for 8–12 months. We were able to obtain usable data from 12 individual genets, 6 (4 male : 2 female) from Mpala Ranch and 6 (4 male : 2 female) from Il Motiok. The average number of fixes recorded for genets from Mpala Ranch was 837 (117–2211) compared to 1336 (91–3999) for Il Motiok. Results and implications for understanding space use dynamics for the common genet will be discussed in light of several problems encountered during the study with suggestions on how to avoid future issues when applying GPS telemetry to small African carnivores of similar size and ecology.

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Spatial distribution and occupancy of bushy-tailed mongoose (*Bdeogale crassicauda*) and miombo genet (*Genetta angolensis*) in a miombo woodland ecosystem, western Tanzania.

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Extended areas of western and south-western Tanzania are still covered by natural habitats, within the miombo woodland biome. Miombo woodlands are home to a large biodiversity, with a mix of forest and savanna species and in addition species that are endemic to the miombo. In a preliminary study based on a camera trap survey and conducted in Mlele beekeeping zone, a forest reserve located north of Katavi National Park, we were able to confirm the presence of over 50 species of medium sized and large mammals, including 10 species of small carnivores. Among this latter guild some species were surprisingly abundant, such as for example the bushy-tailed mongoose (*Bdeogale crassicauda*), that was previously considered uncommon, and the miombo genet (*Genetta angolensis*), a species linked to this habitat but for which there was only few records in and around our study area before our surveys. Since this preliminary study, we have extended our survey protocol and acquired new camera traps with

more sensitive detectors. The data we have acquired since then enables us to have a more precise picture of the spatial behavior of these species and to use occupancy models to have a proxy of their abundance and to investigate if natural or anthropic factors might influence their distribution.

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Spatio-temporal ecology of the rusty-spotted genet, *Genetta maculata*, in Telperion Nature Reserve (Mpumalanga, South Africa).

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The rusty-spotted genet, *Genetta maculata*, is endemic to Africa and poorly studied. We carried out the first exhaustive study in South Africa over a full annual cycle (September 2015 to August 2016). We aimed to describe their 1) activity patterns, 2) resting site ecology, and 3) spatial behaviour. Nine male and six female genets were live-trapped, fitted with motion-sensor radio-collars and tracked for an average of 6 ± 3 nights and 2 ± 1 days per individual. An average of 36 ± 24 resting site locations were also taken for each animal. Genets were primarily nocturnal (nocturnality index: 0.84). Differences in activity were minimal between sexes, but significant between seasons. Genets were less active during winter. The percentage of resting site reuse (37 ± 17% per animal per season) did not differ between sexes or seasons. The distance between resting sites on consecutive days was higher for males (940 m) than females (707 m). Home range sizes of males (2.87 km^2) and females (3.34 km^2) and during the different seasons did not differ. Core areas were small (7% of the home range). Slight inter- and intra-sexual home range overlaps were recorded. Home ranges and specifically core areas were located on dense bushveld vegetation. We suggest that our results can be explained by a combination of factors including food availability, reproductive actions and predator avoidance.

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Methodologies for studying small African carnivores: Can research keep pace with emerging conservation needs?

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Small African carnivores (< 15 kg) represent a biologically and ecologically diverse assemblage. Yet despite their biodiversity and subsequent assumed ecological importance, most species remain vastly understudied in comparison to larger-bodied carnivores. As part of IMC XII's symposium on *Advances in Research and Conservation of Small African Carnivores,* this talk will explore methodologies used for studying these often cryptic, secretive and nocturnal species. Building on another talk in this session that will identify data gaps and priorities for future work, here we will consider current methodologies to identify what methods may be best suited to fill these gaps and to address emerging conservation issues. We will then survey newly available technologies, many of which are evolving rapidly, and assess how they might contribute to future studies of small African carnivores that collectively occupy a wide variety of habitats. This presentation is designed to facilitate information sharing among researchers as to the most recent technologies and approaches available. Audience input on new methods or equipment will be invited at the end of the presentation, time permitting.

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Quaternary bat fossils from southeastern Australia reveal long-term patterns of cave habitation: Implications for conservation of the critically endangered southern bent-wing bat

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Despite representing one around fifth of the world's mammal species bats face an uncertain future. Habitat clearance, human activities, invasive species, and climate change have all been implicated as contributors to bat decline. Teasing apart the discrete impacts of these factors is critical for developing appropriately targeted recovery strategies. Long-term data revealing patterns of bat community dynamics prior to human influence are needed to separate natural and anthropogenic impacts. Here I present evidence from Quaternary fossil deposits at Naracoorte in South Australia that shows continuous habitation of caves by the Critically Endangered southern bent-wing bat (*Miniopterus orianae bassanii*) over at least the past 300,000 years; spanning considerable periods of climate variability. The use of particular caves as maternity or wintering sites has been consistent over this time, and mirrors precisely the patterns of cave use seen at Naracoorte today. This suggests that while the bats have been resilient to long-term change over multiple glacial cycles, the availability of appropriate cave habitat is critical. In some caves, within-cave environmental conditions are influenced by surface climate. Projected temperature increases with anthropogenic climate change may render some currently inhabited caves unsuitable. Modern habitat fragmentation and human impact on many caves has severely limited the capacity of this species to expand or contract its range in response to future climate change. Population monitoring and localised habitat restoration measures may not be enough to prevent extinction of this species. The emerging field of palaeo-conservation may provide a useful tool for planning conservation efforts.

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Changes in survival of large-footed myotis in streams with contrasting disturbance history

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Unlike many other taxa, for bats base-line data to identify changes in status is virtually non-existent. We present mark-recapture analyses (17 years) targeting a habitat specialist, the large-footed myotis *Myotis macropus*, on two streams in northern NSW with contrasting disturbance history. We caught bats annually and banded 529 with a 50% retrap rate. The maximum time to recapture was nine years. Analyses allowed for dependence of survival on time, sex, and age at marking. Bats had a higher probability of recapture at the logged site (mean adult female = 0.74) compared with the undisturbed site (mean adult female = 0.33) and there was no evidence for transiency. Adult survival showed only minor fluctuations over time, suggesting that logging did not influence survival. Adult female survival averaged 0.74 ± 0.01 in the undisturbed site compared to 0.70 ± 0.003 in the seven years post-logging at the second site. Adult female population size was similar between the two sites. Our study spanned extreme *El Nino* and *La Nina* events, yet we found little variation in survival. There was some support for a minor influence of winter temperature (+ve) and rainfall (+ve) on survival. Adult male and female survival was similar at the logged site, but juvenile survival was less than half that of adults, probably because of mortality and dispersal. Our results suggest that riparian buffers retained during logging operations mitigate potential impacts on stream habitat for *M. macropus* and that specialising on aquatic habitats buffers the species from extreme weather.

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How do insectivorous microbats use rainforest-grassland ecotones in a fire-managed, tropical landscape?

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Grassland patches occurring in complex rainforest-woodland dominated landscapes provide important habitat to numerous fauna species, and the ecotones between grasslands and rainforests may contain higher biodiversity than either single ecological community. Different fire regimes result in different ecotone gradients between grassland and surrounding rainforest. Little is known about how insectivorous microbats use these rainforest-grassland ecotones. This study aimed to determine the preference of microbats for abrupt or gradual gradient ecotones, and for distance from the edge of the ecotones. This study was conducted in Cape York Peninsula, Australia, an area of high biodiversity that is facing many emerging Anthropocene threats including changing fire regimes, weed infestation, and the effects of climate change. Bat activity was determined using bat detectors placed along linear transects across five 'gradual', and five 'abrupt' ecotones. Overall bat activity and the activity of three bat guilds (open, edge/open and closed) was compared between ecotone types, and position along the ecotone. It was found that mean total bat activity, open guild and edge/open guild bat activity was significantly higher at grassland and ecotone edge positions than at rainforest positions. For closed guild bats, activity was significantly higher at gradual ecotone sites than at abrupt ecotones sites. It is likely that these findings were attributable to the structural differences associated with the ecotone types and positions, but may also have been driven by insect prey availability. The findings from this study can be used directly by land managers to develop conservative management plans, particularly for future fire regimes.

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Artificial light degrades critical urban habitat for slow-flying insectivorous bat species

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The intensification of artificial light in cities has been identified as a key global threat to biodiversity. Insectivorous bats in urban areas are likely to be some of the most affected species, with a global pattern emerging of slower flying species being most at risk. Remnant patches in cities are critical habitat for bats, therefore identifying a need to understand how we are disturbing this habitat with our public lighting policies and decisions. We aimed to determine if artificial light at the bushland edge affects the activity or diversity of insectivorous bats, and whether light affected the peaks in activity of these urban bats. We acoustically surveyed the interior and the edge of 32 remnant patches with Anabat II detectors. Of the 32 sites, half had mercury vapour lights along the edge sampled, and half had dark edges. At sites where slow flying bats were present, they were significantly more active at dark edges than at light edges. Artificial lights at the bushland edge negatively affect the activity of slow flying bats. The activity peaks of these slow flying bats, however, was affected less by light and more by habitat structure; dark and light habitat edges both supported crepuscular activity, whereas interior bushland sites supported a unimodal peak of activity. Our findings show that light penetration into essential bushland remnants has a negative impact on bat diversity. Our research also highlights the importance of protecting dark interior remnants in cities to conserve the natural activity patterns of nocturnal urban fauna.

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Camera trapping as an alternative to pitfall trapping to sample prey availability of insectivorous mammals

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Pitfall trapping is the standard technique to estimate activity and relative abundance of leaf litter arthropods in ecological studies of prey availability. Pitfall trapping is not ideal for long-term sampling because it is a lethal method that can deplete arthropods over time, it is labour intensive, and it may have taxonomic sampling biases. We test an alternative sampling method that can be left in place for several months: horizontally placed, time-lapse camera traps that have a short focal distance, enabling identification of small arthropods in pictures. Time lapse is necessary to capture small arthropods, but the cameras concurrently use a standard infra red trigger, so small mammals are also captured whenever they move into the field of view. We tested the effectiveness of these time-lapse cameras, and quantified escape and avoidance behaviour of arthropod orders encountering pitfall traps. We also recorded small mammals captured on camera traps. Cameras recorded around twice as many arthropod taxa and a third more individuals per day than pitfall traps. Ants, webspinners and cockroaches frequently escaped from pitfalls so were particularly under-sampled by them. The same cameras recorded as many species of small mammals as concurrent live-trapping in our rainforest sites, and also recorded cryptic species that were not live-trapped. The new close-focus time-lapse camera method effectively samples litter arthropods to collect long-term data on prey availability suitable for ecological studies. We are currently using the cameras to sample arthropods and small mammals to assess prey availability of dasyurids.

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Camera traps at American black bear dens: A case study in undergraduate research

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Students in my Black Bear Management class place camera traps at occupied dens of American Black Bears. Data is accumulated so students have the opportunity to analyze current data as well historical data sets. In small groups, students create a novel question to explore. This presentation will focus on how to successfully create and manage undergraduate research projects for students in their first two years of study. Camera traps have many advantages for undergraduate research. They are easy to operate, produce engaging data and important field study questions can be investigated.

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Do protected areas sustain large mammals? A camera-trap survey across the Isthmus of Panama

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Large mammals play key roles in tropical forests but are currently threatened worldwide. A big question is to what degree protected areas are effective in maintaining these large mammals. Here, we assess whether protected forests effectively protect large mammals along the Isthmus of Panama, a bottleneck in the Mesoamerican Biological Corridor that is essential for species migration and gene flow, but is increasingly fragmented. During 2005-2016, we used camera traps to survey terrestrial mammals in 17 protected forests scattered across Panama. We determined occupancy rates for the nine largest extant species, which differ in their sensitivity to disturbance. Based on 26,000 trap days from > 500 camera trap stations, we found that most protected forests had impoverished, structurally simplified mammal communities, with few or no apex predators and large terrestrial frugivores. Occupancy analysis revealed consistent patterns of avoidance of human disturbance and forest edges by *Tapirus bairdii* and *Tayassu pecari*, which are heavily hunted, and concentration at higher elevations. Only in our most remote site, far away from any anthropogenic activity, did these species still occur in lowland areas. Carnivores, in contrast, when present at a site, were less affected by anthropogenic factors. Our findings indicate that the protected areas of Panama are not effective in maintaining the entire mammal community, and show clear signs of anthropogenic declines in abundance and shifts in habitat use of large terrestrial mammals. Our study also suggests a lack of connectivity between protected areas. We propose recommendations to improve mammal conservation in Mesoamerica.

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On the status and distribution of *Gazella gazella* (Artiodactyla: Mammalia) in Turkey along with some medium and large mammal records from Hatay Province

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Gazella gazella was discovered recently in a restricted area in Hatay. To date, no study of the distribution area of Mountain Gazelle has been carried out. To determine the current distribution area of Mountain Gazelle in Hatay region, 17 camera traps were set along 45 km on a line from south toward north in Hatay Province along the border with Syria. Traps stayed in the field about five months from late May to mid-October in 2016. Additionally, field observations and conversations with local people, wild life officers and researchers were performed. According to data obtained, *Gazella gazella* distributes as two isolated colonies in Kırıkhan and Reyhanlı regions of Hatay Province, along about 50 km of borderline, and the area constitutes the northernmost point of the distribution of the species in the world. The Reyhanlı population of *Gazella gazella* was first discovered by the study. The total area of both populations is about 125 km^2 and population size is estimated about 600. On the other hand, a total of fourteen species of mammals including *Vulpes vulpes, Gazella gazella, Hystrix indica, Canis aureus, Canis lupus, Hyaena hyaena, Meles meles, Martes foina, Herpestes ichneumon, Felis silvestris, Felis chaus, Lepus europaeus, Hemiechinus auratus,* and *Sus scrofa* were recorded by phototraps. *Hemiechinus auratus* is a new record for Hatay region. Results showed that, because of the conservation efforts after the discovery of Mountain Gazelle, their population size has an increasing trend and one additional wild population is present in the Reyhanlı region.

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Ungulates rely less on visual cues, but more on adaptive movement behaviour, when searching for forage

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Finding suitable forage patches in a heterogeneous landscape, where patches change dynamically both spatially and temporally could be challenging to large herbivores, especially if they have no *a priori* knowledge of the location of the patches. We tested whether three large grazing herbivores with a variety of different traits, improve their efficiency when foraging at a heterogeneous habitat patch scale, by using visual cues to gain a priori knowledge about potential higher value foraging patches. For each species (zebra (*Equus burchelli*), red hartebeest (*Alcelaphus buselaphus* subspecies *camaa*) and eland (*Tragelaphus oryx*), we used step lengths and directionality of movement to infer if they were using visual cues to find suitable forage patches at a habitat patch scale. Step lengths were significantly longer for all species when moving to non-visible patches but all movements showed little directionality. These large grazing herbivores did not use visual cues when foraging at a habitat patch scale, but rather adapted their movement behaviour to the heterogeneity of the specific landscape.

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What makes northern quolls “toad-smart”?

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Countless species are currently under threat due to changes to the environment around them, and although many are facing extinction, some are adapting to survive. The cane toad invasion across northern Australia has led to declines in native predators, including the northern quoll, which unwittingly attacks and eats poisonous toads. Yet amongst the widespread loss, a small number of quoll populations have persisted and now coexist with toads, doing so because they avoid toads as a prey item. This “toad-smart” behaviour has long been suspected to be heritable, but has never been empirically tested until now. It is likely that quoll populations can exist alongside cane toads because parents pass toad-smart behaviour to their offspring either genetically or through cultural transmission. We measured the response to toads of wild-caught parents from both toad-infested and toad-free areas of northern Australia, and then bred these quolls in captivity to determine if their offspring exhibited similar behaviour to their parents. We also attempted to link other behavioural traits, such as neophobia and exploratory behaviour, to the ability of northern quolls to survive the cane toad invasion. Taken together, this study demonstrates that some individual quolls are predisposed to survive the cane toad invasion, and that they may be able to pass their “toad-smart” ability onto their offspring.

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The role of subordinate Eurasian beavers (*Castor fiber*) as helpers in the natal family group

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Helper systems where non-breeding group members assist with the territorial defense and care of the young are widespread throughout the animal kingdom. In this study, we examined the role of subordinate Eurasian beavers (*Castor fiber*) as helpers in a population in southeast Norway. We conducted playback scent experiments, simulating a territory intruder. In total, we recorded 349 territorial reactions, and found that subordinates reacted towards simulated intruders according to their proportion in the family group, i.e. they helped with territorial defense. Subordinates reacted more with increasing age of their parents suggesting that they might take over territorial duties with increasing age of their senescing parents. However, the number of subordinates in a family group did not increase the total number of responses. Further, we examined whether the number of subordinate beavers within the family group affected the body weight of kits (n = 120) while controlling for other factors, hypothesizing that subordinates would aid with food provisioning. The body weight of kits was not related to the number of subordinates in the family group, but decreased with increasing precipitation. In conclusion, subordinate beavers might play a role in territorial defense, but did not affect offspring weight. By remaining in the natal family group, subordinates likely learn important behaviours, e.g. territorial defense, that will increase their chances to successfully gain and defend a territory of their own.

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Differences in behavioural responses to two kinds of culling over a short time scale in a sika deer, *Cervus nippon*, population

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Deer behavioural responses to culling, such as transient home range shifts and changes in diel activity patterns, which are factors reducing capture efficiency, become obstacles to achieving long-term management sustainability. However, most studies have analysed these responses on a long time-scale. Furthermore, the differences among various culling methods (e.g., driving versus stalking) have not been evaluated. In this study, photographic data from 28 camera traps of a sika deer (*Cervus nippon*) population in the Tanzawa Mountains, Japan, were analysed to evaluate differences in behavioural responses to different culling methods. First, to compare the duration of transient home range shift between two culling methods, a Cox proportional hazard model was applied to the day period encompassing when culling began to when a deer was re-photographed at a culling site; we found driving required slightly longer days. Second, temporal changes in deer diel activity patterns between disturbed (seven days after culling) and undisturbed (out of the disturbed period) periods were evaluated with kernel density estimation for each culling method. The degree of change in diel activity pattern between the two periods was almost the same between culling methods; however, peak activity during the disturbed period differed between the two culling methods, probably owing to the difference in start time. We conclude that deer immediately changed their behaviour according to the culling method characteristics; therefore, deer behavioural change over a short time period should be incorporated into the planning of population control.

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DNA metabarcoding reveals diet overlap among sympatric three species of forest guenons (*Cercopithecus*) in Uganda

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Three species of forest guenons live sympatrically in a mountain forest, Kalinzu, Uganda. Among them, the blue monkey (*Cercopithecus mitis*) and red-tailed monkey (*C. ascanius*) are arboreal, but l'hoest's monkey (*C. lhoesti*) is highly terrestrial. They often form a mixed-species group to travel and feed together for a long time. In particular, blue and red-tailed monkeys make such associations almost every day. Though forest guenons are generally considered frugivorous, all in this forest spend a very long time searching for and eating invertebrates. Little is known about how these congeneric species coexist and why guenons living in this forest feed for hours on insects. Firstly, I observed them and collected 156 faeces from August to September in 2016. Blue monkeys consumed more kinds of plant parts and ate a wider variety of insects than the other species. For both herbivory and insectivory, blue and red-tailed monkeys commonly used more items than the other two combinations. To reveal the consumed insect fauna, I extracted DNA from faeces, amplified the COI region of mtDNA using insect-specific primers, sequenced the amplifcations with Illumina MiSeq, and compared the obtained sequences to those in reference databases (DNA metabarcoding). Supporting the behavioral observation, blue monkeys consumed more varied insects than the others, and blue and red-tailed commonly ate more items than the other two combinations. These results consistently suggest that blue monkeys have the widest niche breadth, and blue and red-tailed occupy very similar niches even when they form a mixed-species group.

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Where the wild things were: Identifying extinction drivers and correlates of vulnerability and resilience in the Caribbean land mammal fauna

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The Caribbean land mammal fauna was formerly species-rich and diverse, but has experienced extensive postglacial extinctions that have been staggered through time and have varied in intensity between different islands. The Caribbean therefore has the potential to represent an extremely informative study system to understand wide-scale macroecological patterns of mammalian vulnerability and resilience, and provide important insights into global extinction dynamics. However, the spatiotemporal pattern of Caribbean mammal survival and extinction is complex, and research into correlates of extinction risk for this fauna has so far been limited and largely qualitative. We present the results of a new macroecological analysis investigating both intrinsic (biological, evolutionary) and extrinsic (environmental, anthropogenic) correlates of extinction vulnerability and resilience across the endemic Holocene land mammal fauna of the Caribbean (including rodents, sloths, primates and lipotyphlans) within a rigorous statistical and phylogenetically explicit framework, and present a new evidence-base for assessing why some Caribbean species and islands have been more prone to experience extinction through time. Extinction risk data from this analysis of historical baselines are interpreted within the context of the status and ecology of surviving Caribbean mammals, to evaluate the extent to which the past can be used to inform conservation in the present. The "last survivors" of the Caribbean land mammal fauna may now be threatened by multiple factors, and we complement our fauna-wide macroecological analysis with further analysis of remote-sensing data, to evaluate whether primary extinction drivers can be identified for some of Cuba's most threatened mammal species.

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Genomic and isotopic approaches reveal mechanisms of persistence in the endemic Hispaniolan solenodon

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Habitat loss in the form of deforestation and agriculture poses major challenges to species in the Anthropocene. Dietary flexibility has been hypothesised as a mechanism that can promote species survival in transformed habitats. In this study, we test whether dietary flexibility could explain the survival of the Hispaniolan solenodon (*Solenodon paradoxus*) across a variety of land-use types within the Jaragua-Bahoruco-Enriquillo Biosphere Reserve. We collected 54 faecal samples across two seasons from a series of forested and mosaic agriculture sites ranging in elevation and human impact. We characterised dietary flexibility through 1) metabarcoding of prey DNA in faeces and 2) stable isotopes of carbon and nitrogen. We confirmed the validity of isotopic data derived from faeces through comparison with isotopic analysis of hair samples. We applied five molecular markers to account for the taxonomic range of prey consumed by solenodons, including vertebrates, insects, arachnids, and gastropods. The population-level isotopic niche of solenodons is wider than any other known 'insectivore', with no significant differences in isotopic niche width between seasons or habitat types. DNA metabarcoding revealed an incredible diversity of prey items utilised by solenodons across habitat types, although all individuals consume millipedes, suggesting millipedes may be an important and abundant resource across altered landscapes. Critically, we address a local human-wildlife conflict concern, showing that solenodons are not predators of poultry and should not be persecuted. Our findings suggest that the evolutionary history of solenodons and their flexible diet may help them persist in areas altered by people such as mosaic agriculture.

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Modeling the distribution of the endangered Hispaniolan solenodon (*Solenodon paradoxus*) in the face of anthropogenic global change

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During the Holocene, the Caribbean suffered the largest regional postglacial mammalian extinction event, resulting in the extinction of over half of the native terrestrial fauna. The Hispaniolan solenodon (*Solenodon paradoxus*) is one of only two endemic terrestrial mammals from the island of Hispaniola that survived to today. However, despite the species' 72-million-year history and its IUCN endangered status, very little is known about the solenodon's distribution or the factors that drive that distribution. In this study, we employed a maximum entropy (MaxEnt) framework to generate species distribution models (SDMs) of the Hispaniolan solenodon during the late Quaternary and during the last fifty years. For each time period, two models were created. The first model included only bioclimatic variables characteristically included in SDMs. The second model included other potentially relevant factors, including soils and geology for the late Quaternary and soils, geology, land use, forest cover, and human population density for the modern time. The models including these additional factors outperformed the bioclimate-only models. These stronger models suggested that, in the late Quaternary, soils and geology were stronger determinants of solenodon distribution than were temperature or precipitation. In the modern time, human population density was seen to be the main driver of solenodon distribution. These results suggest that solenodons may not have a strictly delimited bioclimatic envelope in which they must live but may instead have a range limited by human encroachment into their habitats. Continued human population expansion will therefore likely threaten their future survival more than anthropogenic climate change.

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Current status and conservation of the non-volant land mammals of the insular Caribbean and priorities for future ecological research and conservation actions

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The insular Caribbean has experienced the world's highest levels of historical mammal extinctions, with at least 29 species lost since AD 1500. Representatives of only two non-volant land mammal families (Capromyidae and Solenodontidae) now survive, and the conservation status of these is surprisingly poorly understood. In the 2008 IUCN Red List assessments 15 endemic species were recognised, of which 13 were assessed as threatened. We reassessed all available baseline data on the current status of these species within the framework of the IUCN Red List, to determine their specific conservation requirements using an evidence-based approach. We now only recognise 13 surviving species, one of which is not formally described and cannot be assessed using IUCN criteria; three further species previously considered valid are interpreted as junior synonyms or subspecies. Of the 12 reassessed species, five have undergone a change in threat status since 2008, with three species (*Capromys pilorides*, *Geocapromys brownii*, *Mesocapromys angelcabrerai*) increasing in extinction risk by one IUCN category, and two species (*Plagiodontia aedium*, *Solenodon paradoxus*) decreasing in extinction risk by two categories. Only one change in threat status represents a genuine change; all other changes are non-genuine changes mainly associated with new information becoming available. Hunting, habitat loss, and invasive species represent major threats to surviving species, and conservation of the highly threatened Caribbean land mammal fauna will require a range of targeted management strategies. We will discuss which species represent high priorities for further ecological research and where urgent conservation actions are needed.

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Poor historical data drive conservation complacency: The vital role of predator accumulations for mammal conservation in south-eastern Australia

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Understanding how native mammals have responded to ecosystem modification since European settlement is critical for their conservation management. Unfortunately, historical data is limited, and our ecological understanding is instead heavily biased towards modern studies, mostly post-1960s. Consequently, critically important information about past conditions and ecological changes is often surmised, with modern conditions and ecological patterns perceived as close to natural or normal. Recently obtained information from subfossil deposits in south-eastern Australia indicates that mammal declines have been recent, rapid and underestimated, and that many assumptions about species' ecology, biogeography, status and overall ecosystem health require re-evaluating. Of particular note, many species now rare and geographically restricted recently occupied a greater range of habitats, often at high abundances. Many species are experiencing niche-denial, whereby they are being excluded from their original niche, and cannot function as they did historically, which has wide-scale consequences for ecosystem function and management. The pattern of decline indicates that predation by exotic predators is the principal causal factor, especially when greatest declines have occurred to terrestrial species in structurally open habitat types, including forested habitats that have experienced limited disturbances by factors considered responsible for declines in other regions of Australia. Researchers must recognise that ecosystems have been highly modified and that species are potentially constrained from carrying out their ecological functions, and therefore need to exercise caution when making broad generalisations from their studies.

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From papers to potholes: Piecing together extinct eastern Australian mammal communities

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The loss of many small and medium mammal species from eastern Australia during the 19th and early 20th centuries greatly outpaced scientific collection or preservation of live-caught specimens for other purposes. Bounties, diaries and newspaper reports provide conclusive evidence of the former distribution of some readily-diagnosed larger bodied species. However, to establish the distribution of small-bodied species such as mice, the only known viable source of information is bone accumulations associated with owl roosts. These deposits also provide potential to determine population genetics and isotopic analyses of dietary shifts, along with tracking natural community changes through pre-historical environmental changes. These deposits record the clear decimation of small mammal faunas across eastern Australia in the wake of European colonisation. Here we discuss the case study of southern highland faunas and an ecological restoration project at Mulligans Flat in the Australian Capital Territory, as well as broader patterns of interest across eastern Australia. Owl pellet deposits were essential in determining species that were suitable for reintroduction into the feral predator-proof fenced area of Mulligans Flat. The fauna revealed by deposits in and around the ACT was far richer than faunal lists suggested. However, like the loss of knowledge that occurred with the passing of early settlers who lived with these species, many bone deposits are prone to disturbance, and are themselves now at risk of being lost.

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Applied conservation palaeobiology in Western Australia: Faure Island, Shark Bay, and Mount Gibson Sanctuary, mainland Mid-West

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Translocating species to areas where significant threats have been removed or ameliorated is an important conservation tool. Two types of translocation are (1) reintroductions, where locally extinct species are re-established and (2) introductions for conservation purposes. In areas where the previous mammal fauna assemblage is poorly understood, remains can provide evidence of the species originally present; information that is integral to planning and justifying translocations. Evidence of 3 mammals was found on Faure Island, but species-area relations of other northwest islands indicate the carrying capacity of Faure is 8 species. Both aspects were taken into account when planning translocations. Four species were successfully translocated to Faure, two as reintroductions (*Pseudomys fieldi*, *Perameles bougainville*) and two as conservation-motivated introductions (*Lagostrophus fasciatus*, *Bettongia lesueur*). *Bettongia lesueur* was selected instead of *B. penicillata*, previously present, due to its higher conservation concern. The previous presence of a *Bettongia* species suggested that the habitat may be suitable for *B. lesueur*, which is now well established. Evidence of 20 non-volant mammals was found at Mt Gibson; 9 of these were subsequently selected for reintroduction. The now extinct *Leporillus apicalis* was confirmed as a former inhabitant, providing impetus for the inclusion of *L. conditor* in the restoration program. Although the program at Mt Gibson is in its infancy, the species translocated so far are establishing satisfactorily. Understanding of the composition of previous faunal assemblages enables translocation programs to re-establish communities of species and make more informed decisions about the suitability of areas for introductions for conservation purposes.

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A brief history of the international theriological/mammalogical congresses

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I will review the history of the 12 ITC/IMC conferences plus the two antecedent symposia held in Brno, Czechoslovakia (now Czechia). These latter two international conferences paved the way for ITC-1. Collectively these meetings spanned a time interval from 1960 to 2017. I attended the second of the two Brno symposia as well as all of the subsequent congresses. Emphasis will be on the role this international cooperation in mammalogical science played in the dissolution of the “Iron Curtain” in Europe, on the leading personalities involved, and on the history of the organizational structure of the program.

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Survival expectations in a wolf-elk system: How selective predation and the environment shift senescence

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Because ungulates can be dangerous prey, predators generally kill vulnerable ones (e.g. juveniles, individuals in poor body condition). Adult female ungulates usually have a high constant survival rate until they become frail at older ages. We tested the hypothesis that relative to other mortality, selective wolf predation on old female elk is the principle driver of actuarial senescence in northern Yellowstone National Park, USA. We monitored radio-collared elk (n = 196) from 2000-2008 and 2011-2016 and determined the cause of mortality for 77 individuals. We used a multi-state survival model in a competing risks framework to estimate age-specific wolf-caused mortality compared to all other causes of mortality. Elk mortality was low (< 5%) for 2-13 year-olds. After age thirteen, the probability of wolf-caused mortality increased sharply. The probability of wolf predation was 0.10 (95% CI = 0.08, 0.14) for 15-year-olds and 0.42 (95% CI = 0.32, 0.54) for 20-year-olds. In contrast, the probability of non-wolf caused mortality was 0.08 (95% CI =0.06, 0.11) for 15-year-olds, and 0.15 (95% CI = 0.11, 0.26) for 20-year-olds. Older elk were more likely to be killed by wolves during severe winters (20-year-old mortality = 0.68, 95% CI = 0.41, 0.85) relative to mild winters (0.32, 95% CI = 0.16, 0.60). These results suggest that prey senescence can be shaped by selective predation and that the population-level impact of predation depends on prey age structure. Additive predation effects are more likely in a population with an older age structure, and among old individuals.

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Behavioural and chemical ecology approaches to novel species interactions: What do we know about naïveté in the Australian mammal fauna?

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Naïveté, or the failure to recognise and respond appropriately and effectively to a novel alien predator, is thought to underpin Australia's dubious record for the world's worst rate of extinctions and declines in small to medium-sized mammalian fauna. We report on three years of research into predator naïveté in Australian native small-medium sized mammals. Australian native prey have an evolutionary history of marsupial predation, with the more recent addition of the placental dingo (*Canis lupus dingo*), which was introduced ~4000 years ago and is generally considered a native species. Placental foxes (*Vulpes vulpes*), dogs (*Canis familiaris*) and cats (*Felis catus*) were introduced around 150 years ago. We used behavioural analysis of remote-sensing camera footage to quantify recognition of predator odours by native *Rattus fuscipes* in the field, and surveyed Sydney, NSW, residents to quantify behavioural responses of native bandicoots (*Isoodon macrourus* and *Perameles nasuta*) to the presence of pet predators (cats and dogs) in back yards. Finally, we used analytical chemistry techniques to compare the chemical profiles of odour cues emitted by placental and marsupial predators. Naïveté in Australian fauna appears to be driven by significant chemical differences in the cues emitted by introduced placental and native marsupial carnivores. Native bush rats and bandicoots both recognised dog odours, which we attribute to thousands of years experience with the very closely related dingo. We present a wholistic picture of the current state of naïveté in Australian fauna, and discuss how it may have changed since placental carnivores were introduced.

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Investigating post-fire recovery in an Australian native rodent: Managing fire for conservation in northern Australia

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Since European arrival, native mammals in Australia have suffered the worst declines of any country in the world. In particular, recent and drastic declines have been seen across northern Australia, a region long considered a haven for wildlife. This is partly due to frequent, intense wildfires occurring later in the dry-season. Therefore, conservation-based fire management focuses on implementing low-intensity burns early in the dry-season, creating a mosaic of burnt and unburnt habitat to prevent late-season wildfires. To design effective fire management for conservation, we need to understand how populations recover after fire. We assessed the immediate response to fire of a vulnerable native rodent, the pale field-rat (*Rattus tunneyi*) and investigated how populations recover after fires of varying size. We carried out fire experiments in the Kimberley region of Western Australia, using 'patchy' and 'thorough' burns to represent early and late dry-season fires. We collected mark-recapture data, genotypes and vegetation measurements before fire and during the post-fire recovery phase over a one-year period. We found that vegetative cover and pale field-rat captures decreased after fire. This was much more dramatic after 'thorough' burns than after 'patchy' burns. One year after fire, both vegetation and pale field-rat populations recovered quickly. However, the mechanisms driving recovery differed between fire types, with recovery driven by *in situ* survival after 'patchy' fires, compared to recolonisation after 'thorough' fires. Understanding this process is vital for designing management strategies that promote recovery for vulnerable native rodents, as well as other mammals declining across similar habitats.

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Dynamics of three flea species parasitizing the Namaqua rock mouse (*Micaelamys namaquensis*) in South Africa

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Rodents are hosts to a multitude of parasites and pathogens and exhibit a large diversity on the African continent. Despite this, most research on rodent parasites has focused on invasive but rarely endemic rodents. The Namaqua rock mouse (*Micaelamys namaquensis*) is widely distributed in sub-Saharan Africa and frequently parasitised by three flea species, *Xenopsylla brasiliensis, Chiastopsylla godfreyi* and *Epirimia aganippes*. While the latter two are probably host specific, *X. brasiliensis* has been identified as a plague vector globally. Nevertheless, little is known about either species' biology. This study aimed to evaluate the contributions of abiotic (e.g. climate) and biotic (e.g. host, parasite) factors to the patterns of prevalence and abundance of these flea species on their natural host. Mice were sampled four times a year between April 2010 and August 2016 in a nature reserve in South Africa's Gauteng Province. We assessed the entire ectoparasite community and took morphometric and condition measurements for all hosts and their fleas. All flea species show seasonal variation in prevalence and abundance that differed between the species. In combination with the marked size differences, this might be indicative of competitive interactions between these fleas. There was little evidence that host condition was linked to flea burden. At the same time, our data suggest that other (non-flea) ectoparasites may affect the distribution of fleas. The implications of these findings for the dynamic of the three flea species will be discussed.

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More variable than we thought: New patterns of social structure in tuco-tucos (Rodentia: Ctenomyidae)

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The social environment in which an individual lives can have profound impacts on numerous aspects of its biology, including fitness, physiology, and gene expression. Long-term field and laboratory studies of the colonial tuco-tuco (*Ctenomys sociabilis*) indicate that whether a yearling female lives alone or with conspecifics impacts each of these parameters. To better understand the effects of the social environment, comparative data from other, independently evolved examples of ctenomyid sociality are required. To date, however, few additional species of tuco-tucos have been studied with regard to social structure; of those species for which appropriate data are available, the majority (N = 7 of 9 species) have been shown to be solitary. Here, we present information indicating that, in addition to *C. sociabilis*, at least two other species of ctenomyids – *C. opimus* and *C. rionegrensis* - display evidence of some degree of sociality. Based on analyses of mark-recapture and radiotelemetry data, we demonstrate that spatial and thus presumably social relationships differ markedly among these species. The distribution of these species within the genus *Ctenomys* suggests that they represent independent origins of non-solitary behavior. Collectively, these analyses indicate that patterns of social structure in ctenomyid rodents are more diverse than previously suspected, thereby creating exciting new opportunities for comparative analyses of the causes and consequences of patterns of social behavior.

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Field physiology of the short-beaked echidna: Flexibility aids success for this Australian mammal.

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The short-beaked echidna (*Tachyglossus aculeatus*) has the widest geographic distribution of any Australian native mammal and has not suffered the same decline post-European settlement as many mammals. Here I evaluate its field physiology in terms of the physiological characteristics that contribute to its success. Its low body temperature (T_b) and basal metabolic rate are not associated with a low field metabolic rate (FMR). Echidnas move over large distances daily, contributing to this typical mammalian FMR and despite limitations imposed by their limb structure. They spend up to 12% of their active time digging, excavating considerable quantities of soil and so are important ecosystem engineers. Echidnas moderate their activity seasonally; they are exclusively nocturnal during hot weather, moving more quickly to and from foraging sites in summer. However, despite earlier hypotheses, echidnas do have physiological heat dissipation in the form of enhanced evaporative water loss at high temperatures. South-west Australian echidnas are heterothermic, using daily torpor regularly and sometimes hibernation, but this heterothermy does not have the strong seasonal pattern observed in colder climates. Heterothermy allows echidnas to avoid unfavourable conditions; for example, echidnas impacted by fire reduced their T_b and activity compared with those not affected. The echidna's physiological flexibility is a factor contributing to their current success and presumably will aid their continued survival in the face of human-induced habitat modification and climate change.

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Body water conservation through selective brain cooling by the carotid rete: A physiological feature for surviving climate change?

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Some mammals have the ability to lower their hypothalamic temperature below that of carotid arterial blood temperature, a process termed selective brain cooling. Although the requisite anatomical structure that facilitates this physiological process, the carotid rete, is present in members of the Cetartiodactyla, Felidae and Canidae, the carotid rete is particularly well developed in the artiodactyls, e.g. antelopes, cattle, sheep and goats. First described in the domestic cat, the seemingly obvious function initially attributed to selective brain cooling was that of protecting the brain from thermal damage. However, hyperthermia is not a prerequisite for selective brain cooling, and selective brain cooling can be exhibited at all times of the day, even when carotid arterial blood temperature is relatively low. More recently, it has been shown that selective brain cooling functions primarily as a water-conservation mechanism, allowing artiodactyls to save more than half of their daily water requirements. Here, we argue

that the evolutionary success of the artiodactyls may, in part, be attributed to the evolution of the carotid rete and the resulting ability to conserve body water during past environmental conditions, and we suggest that this group of mammals may therefore have a selective advantage in the hotter and drier conditions associated with current anthropogenic climate change. A better understanding of how selective brain cooling provides physiological plasticity to mammals in changing environments will improve our ability to predict their responses and to implement appropriate conservation measures.

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Towards accurate calculation of field metabolic rates for bats

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A balanced energy budget is the key element in an animal's ability to survive and reproduce. Accurately understanding this budget, called the field metabolic rate (FMR), throughout an annual cycle is a very difficult challenge. Typically, previous estimates for bats have been accurate to +/- 50%. A practical method for calculation of FMR for bats to a high level of accuracy is possible using a model based on physiology and quasi-steady aerodynamics. The fidelity of this modelling approach has been cross-checked using twenty three empirical data measurements using doubly labelled water methods published for fifteen Old and New World species. Predictions have been made for adult bats in non-reproductive, pregnant and lactating conditions. Predictions were generally within 5% of the empirical values for non-reproductive adult bats and pregnant females (average 4.4%, s.d. 5.6%, n = 19). Predictions with errors over 10% were limited to lactating females from one of four species where the timing of the collection of the empirical data may have been a contributing factor. Calculation of metabolic power at these improved accuracies can provide inter-species level energy budget assessments for bats in guilds, communities and also at a continental level.

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Wild mammal ecophysiology in a changing world: A role for plasticity?

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Ecological physiology (ecophysiology) has transformed thinking about mammal survival beyond an appreciation of the mechanisms of physiology, to an appreciation of the ecological consequences of their physiological constrains and abilities. Ecophysiology has emerged from the long-standing traditions of comparative physiology, but deeper understanding of the contributions of mammalian physiological traits to ecological interactions is scant, and ecological research remains focussed on animal abundance and distribution. Here I describe the role that physiological plasticity of mammals (or lack thereof) may play at finer ecological scales, and argue that such plasticity could be considered as a key factor affecting mammalian survival. This is especially relevant in light of global climate change, but may also be important for understanding and predicting the ecological consequences of invasive mammals, conservation physiology, and factors affecting biodiversity. In this regard, mammals at extreme climates offer opportunity to test hypotheses about the strength of plasticity as a driver or cog for ecological interactions and processes. Mammal abundance and distribution, therefore, may be necessary, but not sufficient, for explaining ecological changes in some systems, and the role of plasticity in affecting mammalian survival and fecundity (and hence abundance) needs to be explored.

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Peeing poison: The biochemistry of bamboo lemur cyanide survival

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Bamboo lemurs (*Prolemur simus* and *Hapalemur* spp.) survive eating typically deadly concentrations of cyanide in their natural diet of bamboo. This survival is an evolutionary novelty, likely shared only by giant pandas (*Ailuropoda melanoleuca*), red pandas (*Ailurus fulgens*), and some bamboo rats (*Dactylomys* spp., *Rhizomys* spp.). To understand the nature of this adaptation we must understand the biochemical and metabolic processes at work. However, the Critically Endangered status of bamboo lemurs and the Vulnerable and Endangered statuses of other bamboo eating mammals limit options for study. We used a novel approach by examining the form of cyanide excreted in urine. The form (cyanide ion or a detoxification product) is informative of the biochemical processes allowing survival. To determine the chemical structure of excreted cyanide compounds, we collected urine samples from wild (N = 46) and captive (N = 5) bamboo lemurs (*P. simus*, *H. aureus*, and *H. griseus*) from Madagascar and comparative samples from non-bamboo eating (non-cyanide consuming) lemurs at the Duke Lemur Center. We adapted gas-chromatography mass-spectrometry analytical methods to quantify cyanide and thiocyanate (the primary mammalian detoxification product) in lemur urine. Concentrations of both cyanide and thiocyanate in bamboo lemur urine, but not that of non-bamboo eating lemurs, were 10-20 times higher than concentrations in other mammals killed by acute cyanide poisoning. This implicates two co-acting mechanisms: 1) increased activity of the enzymatic detoxification pathway and 2) increased tolerance to residual cyanide. This provides the first evidence for the biochemical mechanisms behind this extreme dietary adaptation.

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Can apex predators retain their ecosystem function when the world changes?

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Apex predators play an important role in structuring ecosystems. Can they retain this function when the world changes? We applied a space for time approach to explore a recolonising apex predator´s ability to limit mesopredator abundance when land use and climate have changed. First, we estimated to what extent Eurasian lynx (*Lynx lynx*, apex predator), cropland and winter temperatures drive red fox (*Vulpes vulpes*, mesopredator) abundance at a spatial scale. Second, we estimated lynx abundance, proportion of cropland and winter temperatures over time. Third, we used the estimates from the initial steps to project fox abundance in 1830, 1920, 2010 and 2050. Projected fox abundance was lowest in 1830 when lynx abundance was high, the proportion of cropland was low and winters were harsh. Persecution of lynx during the 19th century caused a mesopredator release that was boosted by agricultural expansion and global warming; the highest fox abundance was therefore reached in 1920 when lynx were extinct. In 2010, lynx recolonisation had suppressed fox abundance but not to the same level as in 1830, because of a smaller lynx population and an enriched environment with more crop fields and milder climate compared to 1830. Assuming that winter temperatures will increase yet another 1.5°C, lynx abundance is required to increase by 79% compared to 2010 to buffer the impact of global warming on foxes, and prevent increased mesopredator abundance. We suggest that environmental enrichment can give mesopredators and herbivores an opportunity to thrive unless apex predators can respond numerically or behaviourally.

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Evidencing new areas of endemism in the Atlantic Forest Biome: An approach for non-volant small mammals

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Knowledge of distributional patterns and areas of endemism (AE) is an important source to protect the biodiversity. The Atlantic Forest (AF) is the second major rainforest of the Americas, and combining an extensive latitudinal range with altitudinal gradient, hosts one of the most important faunal diversities of the world, here highlighted by the high diversity of non-volant small mammals. However, the AF is one of the more threatened biomes, with significant habitat loss to urbanisation and expansion of agricultural frontiers. Based on 283 inventory records of 105 species of small mammals we employed parsimony analysis of endemicity (PAE) and endemicity analysis (EA) implemented in the programs NDM and VNDM to delimitate AEs in the AF. Using 25% for radius to fill and 50% to radius to assume, the PAE results show 11 individual AEs and nine consensus AE. For EA analyses, using the grid size of 0.75° with two points, we detect 15 areas of endemism. Ours results indicate that nine of them are congruent AE. Our results highlighted the following AE: Misiones; coastal Southern; Serra do Mar; Highlands of Espirito Santo and Minas Gerais; coastal Northeastern. Most of these areas are within conservation units and have already been identified as AE for other vertebrates, highlighting their importance for the maintenance of biodiversity. However, we also have identified unprotected areas that deserve priority attention. The AEs identified here represent a major advance in mammal quantitative distribution patterns in the AF, contributing to biogeography studies and conservation planning.

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Niche separation of three species of tree-rat in north western Australia

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Conilurus penicillatus, *Mesembriomys macrurus* and *M. gouldii* have undergone significant contraction in distribution and abundance since European settlement. The Kimberley region is one where they co-occurred and the project's aim was to determine niche separation within a restricted area of the Mitchell Plateau. Trapping at ground level, observations and radio telemetry at nine sites in vine thicket and open eucalypt forest were used to describe habitat preference, use and diet. Vegetation requirements were characterized using PATN analysis. Vegetation analysis showed little overlap in habitat preference. *Mesembriomys gouldii* preferred relatively stable open forest with a well-developed shrub layer, nesting in tree hollows and palm fronds. *Mesembriomys macrurus* selected several habitats, especially the edges between vine thicket and open forest, nesting in hollows in large eucalypt trees. *Conilurus penicillatus* occupied the greatest variety of habitats, nesting in eucalypts and ground-level sites. *C. penicillatus* was the most frequently trapped and found in both trees and on the ground. *M. gouldii* was predominantly arboreal while *M. macrurus* was mostly arboreal but also spent time on the ground. While there is substantial overlap in diet, niches were identified: *M. gouldii* a granivore/frugivore, eating seeds almost exclusively; *M. macrurus* an omnivore with a diet of seeds, fruits, flowers, termites and other invertebrates; and *C. penicillatus* a generalist whose diet included monocot

and dicot leaves, seeds, flowers, fruits and arthropods. Landscape-wide changes in northern Australia since European settlement may have reduced the availability of the vital and differing resources required by these tree-rat species.

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Kangaroos in the backyard: A case study from the Coffs Harbour Northern Beaches, New South Wales.

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The proximity of eastern grey kangaroos to human residents is an emerging management issue in the Coffs Harbour Northern Beaches region of New South Wales. The small rural estate of Heritage Park, located within this region, is a 'hotspot' for frequent human-kangaroo interactions. While interactions are generally positive, there have been 17 reports of kangaroo attacks since 2007. This study investigated human dimensions and kangaroo ecology to understand community perceptions towards kangaroos, and the abundance, demographics and movement patterns of kangaroos in the peri-urban environment. Heritage Park residents were surveyed using an online questionnaire and responses revealed an overall positive perception of kangaroos. However, there were concerns among residents on potential conflict with kangaroos, especially large males, as well as concerns for vehicle collisions. Responses also showed a lack of educational exposure on how to coexist peacefully with kangaroos. Kangaroos were counted every two months throughout 2016 and abundance ranged from 260 individuals in June to 312 individuals in October. GPS telemetry units were also used to monitor the movement patterns of 14 male kangaroos. Kangaroos primarily occurred within the peri-urban landscape, with some individuals occupying the surrounding forests for short periods of time. On average, kangaroos occupied 4.6 properties per day and showed temporal shifts in their proximity to housing, being closer to houses overnight and further away during the day. The results of this research increased our understanding of peri-urban kangaroos to assist in the development of appropriate management strategies with a focus on Heritage Park.

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Newfound insights into the host range, geographic distribution and genetic diversity of hantaviruses gained from natural history collections of shrews, moles and bats

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Rodents (order Rodentia) were initially believed to serve as the exclusive reservoir hosts of hantaviruses. Moreover, the conventional view contended that each genetically distinct hantavirus was hosted by a single rodent species, with which it co-evolved. Recently, however, a new frontier in hantavirology has dawned with the discovery of highly divergent lineages of hantaviruses in multiple species of shrews and moles (order Eulipotyphla) and bats (order Chiroptera) from widely separated geographic regions in Asia, Europe, Africa and North America. Close collaborations with museum curators and field mammalogists have accelerated the acquisition of new knowledge about the spatial and temporal dynamics of 23 shrew-, 7 mole- and 11 bat-borne hantaviruses. Also, particularly in light of the expanded host range and genetic diversity of hantaviruses, mounting evidence supports the concepts of extensive host sharing and host switching. That is, the same hantavirus species may be harbored by more than one reservoir host species. The converse is also true; that is, the same reservoir host species can harbor more than one hantavirus species. Phylogeographic analysis indicates that shrew- and mole-borne hantaviruses exhibit geographic-specific lineages, akin to that reported for rodent-borne hantaviruses. Also, based on the geographic origin of the newfound non-rodent-borne hantaviruses, primordial hantaviruses probably originated in Asia, rather than Africa or the Americas. Moreover, phylogenetic analyses suggest that ancestral shrews and moles and/or bats may have predated rodents as the early reservoir hosts of primordial hantaviruses. Thus, the phylogeography and evolutionary history of hantaviruses are far more complex than originally imagined.

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High parasite infection level in non-native invasive species – It is just a matter of time

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The Enemy Release Hypothesis (ERH) is often used to explain the success of non-native species invasions. Growing evidence indicates that parasite or pathogen species richness increases over time in invasive non-native species. However, this increase should not directly translate into release from enemy pressure as infection intensity of parasites (number of parasites per host) has a more profound impact on host fitness. The changes in intensity of parasitic infections in invasive non-native species have not yet been thoroughly analysed in newly colonized areas. The goal of this study was to determine whether gastrointestinal parasite (nematodes and trematodes) infection intensity has increased with time since the populations of American mink (*Neovison vison*) were established and how parasite-mediated selection might drive mink major histocompatibility complex (MHC) diversity. We tested the ERH by substituting space for time, evaluating parasite abundance in American mink at sites along a chronosequence of mink invasion history. Nematode and trematode abundance increased with time since mink introduction and mink populations established 30-35 years ago had similar parasite abundance to native populations. The rate of increase in infection intensity varied among demographic groups of mink (sex and age). Our results provide evidence that non-native species are released from enemy pressure only in the first phase of invasion. The delay in parasite infection may explain the dynamics of invasive non-native species populations during expansion. Examination of parasite abundance and MHC genes provide an improved understanding of the mechanisms driving MHC diversity.

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Transmission of chlamydia using naturally-infected koala semen

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Koala numbers in Eastern Australia have declined dramatically over the last 20 years. Over this time an increase in infectious diseases in the species, including chlamydia, has been observed. *Chlamydia pecorum* infection is estimated to effect approximately 70% of koalas in SEQ. In females, infection of koalas has shown to induce reproductive tract pathology resulting in infertility. To date, minimal studies have investigated the effects of *C. pecorum* infection on male fertility. This study was undertaken to investigate whether naturally occurring chlamydia-infection identified in koala semen is viable to inoculate a cell line and act as a source of bacterial transmission. Semen collected from 120 wild koalas were assessed for motility and rate, % live/dead, concentration, morphology, % DNA fragmentation and chlamydial speciation and quantitation determined through qPCR of seminal fluid. Chlamydia-positive koala semen, with PCR quantitated infectious load, was inoculated into a clean McCoy cell line and incubated. Fluorescently-conjugated chlamydia MOMP antibody was used for the detection of chlamydial inclusion bodies within cell cytoplasm. Results show inoculation of a cell line using naturally-infected koala semen. Observation of small chlamydial inclusion bodies and remnants of sperm flagella within the culture medium indicates presence of infection. With the absence of experimental animals available, we have developed a secondary method that can assist in determining the infectious load of chlamydia within a koala semen sample. Results confirm that infectious chlamydial elementary bodies can be shed into koala semen and serve as a source of bacterial transmission to the female.

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Let’s go to the dogs: Domestic dog ecology in rural villages west of Serengeti National Park in Tanzania

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Free-roaming dogs, *Canis lupus familiaris,* can be both a public health and conservation concern because they are a disease reservoir. Between 2010 and 2013, we identified 2,649 dogs in four rural villages in Tanzania. We characterized dog demography and ownership practices and investigated whether vaccination influences dog population dynamics. We found that adult dogs had higher survival than puppies in all villages. We observed a male-biased sex ratio across all age classes and higher adult male dog survival. Within the vaccination villages, vaccinated dogs had a decreased risk of death. However, overall mortality in one non-vaccination village was significantly higher than in the two vaccination villages and other non-vaccination villages. Dogs in poor body condition had lower survival than dogs in ideal body condition in all villages. Sickness and spotted hyaena (*Crocuta crocuta*) predation were the two main causes of dog death. We found that dog ownership was related to livestock ownership, household size, education, and house type. Thus, the number of dogs increases with household wealth. Free-roaming domestic dogs in rural communities exist in the context of their human owners as well as the surrounding wildlife. Our results demonstrate that vaccination alone does not impact domestic dog population dynamics and that they may be mediated by humans. Understanding the role of dogs and their care within these communities is important for planning and implement rabies control measures such as mass dog vaccination.

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What makes a stud? Understanding high reproductive skew in male African ground squirrels with no dominance or territoriality

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Reproductive skew among male mammals is common, often reflecting differences in morphology, physiology, and/or behaviour, with some males gaining a high number of matings compared to others. Differences in competitive abilities (e.g., territories or dominance) are often the most important factors influencing copulatory success, although post-copulatory mechanisms (e.g. sperm competition) can confound these pre-copulatory mechanisms. Less is known about the factors influencing reproductive distribution in what appear to be egalitarian societies that do not use aggressive pre-copulatory means of competing for mates. Male Cape ground squirrels (*Xerus inauris*) typically associate in all-male bands where aggressive interactions are rare. In our study population in central South Africa, males do not form dominance hierarchies, and all males are equally likely to copulate; however less than 30% of all adult males sire offspring. Males competitively search for females but there is no relationship between fertilization success and mate order. We examined the factors that may influence male reproductive success, including reproductive tactic (dispersed vs non-dispersed), years on site, scrotal size, parasites, hormones, and body condition. We found that factors such as tactic, body condition, scrotal size, and age appeared to influence male reproductive success, but the importance of these factors appeared to vary from year to year and may reflect annual fluctuations in resources. Why male reproduction is so highly skewed in this highly social species is still unclear.

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Trophy hunting: The good, the bad, and the ugly - how to tell them apart

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Trophy hunting is the subject of intense debate and polarised positions, particularly in the current context of acute concern for iconic species such as rhinos, elephants and lions in the face of a surge in poaching and illegal wildlife trade. The controversy has sparked moves at various levels to end or restrict trophy hunting, including through bans on the carriage or import of hunting trophies. Although there is a pressing need for the reform of hunting governance and practice in many countries, calls for blanket restrictions on trophy hunting assume that it is uniformly detrimental to conservation; such calls are frequently made based on poor information and inaccurate assumptions. Like it or not, trophy hunting can demonstrably play a positive role in supporting conservation and community rights and livelihoods, but only where there is adequate governance and responsible management. Here I examine examples of trophy hunting around the world (good, bad, and ugly) to highlight and illustrate some key characteristics of successful programmes. Characteristics discussed include the distribution of benefits from hunting, the economic pressures on landowners, the impacts of corruption, the nature of tenure arrangements, and the transparency of benefit flows and other aspects of management.

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Patterns of selective hunting and its indirect effects on ungulate populations

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Selective hunting is an old and wide-spread management tradition for ungulate populations. Hunter selectivity is most commonly driven by either a desire to shoot males with large trophies (such as antlers and horns), or to avoid shooting females with offspring and to rather target individuals with low reproductive value (such as juveniles) to enhance population growth. Intentional selectivity due to hunter preferences is clearly a very important force. Many countries already have management practices for avoiding undesirable consequences of unregulated trophy hunting. Selectivity is often largely modified by management (through specific quotas), culture, time constraints and economic incentives. Selectivity may also arise due to differences in behaviour among animals making them more or less prone to being shot. Any level of hunting of an animal population may have an impact on population dynamics by removing individuals. When hunting is selective, it largely affects the remaining sex-ratio and age-structure, and thereby also indirectly a range of other processes that is less well documented. In theory, differing mortality patterns and skewed sex-ratio and age-structure due to selective hunting will yield markedly different selective pressures from those impinging on populations without hunting or with large predators. The aim of this talk is to present empirical patterns of hunter selectivity and analysis of why they arise, and empirical evidence of indirect effects related to changes in age structure and sex ratio.

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When does selective hunting select, and is that a problem?

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Trophy hunting can be a major component of conservation strategies for large mammals, but it must be both ecologically and evolutionarily sustainable. Selection will not necessarily lead to evolution. To affect evolution, selective hunting must target an inheritable trait and be stronger than natural or sexual selective pressures that it may oppose. For some ungulates, horn or antler size, the trait usually targeted by trophy hunting, is strongly correlated with mating success, often in interaction with male age.

For other species the correlation is weak, and for most species it is unknown. Selective hunting is more likely to induce genetic change if it targets a trait expressed early in life, if it causes strong trait-based selective mortality, and if hunting regulations remain similar over a wide area and for multiple generations. Protected areas may be a source of unselected males that could dampen artificial selection, but only if those males migrate out of protected areas for the rut after the hunting season, otherwise they are likely to be shot before they breed. Using long-term data from bighorn sheep, Stone's sheep, red deer, mountain goat and chamois I will illustrate when selective hunting is most likely to select and what management strategies can be used to prevent or reduce this selective effect. Those strategies include a reduction in hunting pressure, an increase in harvest age, and protection of males that emigrate from protected areas to breed.

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Evolutionary and demographic consequences of exploitation: Wild boar as a case study

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Understanding how some species respond quickly enough to deal with anthropogenic pressure is of prime interest in evolutionary biology, conservation, and management. Wild boar (*Sus scrofa*) populations are mainly regulated by hunting and seed availability (acorns/beechnuts) in Europe. From a long-term monitoring of two populations subjected to markedly different environmental contexts in terms of both frequency of pulsed resources and hunting pressure, we assessed how pulsed resources shape the reproductive output of females. Using path analyses, we showed that in both populations, abundant seed availability increases body mass and both the absolute and the relative (to body mass) allocation to reproduction through higher fertility. In the lightly hunted population also characterised by few resources, females equally relied on past and current resources for reproduction and ranked at an intermediate position along the capital-income continuum of breeding tactics. In contrast, in the heavily hunted population with high availability of food resources, females relied on current more than past resources and ranked closer to the income end of the continuum. We discussed these results at the light of recent works showing different wild boar life history strategies in populations subjected to contrasting hunting pressures.

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Hunting of introduced deer vs native species conservation: Wapiti management in New Zealand

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Management of introduced deer in New Zealand has long been controversial. Deer were introduced into native ecosystems previously free of large mammals, driving unwanted changes in those ecosystems. In national parks, where protecting the native biota is a primary aim, deer and other introduced species are effectively designated as pests, with the law stating that they 'shall as far as possible be exterminated'. However, deer are too widespread for that to be affordable and they are also valued as a hunting resource by some stakeholders. We describe the management of New Zealand's only wild herd of wapiti (*Cervus canadensis*), the Fiordland National Park herd. The Fiordland Wapiti Foundation (FWF) generates revenue from recreational hunters and aims to improve the recreational trophy hunting value of the wapiti herd without increasing unwanted impacts on the native biota. The FWF also manages and (when necessary) subsidises commercial helicopter-based hunting for venison. The commercial hunters take the greatest numbers of deer but target only sympatric red deer (*C. elaphus*) and red deer–wapiti hybrids, aiming to reverse the loss of wapiti genes from the population whilst ensuring the unwanted impacts of deer are no worse than in unmanaged areas elsewhere. A key issue is determining deer densities and density–impact relationships, and how to affordably measure these. We discuss the underlying principles and complexities implicit in this management system, and assess whether it provides a useful model for the management of some other deer herds of special interest to New Zealand hunters.

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Who's calling? The importance of acoustic studies for the conservation of Brazilian bats

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Brazil is a megadiverse country with more than 180 bat species. However, bat conservation in Brazil is limited by knowledge gaps concerning the ecology and distribution of many species. This is especially severe for aerial insectivores, comprising eight of the nine families present in the country. Reliable data on echolocation calls is thus key to gather information on the occurrence, activity patterns, habitat preferences and, consequently, on the conservation status of those species. We integrated information on echolocation calls of aerial insectivores occurring in Brazil from the literature and our own data. Then we identified regional changes in species acoustic profiles, uncovered gaps of knowledge, both in terms of species and regions sampled, and pointed out which species are acoustically recognisable in a reliable way. From the 93 aerial insectivores we considered to occur in Brazil, 65 have been acoustically described. However, for at least 26 species there is no information on their echolocation calls, nor sound files available to allow their identification. We found regional acoustic variability in at least 10 bat species, which may reflect previous changes in other aspects of the phenotype and local adaptations, making them priority candidates for investigating the actual magnitude of such variation, morphological variations among populations, or the existence of cryptic species complexes. We believe large-scale and long-term acoustic monitoring is fundamental to elucidate how Brazilian bats respond to the severe human-induced landscape modifications in this megadiverse country and their possible associations with climatic changes.

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Detecting seasonal changes in micro-bat species richness in a South African National Park using acoustic receivers

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Insectivorous or micro-bats are a notoriously difficult group of mammals to survey because they are small, nocturnal, fly and roost in hard to reach places during the day. However, micro-bats should not be neglected from biodiversity assessments because they play pivotal roles in pest regulation and as biological indicators. We used acoustic receivers (n = 20 trap nights) to sample micro-bat species richness at three sites within the Mapungubwe National Park, South Africa during the austral winter and summer of 2013. Twenty micro-bat species from six families were recorded, with the plain-faced/clutter-edge foraging bats (Miniopteridae and Vespertilionidae) and free-tailed (Molossidae) or open-air foraging bats dominating. Bat activity was significantly higher in summer compared to winter and this is likely linked to higher prey availability and reduced thermoregulatory costs at this time. Our results represent the first comprehensive assessment of micro-bat species richness in the Mapungubwe National Park and our data compare favourably with historical records for the region. In addition, we provide evidence for the presence of at least one undescribed species. We advocate the use of acoustic receivers for future micro-bat surveys as long as comprehensive reference call library data are available.

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Habitat islands in the sky: Bat use of green roofs in a tropical city

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Green roofs, which are building rooftops with a growing substrate and vegetation, have great potential for urban biodiversity conservation, apart from providing other ecosystem services such as reduction in storm-water runoff. We investigated the habitat value of intensive green roofs for bats in highly urbanised Singapore using an acoustic approach. Bat activity (as measured by bat passes) was monitored using stationary bat detectors for seven nights each over 24 green roofs, which were stratified into 'low' (≤ 24 m) and 'high' roofs (> 24 m). Roof characteristics, management regimes and surrounding land cover metrics were investigated as possible predictors of bat activity using generalised linear mixed models (GLMMs). Four bat species (*Scotophilus kuhlii*, *Saccolaimus saccolaimus*, *Taphozous melanopogon* and *Myotis muricola*) were recorded. The most common species was *S. kuhlii*, which accounted for 80.3% of all bat passes, and the mean number of bat passes recorded per night was 30.6, pooled across all four species. Planted roof area was not a predictor of bat activity but the age and height of roofs had a strong negative influence. Bats responded positively to structural features of the roof vegetation. Green roof maintenance operations such as pruning and pesticide application had positive and negative effects respectively on bat activity. Finally, at a landscape scale, there was some evidence that the lack of vegetation in the immediate area of the roof (125 m buffer) negatively affected bat activity. Some recommendations are made to improve green roofs as habitats for tropical bats.

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Flying-foxes in the warming Anthropocene

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Among the greatest challenges that Australian flying-foxes (*Pteropus* spp.) face in the warming Anthropocene are shifts in the intensity and frequency of extreme heat events. Drawing from a suite of behavioural, physiological, demographic, and weather data, we show that such events have dramatic effects on these species, with temperatures exceeding 42°C causing species-, sex- and age class-specific mass mortality at landscape scales. We illustrate this using our data from recent summer heat events, during which more than 60,000 flying-foxes died. In addition, we demonstrate that extreme heat events are already frequent sources of extrinsic mortality for flying-foxes, which is of increasing concern given that temperature extremes are set to escalate further this century. To help land managers, wildlife carers, and other stakeholders respond effectively to these events, we have developed an online flying-fox heat stress forecaster (bit.ly/FF-heat-stress-forecaster). This forecaster makes explicit, up to 72 hours in advance, where and when flying-foxes are most likely to be exposed to heat stress, and thus enables efficient allocation of wildlife management resources towards colonies that are most at risk. Furthermore, our forecaster includes a data portal where citizen scientists can provide urgently needed data about these events. Flying-fox die-offs are particularly conspicuous due to the colonial nature of the species, and it is likely that heat events have similar impacts in wildlife with more solitary and cryptic lifestyles. Thus, flying-foxes provide a rare and valuable opportunity to understand and manage the impacts of extreme heat events on natural systems.

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Monitoring postfire survivorship and recolonisation of quokkas (*Setonix brachyurus*) in southwest Australian forests

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The effect of large scale and homogenising wildfires on threatened species is of increasing concern in southern Australia, given predictions for an increase in the frequency and severity of such fires. We assessed the effect of a fire, 98,000ha in size, on occupancy patterns for the quokka (*Setonix brachyurus*), a threatened macropod endemic to south-western Australia. The fire resulted in the loss of 77 % of known sub-populations. All post-fire activity by quokka was restricted to the edge of the fire or to a small number of isolated internal sites. Internal refuge sites were smaller than 0.5 ha, were surrounded by intensely burnt vegetation, and contained low densities of individuals. Occupancy of the post-fire environment was strongly influenced by retained vegetation structure (3-7 layers), presence of sedges in the understorey, low areas of pig damage (< 10 m^2) and proximity to unburnt canopy (0-189 m). A large proportion of the fire-affected area was unoccupied, with large distances (up to 36 km) separating occupied areas. Cumulative threats that reduce survivorship or increase the distance between suitable habitat patches could reduce the ability of the species to recolonise core areas of the fire. This could in turn affect metapopulation function in this area. To avoid this, it is important that internal refuge patches are protected, habitat connectivity is re-established, and cumulative threats such as prescribed burning, introduced predators and feral pigs are managed.

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Monitoring population size and structure by individual recognition in brush-tailed rock wallabies (*Petrogale penicillata*)

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Population size is one of the fundamental measures in conservation biology and many different methods have been devised to measure it. For rock wallabies, these encompass scat counts, trapping, observations and scat DNA analysis. As colonies are usually small, the precision of the chosen method is of utmost importance. In this study we attempted individual identification from high quality photographs relying on fur colouration and facial scarring. Six colonies of brush-tailed rock wallabies were sampled yearly in northern New South Wales from 2010 to 2016. Only individuals that had permanently left the pouch were counted. Colony size ranged from 1 to 21 individuals, but for any given colony size remained relative stable over the years. Overall, 116 wallabies were identified and the sex ratio appeared to be close to parity, with a quarter of all individuals being subadults. Although rock wallabies generally exhibit high site fidelity, about half of all individuals were photographed during only one survey and only five were known to be alive during all seven years, implying that few individuals realize their greater than ten year lifespan. There was a trend for females to persist longer in colonies than males. Overall, the high turnover in these colonies indicates dispersal, particularly of young animals, but probably also predation. The poor body condition of some wallabies further suggests that parasites or disease are prevalent. Nevertheless, currently recruitment appears to be sufficient to compensate for these losses as we observed little fluctuations in population size.

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Investigating Tasmanian devil behaviour using collar-mounted Crittercam™ video cameras

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Reintroduction of captive-bred animals to the wild is an important component of threatened species conservation. For the threatened Tasmanian devil *(Sarcophilus harrisii)*, reintroductions from the captive "insurance" population may be crucial to the species' survival. The success of such reintroductions may depend on zoos' ability to maintain wild behaviours in captive devils across multiple generations in captivity. But, zookeepers cannot maintain behaviours of which they are not aware. It is thus crucial to document as much wild devil behaviour as possible while we still can. The animal-borne Crittercam™ video camera technology developed by National Geographic can provide a valuable tool in studying devil behaviour.

We deployed Crittercams on Tasmanian devils in two pilot studies, one with six captive adults at Healesville Sanctuary, Victoria, and one with seven wild adults in north-western Tasmania. Devils were fitted with collar-mounted, motion-activated Crittercams with automatic drop-off capability. The technology was highly effective, capturing clear, easy-to-interpret footage, and the collars and cameras were well tolerated by both captive and wild devils. The pilot studies identified some potential refinements of the deployment protocol that should increase the amount of footage recorded. The video footage revealed several unexpected behaviours, including some never before observed in the species. Additional Crittercam deployments will occur prior to the conference, adding further behavioural observations to our findings.

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Cameras, collars and carnivores: Using contemporary techniques to inform the conservation of an endangered Australian predator, the spotted-tailed quoll (*Dasyurus maculatus*).

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Until relatively recently, quolls were part of a marsupial carnivore assemblage that covered the Australian continent. Following the extinctions of *Thylacinus* and *Sarcophilus*, the spotted-tailed quoll (*Dasyurus maculatus*) became, and still is today, the largest marsupial carnivore extant on the Australian mainland. Since European settlement, however, anthropogenic habitat modification and competition from introduced predators contributed to significant declines in the species' abundance and distribution, and it is now listed as Endangered. Effective conservation and recovery of quolls will be partly dependent upon sound monitoring, which is in turn reliant on knowledge of quoll ecology. Previously, monitoring protocols had barely developed beyond cage trapping or latrine surveys and knowledge of the species' spatial ecology was coarse, having been derived mostly from VHF telemetry with camera trapping and GPS telemetry, during a study in the northern tablelands of New South Wales. Between 2013 and 2016, we developed and field-tested camera trap protocols for detecting and individually identifying spotted-tailed quolls. Ultimately, 95% of detected quolls could be identified to individual level. During the same period, we tracked male and female spotted-tailed quolls with GPS-VHF collars. In addition to describing the ranges and activities of quolls, we unexpectedly learned that many individuals, including females with denned litters, utilised cleared agricultural lands outside the conservation areas intended to protect them. The findings of this research are now being used to inform state-wide recovery actions for this iconic predator.

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Elevational patterns of co-existence and replacement in medium-large species of terrestrial mammals on Sumaco Volcano, Ecuador

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Assessing the occurrence, geographic distribution, and spatial and temporal activity patterns of species is essential for a full understanding of their ecology, biogeography and interactions with sympatric species. Camera trapping techniques are useful in conducting such studies on mammals, as they are non-invasive and minimize disturbance of natural activity patterns. We report findings of camera trap studies of medium-large mammals on Sumaco Volcano, Ecuador, between 2010 and 2016. Sumaco Volcano lies in the heart of the Tropical Andes biodiversity hotspot and is noteworthy for having one of the most extensive, intact elevational habitat gradients in the Neotropics, ranging from the lowland rainforests of the western Amazon basin at 300 m to páramo vegetation near the volcano's 3,800 m peak. We characterize the medium-large mammal fauna at five elevational zones on Sumaco Volcano: one located in the lower montane rainforest at approximately 1350 m, and four located in the cloud forest at approximately 1750, 2200, 2500, and 2900 m. We determined species diversity for each zone and species turnover (beta diversity) between zones. Our major conclusions are 1) that species turnover between the 1750 m and 2200 m sites was the most pronounced; however, we also found substantial turnover among upper elevation sites, suggesting that elevational differences in mammalian communities within Neotropical upper montane rainforest biomes also can be surprisingly high; and 2) that typical Amazonian lowland species occurred at all elevations (including 2900 m, far above the rainforest-cloud forest ecotone), but that no "Andean" species were found below this ecotone.

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Optimising the detection and enumeration of northern quoll (*Dasyurus hallucatus*) populations using trail cameras

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Trail cameras have rightly replaced cage traps as the instrument of choice in many ecological studies. The quolls (*Dasyurus* spp.) are excellent candidates for trail camera detection studies given their opportunistic dietary behaviour and their uniquely marked coats; however there has been limited benchmarking of trail camera performance against live-trapping approaches, nor research into deployment methods to optimise quoll detection. We therefore compared the relative ability of trail cameras compared to cage traps, and of various trail camera orientations, spacings and duration to; (i) detect northern quolls at a site, (ii) detect the largest number of northern quolls at a site and, (iii) collect data suitable for Mark-Recapture and SECR analyses. We show that on our 1 km long transects in north-east Queensland, trail cameras perform at least as well as cage traps in all parameters measured. We further demonstrate that camera orientation on the horizontal plane does not influence the probability of detecting a quoll and that new quoll individuals continue to accumulate steadily up to 12-14 days. Camera trap spacing has a strong influence on the number of quolls detected over a 1 km transect, with 100 m -apart spacings resulting in twice as many individuals detected as 250 m spacings. Even in these high-density quoll populations, linear transects don't generate sufficient recaptures to facilitate mark-recapture or SECR modelling and a grid-based approach is recommended for studies where population size estimation is an objective.

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Preliminary findings of behavioral patterns under captivity conditions in Chinkara (*Gazella bennettii*) with prospects for future conservation strategies

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The present study was conducted from April 2013 to March 2014 to observe the behavioral parameters of Chinkara (*Gazella bennettii*) under captive conditions by comparing the captive-born and wild-caught animals for conservation strategies. Understanding the behavioral conformations plays a significant role for captive management. Due to human population increase and mechanized hunting, the captive breeding seems to be the best way for sport hunting, bush meat, leather and horns for traditional medicinal usage. Primarily, captive management has been, used on a trial and error basis due to deficiency of ethology of this least concerned species. Behavior of 20 wild-caught (WC) and 10 captive-bred (CB) adult Chinkara was observed at captive breeding facilities for ungulates at Ravi Campus, University of Veterinary and Animal Sciences, in the Kasur district which is situated on southeast side of Lahore. The average annual rainfall is about 650 mm, with frequent rain during monsoons. A focal sample was used to observe the various (12) behavioral patterns for CB & WC chinkara. A similarity was observed in behavioral parameters in WC & CB animals, but when the differences were considered WC male deer showed a significantly higher degree of agonistic interaction as compared to the CB male chinkara. These findings suggest that there is no immediate impact of captivity on behavior of chinkara despite 10 generations in captivity. It is suggested that the Chinkara is not suitable for domestication or for successful deer farming, and further study is recommended for the ethology of chinkara.

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Are aggressive calls the honest signals of body size and quality in female Asian particoloured bats (*Vespertilio sinensis*)?

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Animals need information about the callers to make decisions that affect survival and reproduction. However, there is unreliable information in some communications. Generally, the honesty signal is costly to produce or is controlled by physical or physiological constraints that cannot be faked. Aggressive calls meet the above two points at the same time. In the bat *Vespertilio sinensis*, aggressive displays and vocalizations are produced when an intruder bat crawls over native bats for a roost position. Thus, we examined whether the aggressive calls of female Asian particolored bats encode reliable information about the body size and quality of callers. For syllables, different syllable parameters were associated with different body size and quality indexes in different syllable types. Frequency-related parameters were negatively correlated with the bats' body mass and immune response, and other syllable parameters were positively correlated with the bats' body mass and immune response. Forearm length, body length and bite force were all positively correlated with syllable parameters. For calls, heavier bats produced shorter mean inter-syllable silence and that shorter mean inter-syllable silence predicted better immune response. For repertoire, a negative relationship between body length and vocal complexity and a positive relationship between immune response and vocal complexity were observed. These data demonstrate that female Asian particolored bat aggressive calls are honest signals of body size and quality of callers.

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Alloparental care and infant carrying in bottlenose dolphins

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Alloparental care, where an individual provides care to a nonfilial offspring, has been reported in a number of mammalian species. Such care ranges from short-term such as holding, defending or escorting, to long-term care such as adoption. Such behaviours are energetically costly, and their causes and functions remain unclear. To assess or ascertain the prevalence of parental care in cetaceans is difficult, yet descriptive accounts in several species have occurred (e.g. bottlenose dolphins, *Tursiops truncatus*; sperm whales, *Physeter microcephalus*; spinner dolphins, *Stenella longirostris*; killer whales, *Orcinus orca*; harbor porpoise, *Phocoena phocoena*; pilot whales, *Globicephala melas*). However, most of these studies defined parental care whenever an infant associated with a conspecific away from its mother or with more than one conspecific. None have specifically looked at the benefits to the offspring or the carer. Here, we analyze data on wild bottlenose dolphins from Shark Bay, Western Australia from 1985 to 2016. We specifically look at the most expensive form of parental care after lactation, infant carrying and discuss the benefits to young and the "learning to parent" hypothesis.

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Molecular genetics used for analyzing Eurasian beaver dispersal - 20 years after reintroduction in Romania

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The Eurasian beaver disappeared from Romania in the beginning of the 18th century; recently (1998-2003), 190 individuals from Bavaria (Germany) were reintroduced into 3 main river basins. Nowadays, more than 2500 individuals are occupying habitats across the country on tributaries, with beaver dispersal being realized first over short distances. After the reintroduction, methods used for monitoring species dispersal were presence indices (tree cut, footprint, lodge, dam) and direct observations. Starting in 2015, genetic analyses were used for determining species diversity, dispersal directions and characteristics at the national level. Thus, 62 individuals (genotyped for 11 SSR markers) were captured and biological samples were collected.

Genetic diversity of the species is similar with that in other studies; statistical tests have indicated that beaver individuals are isolated by distance in 5 distance classes (0-50 km, 51-165 km, 166-300 km, 301-360 km and 361-480 km), which can result from the gradual expansion of the reintroduced individuals. Approximately 17 percent of the genetic differences between individuals can be explained by the geographic separation, results confirmed by the appartenance tests. Spatial analysis showed significant and positive autocorrelation within the first 50 km, indicating the presence of related individuals. We identified two directions of the gene flow (west and east); east direction expansion seems to be facilitated by the good quality of the habitats, which are situated along long distances. These results offer a good resolution in determining species evolution, offering an excellent tool for permanent monitoring, determining if the population requires new genetic material from different areas.

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Tracking Cats, Dingoes and Bilbies: Results of a collaborative two-way science project with Wiluna Martu Women Rangers

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Fauna surveys using a modified form of the standardised Moseby, Nano & Southgate 2 ha track plot method were conducted by Martu Women Rangers at twelve sites each at Jundee Pastoral Lease and at Matuwa (formerly Lorna Glen Pastoral Lease, now part of the Matuwa Kurrara Kurrara IPA) within the Wiluna Native Title area, Western Australia. Plot locations were based on sites used in previous research that were culturally acceptable to the Martu women. Three surveys were completed at each site approximately one month apart between late August and early November in both 2015 and 2016. Each survey involved 4 rangers walking around the 2 ha plot for about 20 minutes recording all observed tracks, scats, burrows and diggings. The original aim of the surveys was to compare the presence of cats, dogs/dingoes and threatened species (particularly bilbies, *Macrotis lagotis*) at Jundee with their occurrence at Matuwa, where annual aerial cat baiting and targeted threatened species management (eg translocations) are being carried out. Initial data recorded included presence/absence & estimated freshness of sign for each species, landform, vegetation and fire age. As the work progressed the Martu women's tracking skills and suggestions for additional information to record resulted in extension of data collection to include, where possible, species abundance estimates, number and age of individual cats/dingoes present and behavioural observations (eg hunting). The results of this work demonstrate the potential to research detailed questions about predator interactions and threatened species management using collaborative two-way science methods.

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Bats: A macro-evolutionary exception

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Phylogenies are primary sources for macroevolutionary research. Here I investigate how the two principal aspects of phylogenies, character evolution and taxon relationships, contribute to reveal exceptional evolutionary patterns and processes in one outstanding mammalian lineage, Chiroptera. Bats are the only group of mammals capable of powered flight. Understanding the origin of flight ultimately explains bats as a group, their singularities, and much of their historical and current diversity. Flight enabled bats to reach all continents they inhabit today by the early Eocene. Systematic studies have placed bats among laurasiatherian mammals, with a divergence time estimated near the K-Pg boundary. First (c. 52-my-old) complete fossils exhibit a mosaic of character states but their morphology indicates that these species were accomplished volant mammals. Bats accumulate a large number of un-reversed synapomorphies, including many of the flight apparatus. Detailed morphological and developmental comparisons allow us to identify the homology of all of the aerofoil components. These homologies and their relative ontogenetic timing can help resolve the origin of bat flight. A recent, large-scale supermatrix phylogeny corroborated most of current bat clades, from species groups to superfamilies, albeit some new groups imply considerable biogeographic rethinking of the bat history. Size, a key functional character for volant animals, evolved in that phylogeny in ways that challenge everything we know about evolution of this character in mammals as a group. Neither neutral nor adaptive mammalian models satisfactorily explain the reconstructed pattern of initial nanism, backbone stasis, low-scale size evolution inside subclades and explosive size evolution in a few groups (chiefly pteropodid bats). As proposed two decades ago, various constraints from echolocation parameters emerge as strong candidates to account for body size evolution in bats, from a scaling perspective. Ecological release from echolocation loss may explain megabat size evolution. Size may start acting as a strong evolutionary constraint within a few million years, when the largest megabats of the Recent eventually approach the theoretical maximum size in bats. Thus, a model of nested constraints from echolocation and flight, encompassing the past and the future, is proposed to explain bat evolution.

From this point of view, bat evolution is unique among mammals. Beyond exclusively macro-evolutionary patterns, recent analyses of morphological evolution reject drift and compellingly support natural selection acting on correlated cranial characters in all nodes of the phyllostomid phylogeny. Thus, bat phylogenies also help bridge the controversial micro-macro-evolutionary gap.

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Working for wildlife: The role of zoos in conservation action

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Given the dire situation facing wildlife globally, leadership by wildlife conservationists and conservation organisations is becoming increasingly important. In this rapidly moving world, how do we break through the increasing noise to effectively make a difference for wildlife and wild places? What are the key messages, actions and how can we best operate? In leading zoos and aquariums around the world, this has been a core issue and over recent years there has been a substantive and conscious re-positioning of leading zoological institutions as conservation organisations. This has involved the adoption of new strategic directions and an integrated conservation model, the One Plan Approach to conservation action. This presentation will outline the species conservation role of zoos; conservation leadership; the One Plan Approach; the two new global zoo strategies *Committing to Conservation* and *Caring for Wildlife*; and how we are bridging the gap between in-situ and ex-situ conservation.

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DNA detection and population genetics of the red fox in Australia

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DNA analyses of wildlife can provide valuable diagnostic tools and have direct application to the study of ecological and other environmental phenomena. Yet, well documented and tested markers exist for only a handful of species. One of the reasons for this is that good sequence information and robust sampling at the appropriate level of resolution is lacking for many taxa. We report on the development of DNA markers that enable us to detect red foxes from trace samples such as scats (faeces) in Australia and then use genotype-by-sequencing and a citizen science based collection of tissue samples to conduct a continental analysis that recapitulates the invasion sequence of red foxes into Australia. We demonstrate that technologies have the potential to substantially enrich our knowledge of mammalian ecology but that the development of comprehensive and good quality tissue collections matched to accurate locational information, better marker resolution, regular repeat collections of DNA samples, high quality sequences in online databases, and minimisation of laboratory errors are the key to maximising that potential.

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Molecular phylogeography of mustelid species endemic to the Japanese islands and closely related species

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On the Japanese islands, there are several endemic species of mustelids. The biogeographical feature common to the endemic species is their distribution on the three main islands (Honshu, Shikoku and Kyushu, not Hokkaido) among the Japanese islands. One of the endemic mustelids is the Japanese weasel (*Mustela itatsi*), whereas the sister species, the Siberian weasel (*Mustela sibirica*), is distributed widely on the Eurasian Continent and some continental islands. To further understand the biogeographical history, we recently analysed the complete mitochondrial genome for both species and calculated the divergence times between the two species and within each species (Shalabi et al. 2017). The results clearly show the Japanese weasel was separated into two allopatric lineages, the northern and southern groups. The phylogeographical features reflect the palaeoenvironmental changes of the Japanese islands after the last glacial period. The southern group could have remained in place, whereas the northern lineage expanded stepwise from southwestern to northern Honshu during the Holocene. On the other hand, the Siberian weasel consisted of the two lineages, the Far Eastern and Inner continental groups. Interestingly, the Tsushima Island population of *M. sibirica* is likely a relict from the continental Russian lineage. In addition, the phylogeography on the Japanese badger, *Meles anakuma*, as another Japan-endemic mustelid is discussed using molecular data of mitochondrial DNA and Y-chromosomal DNA, compared with the continental related species. This badger is also differentiated from the other three *Meles* species of the continent.

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Introduction to the systematics of Peruvian forms of *Caenolestes caniventer* (Paucituberculata: Caenolestidae)

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Caenolestes caniventer is a shrew opossum widely distributed in the mountain forests of southern Ecuador and northern Peru, where the Huancabamba depression (HD) was considered as its southern limit of distribution. Currently, this species is considered monotypic, however *C. sangay* from the eastern of Ecuador was recently differentiated from *C. caniventer* by molecular analysis prompting us to re-examine Peruvian populations. We performed a morphological and morphometric study, and a phylogenetic analysis of mitochondrial DNA sequences, for Peruvian populations. We found that populations known as *caniventer*, correspond to two different clades. The first includes to *C. sangay* which is sister group to two hypothetical new taxa: *Caenolestes* sp. 1, from Cañaris (Lambayeque) and La Granja (Cajamarca), south of the HD; and *Caenolestes* sp. 2, from Río Majaz (Piura), north of the HD. These putative taxa are different from *C. sangay* with a genetic distance of 8.8-9.1% and 7.5% respectively. The second clade that apparently comprise the true *C. caniventer* includes the populations from Huamantanga and Las Ashitas (Cajamarca), and Alto Samaniego (Piura), and differs from the first by no less than 6%. A canonical component analysis with 58 specimens, assigned to *C. caniventer* from Peru, recognised these groups. Therefore, morphological, morphometric and molecular analysis suggest that *Caenolestes* sp. 1 and sp. 2 are likely new species related to *C. sangay*. The biogeography of *C. caniventer* complex does not fit with the hypothesis of HD as a barrier.

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Tempo and mode of the diversification of extant didelphids (Didelphimorphia)

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The family Didelphidae represents the most diverse group of New World living marsupials. Most didelphids are endemic to South America and are distributed in tropical areas, although some species reach open and forested areas at high latitudes of South and North America. Several studies have focused on the shape and timing of the extant didelphid radiation, but much less is known about the rates and drivers of their diversification. We structured this talk into two parts. First, we review previous findings characterising the extent and rates of the extant didelphid radiation. Second, we present novel results conducted on the basis of analyses of a matrix with a broad taxonomic (117 didelphid species) and character (10 genes) sampling. We present age estimates for didelphid clades (e.g., ca. 14 MYA for the most recent common ancestor of the family). Our analyses of diversification rates found a single macroevolutionary dynamic across the radiation of the family and evidence of a slight increase of speciation towards the present. Financial support: FONDECYT 1141055, FONDECYT-Postdoctorado 3150604.

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You can lead a horse to water... providing effective reintroduction support is difficult, but does it matter?

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Reintroductions are an increasingly common conservation tool used to reverse the decline of threatened species, yet globally reintroduction success remains low. Release methods have the potential to influence the outcome of a reintroduction. We used a brushtail possum (*Trichosurus vulpecula*) reintroduction to test the use and effect of supportive release measures, testing delayed, immediate and nest-box release treatments. Intensive monitoring of 48 radio-collared possums showed release treatment had no effect on dispersal distance, weight change, reproduction or survival; however, possums were generally reluctant to utilise supplementary food or shelter. Dispersal rates varied by treatment, with immediate release possums settling fastest. Equal proportions of possums from each treatment lost weight and used unsafe shelter sites immediately after release, but eventually gained weight and chose safer shelter. Unsafe behaviour combined with weight loss suggests that supplementary food and shelter would be beneficial, yet the efficacy of both was low, presenting a reintroduction conundrum not considered in previous research. In environments with low predation risk and where sufficient shelter is available, weight loss and risky behaviour may not affect long-term reintroduction success and immediate releases are recommended as the most effective reintroduction technique. In contrast, in environments where post-release predation risk is high, the inability of possums to quickly adapt to suitable new food or shelter resources could lead to high post-release mortality unless release methods can be specifically tailored to overcome poor adaptability. An assessment of a species adaptability to new conditions should be used to inform release methods for future reintroductions.

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Translocation success for dibblers (*Parantechinus apicalis*) in Western Australia is explained by invertebrate abundance.

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The dibbler is a 40-120g Australian dasyurid marsupial with a high dietary dependence on surface-active invertebrates. Its distribution declined greatly in the last 150 years largely due to predation by introduced foxes and cats. Although some small populations remain on offshore islands, the stronghold of the species is the 2,972 km² Fitzgerald River National Park (FRNP) on the south coast of Western Australia. Since 2000, three attempts have been made using captive bred animals of FRNP stock to establish new mainland populations in sites where vegetation structure and floristics resemble those at dibbler sites in FRNP and where cats and foxes are controlled. Only one has been successful. This study examined litter invertebrate abundance at all sites as a possible determining factor in translocation success. To compare invertebrate abundance between the four sites, samples of leaf litter on the ground surface at 10 randomly selected points at each dibbler site were collected. All surface litter within a 0.25 m^2 plot was collected and transported directly to the laboratory, where invertebrates were extracted using Berlese-Tullgren funnels. Invertebrates were sorted to order and individuals over 2 mm in body length were counted. The abundance of invertebrates over 2 mm in length increased progressively from Stirling Range (failed site) to Waychinicup (failed) to Peniup (successful) to FRNP (source). Abundance at each of the failed translocation sites was significantly different to the source site. It is recommended that measurement of invertebrate abundance becomes an essential element of site assessment for future dibbler translocations.

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Recent trends in the global extinction risk of mammals

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The 2017 IUCN Red List of Threatened Species includes ca. 6000 species of mammals, approximately 500 species more than in the last complete mammal assessment published in 2008. This dataset provided the basis for the calculation of the Red List Index (RLI), which is an indicator of the aggregated risk of extinction of a group of species. The 2017 RLI was compared to the RLI in 1996 and 2008, the two years for which complete mammal assessments are available, providing a 21-year trend in extinction risk for the world's mammals. For large mammals (carnivores and ungulates), the RLI backcasted to 1975 allowed the extension of the comparison across a 42-year period. The RLI of all mammals, as well as that of large mammals, showed a steady decrease over time, with far more species moving towards extinction than species averting extinctions at any time-step considered. Several iconic species and subspecies, including the eastern gorilla, Bornean orangutan, plains zebra, and lowlands tree kangaroo are now at higher risk of extinction that nine years ago. Despite conservation efforts and some conservation success, increasing pressures on biodiversity continue to drive the decline of mammals globally.

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Intrinsic and extrinsic correlates of range reduction in mammals

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The global conservation status of all mammals has been evaluated for the first time in 2008, and in 2010 Hoffman et al. (2010) made a retrospective assessment related to the year 1996. A recent study by Di Marco et al. (2014) assigned species to a threat category in 1970, based on information in the published literature. Despite the great efforts made in understanding the situation of mammals in the recent past, most of the existing studies lack information on changes in the spatial distribution of the species. In this study, we aimed at filling this gap by collecting data on the distribution of mammals in the 1970s, when this information was available and reliable, and we then compared the past range of species to their current range. We identified the areas gained or lost by each selected mammal, and analysed the relationship between the loss or gain of part of the distributional range and a set of intrinsic traits and drivers of threat. For most of the species that experienced a range reduction, the increase in human population and pressure have been the major drivers of decline. This work will help to understand the success of past and current conservation actions on species and also the identification of sites potentially exposed to human influence in the near future.

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Strong sexual segregation amplifies road-kill risk in urban eastern grey kangaroos

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The urban environment is hostile to many mammalian species, yet some are recognised as ‘urban adaptors’. Research tends to focus on these species and their adaptations to urban habitats, which can arise through behavioural plasticity or microevolutionary change. Far less attention has been given to traits showing inertia at behavioural or evolutionary scales. We examined one such trait, sexual segregation, and evaluated its impact on sex-specific survival of eastern grey kangaroos (*Macropus giganteus*) in the seaside town of Anglesea, southern Australia. We captured and marked over 500 individual kangaroos at a golf course on the edge of town, where the population was concentrated. This population had the three precursors of sexual segregation: sexual dimorphism, seasonal breeding and polygynous mating. Median body mass of adult females was 27 kg (range 17–34 kg); median male mass was 46 kg (range 22–73 kg). Mating was concentrated in the austral spring and summer, followed by a birth peak in December, with 80% of births from November to February. Each year, at least 43% of adult males sired 1.7 offspring on average (range 1–9). Sexual segregation was strong in the non-mating season: most adult females remained on the golf course and properties nearby, whereas most adult males left the course and ranged throughout the town and adjacent native bushland in autumn and winter. Males were thus at greater risk of road-kill, which caused 50% of deaths versus 20% of females. Given the intensity of selection on this behavioural trait, we predict that sexual segregation will diminish in this urban kangaroo population.

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Human-wildlife conflict: Flying-foxes in the city also provide landscape scale ecosystem services

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The Royal Botanic Garden, Sydney is a green oasis positioned on Sydney Harbour surrounded by city skyscrapers. As an urban island the garden provides resources (habitat, water and food) to a range of fauna, including species listed as vulnerable to extinction (e.g. powerful owl, *Ninox strenua*; eastern bentwing-bat, *Miniopterus schreibersii oceanensis*). By far the most well-known species associated with the garden is the grey-headed flying-fox (*Pteropus poliocephalus*), a species also listed as vulnerable. The flying-foxes currently visit the garden at night to forage, they formerly roosted in the garden but this behaviour resulted in the death of over 60 trees and palms due to defoliation and a colony dispersal was implemented under approval from the Australian Government. However, flying-foxes are essential pollinators of Australian forest species (mainly Eucalypts). For example, we fitted 50 male and 50 female flying-foxes with satellite transmitters, these animals visited over 200 colonies from Geelong in Victoria to Gladstone in Queensland over a 12-month period. This study shows that grey-headed flying-fox colonies are not static entities; rather, they are hubs in an extensive network spanning much of Australia's east coast.

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Testing the response of the threatened New Holland mouse to management burns

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Almost half of Australia’s 30 recent mammal extinctions have occurred in one of our most poorly understood groups – rodents. Of 64 native species of Australian rats and mice, 14 are already extinct and another 24 are of conservation concern. Among other factors, inappropriate fire regimes may contribute to the decline of many Australian rodent species. Over the past 40 years, the threatened New Holland Mouse (*Pseudomys novaehollandiae*) has been extirpated from most of its known range in Victoria. Of the ten locations where *P. novaehollandiae* were once found in the State, only three are known to still support populations. The areas where *P. novaehollandiae* persists are highly fire prone and subject to regular ‘management’ burns. Ideally, these fires would maintain vegetation in a way that is suitable for *P. novaehollandiae*; however, if fires are too large, too frequent, or too infrequent they may instead eliminate the species from an area. Using radio tracking to map burrow locations and home range size before and after management burns, I am testing the influence of fire on the short-term survival and habitat use of NHMs. Additionally, I am using a long-term Victorian dataset to test whether putative *P. novaehollandiae* associations with early post-fire successional classes are upheld. With this information, I am developing recommendations for burning, including suitable fire scales, to promote conservation of the species in its remaining Victorian strongholds.

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Effects of large spatiotemporal heterogeneity of environmental conditions on conservation of wild ungulates in Mongolia

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Southern Mongolia is an important area for wildlife conservation, because several long-distance migratory ungulate species inhabit it, but mining development and new railroad construction are progressing. To assess habitat fragmentation by new railroad construction on wild ungulates, we evaluated habitat suitability and important environmental factors for Mongolian gazelles (*Procapra gutturosa*) in summer and winter by using tracking data for 8 gazelles and environmental variables from September 2013 to September 2014 and species distribution models. We made habitat suitability maps for Mongolian gazelles in a wider range with similar environmental conditions from 2007 to 2014 by applying the best models to the past environmental data of vegetation index (NDVI) and snow cover. Spatial distribution of habitat suitability in winter was largely changed between the years due to the large interannual fluctuation of spatial distribution of snow-cover duration. Interannual change of spatial distribution of habitat suitability in summer was relatively slight. In areas potentially fragmented by new railroad construction, areas with >0.5 habitat suitability index was only 0.1% in the severest winter (2009-10) and decreased 99% from the former winter (2008-09). The drastic reduction of suitable areas within the range in severe winters suggests a serious threat of habitat fragmentation for long-distance migratory ungulates and the necessity for conservation measures to allow access to wide ranges across new railroads for wild ungulates.

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Using the past to explore the impact of extreme and abrupt climate changes on biodiversity and ecosystem services

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Projected changes in climate and variability are considered to be significant stressors on biodiversity (from the individual organism to biome level) and ecosystem services, both today and in the future, rivalling human land use. Determining the impact of future climate on biodiversity and ecosystem services remains extremely challenging given the uncertainty around the magnitude and rate of projected changes of a range of different climate parameters, the creation of 'novel' climates, and the diverse range of species responses to different climate variables, including their vulnerability, sensitivity and adaptive capacity. A better understanding of the complex interactions is critical if we are to adopt proactive conservation planning measures to future proof against projected climate changes. Fortunately, in these regards, the recent geological record provides potential analogues for different aspects of future climate and environmental change. During the late Pleistocene alone (the last 130,000 years), pronounced warming, megadroughts and sustained sea level rise occurred across a range of timescales, from sub-decadal to millennial in duration. Here we will explore key periods in the past during which these climatic events occurred in Australia and globally, and explore the potential impacts (and thresholds) of ecological systems to extreme and abrupt change.

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Climatic and vegetational drivers of mammoth range reduction in the approach to extinction

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Mapping a global database of some 2,000 audited radiocarbon dates indicates major shifts in mammoth range after 40 ka, corresponding to climatic and vegetational events and suggesting these as the main driving force. The species vacated much of Europe for the interval 21.5-19.5 ka, corresponding to the maximum extent of the European ice sheet. The range then re-expanded and remained widespread into the Bølling warming (14.6-13.9 ka). With the afforestation of the Allerød (13.9-12.8 ka), however, Europe and western Siberia were completely vacated by mammoths; this suggests that it was the vegetational change triggered by, but lagging behind, global warming that reduced mammoth range. The Younger Dryas (GS-1, 12.8-11.7 ka) saw the extirpation of mammoths in North America, and Eurasian populations restricted to northernmost Siberia, with a short-lived re-invasion of north-east Europe. By 11 ka (within the earliest Holocene), the mammoth was extinct in mainland Eurasia. Terminal island populations in the Beringian region expired on St Paul (Pribilof Islands) around 5.6 ka and Wrangel Island around 4 ka. Although distributional gaps are hard to deduce from fossil data, the terminal distribution of *M. primigenius* is consistent with fragmentation as well as severe range reduction prior to extinction. Such reduction to small, refugial populations led to their sequential extirpation by climatic, stochastic, or potentially anthropogenic effects.

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Multifaceted mammal management: Dealing with multiple threats in novel communities

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Mammals are arguably the most successful group of vertebrates on Earth, ranging from the depths of the oceans, to the morth and south poles, and the skies above. Despite their success, modern stressors have radically changed mammal communities around the world—while some species have greatly expanded their ranges, others have disappeared among a raft of extinctions. In a world that is experiencing unprecedented environmental change, including the confluence of multiple threats, such as habitat loss and modification, climate change, and biological invasion, integrated and multifaceted approaches are urgently required for ecologically and cost effective management of novel mammal communities. Using case examples from around the world, here we review innovative and emerging field-based and modelling approaches and tools, and ecological and evolutionary perspectives, for meeting this challenge.

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An eco-evolutionary approach to restoring native wildlife in invaded ecosystems

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New approaches are needed to tackle the global loss of biodiversity from novel impacts, such as invasive species and emerging infectious diseases (EIDs). This requires innovative thinking and integrated approaches that harness the power of natural ecological interactions and conserve the natural evolutionary processes inherent within complex ecological systems. Australian ecosystems are broadly dominated by invasive predators maintained at high density by the highly fecund invasive prey species with which they were co-introduced. Native mammals, which have lower fecundity, cannot withstand this amplified predation pressure. In addition, populations of Tasmania's apex mammalian predator, the devil, has been decimated by an EID, which will likely release feral cats from competition, with cascading loss of smaller biodiversity. Direct control of invasive predators and infectious diseases of wildlife frequently fail because it needs to be maintained at high intensity over large areas and in perpetuity. I will present a multifaceted approach to facilitating native species recovery in invaded landscapes. The ecological component involves manipulating 'leverage points' in food webs; these being nodes where a small intervention can trigger cascading changes of larger effect elsewhere. Leverage points include: restoring native apex and meso-predators to outcompete cats, controlling rabbits to reduce cats, and restoring habitat structure to provide refuge from predators. The evolutionary approach focuses on facilitating host adaptation to novel challenges, in this case rapid evolution of the Tasmanian devil to facial tumour disease (DFTD). These approaches are multi-scaled and animal-centric, linking individual-level behavioural decisions with occupancy and community structure at larger scales.

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Impact of feeding behavior on the deformations of the macaque mandible

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Finite element models (FEM) of cranial design (structure-function relationships) have played an important role in attempts to reconstruct the ecological niches of fossil hominins, but the morphological and functional complexity of the cranium make it a challenging place to look for dietary signals. The lower structural and developmental complexity of the mandible in comparison with the cranium suggests that it should provide a clearer functional link to feeding behaviour and diet, yet attempts to link diet to mandible morphology have had mixed success. Here we used a validated FEM of a rhesus monkey (*Macaca mulatta*) mandible to assess the effects on mandibular strain regimes of chewing on food items with varied material properties and of biting at different points along the toothrow. Chewing on items with different material properties and using different bite points elicit variation in strain regimes around the symphysis where strain magnitudes are high, but strain magnitudes in the corpora vary little with food type and are of lower magnitude than the symphysis. The lack of distinctive strain regimes in the macaque corpus during chewing suggests that symphyseal morphology might be more closely related to the kinds of food being chewed than corpus morphology. This suggests that different parts of the primate mandible might reflect variation in different aspects of feeding behaviour and ecology.

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Factors affecting individual participation during intergroup interactions in mountain gorillas (*Gorilla beringei beringei*)

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In group-living species, encounters between groups can range from aggressive to affiliative and often involve multiple individuals exchanging behaviours with the opposing group. Although intergroup interactions are a collective action, individuals differ in their incentives to participate. Individuals must assess the potential payoffs of participation, which can be influenced by a combination of the value of the disputed resource, the individual's fighting ability, and the fighting ability of their opponent. We examined how these factors affect individual participation in intergroup interactions involving 22 social units comprised of 170 fully-habituated, free-living mountain gorillas at Volcanoes National Park, Rwanda. We used 14 years of observations of 538 naturally occurring intergroup interactions, which ranged from aggressive disputes to peaceful mingling between extra-group individuals. Females participated less frequently in aggressive group encounters than males, and there was no evidence that ecological conditions or individual characteristics created significant differences in participation levels during group encounters. Males were less likely to participate when there were a greater number of adult males within his group, suggesting that group encounters in mountain gorillas may be subjected to the collective action problem. Females demonstrated the greatest participation in peaceful interactions, especially when there were more participants in the opposing group, suggesting that females may benefit from social encounters with extra-group gorillas. In a group-living mammal where intergroup interactions are frequent, patterns of individual participation in group encounters are evidently influenced by the variable circumstances of each encounter, which may contribute to our understanding of the complexity of intergroup relations.

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Eastern chimpanzee (*Pan troglodytes schweinfurthii*) space use patterns in Nyungwe National Park, Rwanda

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Populations of the endangered eastern chimpanzee (*Pan troglodytes schweinfurthii*) are declining throughout their range. Although Nyungwe National Park (NNP), Rwanda, harbors the largest remaining eastern chimpanzee population in the country, we know little about their movement or space use patterns. We studied these patterns for three troops of chimpanzees, Mayebe, Gisovu, and Cyamudongo, in Nyungwe using daily tracking data (6:00 am to 6:00 pm) collected from 2000-2016, as well as factors that potentially influence these patterns. Chimpanzee troop home range calculated using the 95% minimum convex polygon (MCP) method was 25 km^2 for the Mayebe group, 11 km^2 for the Gisovu group, and 5 km^2 for the Cyamudongo group. Our estimate of home range size for the Cyamudongo group (which occupies a 4 km^2 forest fragment) is the smallest recorded for this species, and also suggests that forest fragmentation can substantially alter the chimpanzee space use patterns. Chimpanzee home range sizes were smaller during the dry season compared to the wet season. Data on home range size and space use will be presented in relation to average group size, elevation, habitat type, and distance to park boundary. Our study provides the first comparison estimates of home range size and factors affecting space use patterns for the three groups of chimpanzees in Rwanda. The information generated in this study can be used to improve efficacy of ranger patrols to reduce accidental snaring of this species, which is a threat to their continued presence in this forest.

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Differential nocturnal and circumlunar movement patterns suggest temporal partitioning between coyotes and bobcats in east Texas

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Sympatric mesopredators, such as coyotes and bobcats in east Texas, rely on a similar spectrum of biotic and abiotic resources. There is a high degree of intraguild competition for those resources and particularly for prey. To persist under these circumstances, it is necessary for sympatric mesopredators to mitigate competitive interactions. Species' responses to abiotic environmental factors may influence activity patterns. Temporal segregation between species may facilitate a reduction in competition. Using movement data from 10 bobcats and 10 coyotes, which I fitted with GPS collars programmed to record hourly locations throughout the night, I compared nocturnal movements by bobcats and coyotes relative to abiotic environmental and lunar cycle variables. Coyote and bobcat movements differed relative to crepuscularity, the presence of lunar illumination, and night portion. Coyote movements were influenced by crepuscularity while bobcat movements were not. Coyote movements were significantly greater when lunar light was available, while bobcat movements were unaffected by the presence of lunar light. Coyote movements peaked in the middle of the night while bobcat movements were bimodal, peaking in the evening and the morning before and after the coyote activity peak. It therefore seems plausible that differential responses to lunar light and the temporal partitioning of activity may partially mitigate the effects of competition for resources and facilitate sympatry between these mesopredators in the Pineywoods of east Texas.

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Genetic variation of MHC class II DRB genes among three weasel species: Japanese weasel (*Mustela itatsi*), Siberian weasel (*M. sibirica*) and least weasel (*M. nivalis*)

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We performed molecular phylogenetic analysis of MHC class II *DRB* genes among the Japanese weasel (*Mustela itatsi*), a species endemic to Japan, the Siberian weasel (*Mustela sibirica*), a closely related species on the continent, and the least weasel (*M. nivalis*), widely distributed in the Holarctic, including Japan. The 242-bp region of exon 2, which encodes antigen binding sites, were sequenced and found 24 sequences representative of *DRB* alleles from 31 *M. itatsi* individuals, 17 alleles from 21 *M. sibirica* individuals, and 28 alleles from 35 *M. nivalis* individuals, including broadly distributed, species-specific and/or geographically restricted alleles. In addition, MEME analyses demonstrated positive selection sites that could be committed to maintain the diversity of the *DRB* alleles. According to the reconstructed Bayesian phylogenetic tree, all alleles from *M. itatsi*, *M. sibirica*, and *M. nivalis* were grouped within the Mustelidae clade. Some alleles from the other species are more closely related to one another than to alleles from the same species, the *DRB* alleles obtained in this study showed trans-species polymorphism in related *Mustela* species, that could have appeared to be evolved under long-lasting balancing selection. However, the sister-group patterns suggested that *M. itatsi* and *M. sibirica* alleles are much more closely related to one another than either are to *M. nivalis* alleles (Nishita *et al*., 2015 and *in press*). This result correlates with the large genetic distance separating *M. nivalis* from *M. itatsi* or *M. sibirica*, data for which we have previously reported based on mtDNA sequences (Kurose *et al*., 2000).

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Lineage diversity and size disparity in Musteloidea: testing patterns of adaptive radiation using molecular and fossil-based methods

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Tests for adaptive radiation in extant taxa are traditionally estimated from calibrated molecular phylogenies with little input from extinct taxa. With 85 species in 33 genera and over 400 extinct species, Musteloidea is a prime candidate to investigate patterns of adaptive radiation using both extant- and fossil-based macroevolutionary methods. The species diversity and equally impressive phenotypic diversity found across Musteloidea is often attributed to 2 adaptive radiations coinciding with the Eocene-Oligocene transition and the Mid-Miocene Climate Transition. Here, we compiled a dated phylogeny for 88% of extant musteloids to test the predictions of adaptive radiation hypotheses with respect to rates of lineage diversification and phenotypic evolution. Contrary to expectations, we found no evidence for rapid bursts of lineage diversification at the origin of Musteloidea, and further analyses of lineage diversification rates using molecular and fossil-based methods did not find associations between rates of lineage diversification and climate transitions as previously hypothesised. Rather, we found strong support for decoupled diversification dynamics driven by increased clade carrying capacity in the branches leading to a subclade of elongate mustelids. Supporting decoupled diversification dynamics between the subclade of elongate mustelids and the ancestral musteloid regime is our finding of increased rates of body length evolution, but not body mass evolution, within the decoupled mustelid subclade. The discordance in evolutionary rates between body length and body mass along with evidence of decoupled diversification dynamics suggests that body elongation might be an innovation for the exploitation of Mid-Miocene resources, resulting in the radiation of some musteloids.

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Geographic variation and taxonomy of the marbled polecat *Vormela peregusna*

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The distribution range of the marbled polecat *Vormela peregusna* extends from southeast Europe, through Asia Minor and Middle East, the Caucasus and Middle Asia, to Mongolia and northern China. Geographic variation of the species was studied across the whole distribution range. Analysis of the cranial variation revealed two morphological groups – western and eastern. These groups were treated as two distinct subspecies. Nominotypical *V. p. peregusna* (Güldenstädt, 1770) (syn. *sarmatica*, *euxina*) is found in southern and eastern Europe, Asia Minor and Caucasus. The eastern subspecies *V. p. koshewnikowi* Satunin, 1910 (syn. *alpherakii*, *chinensis*, *negans*, *obscura*, *ornata*, *pallidior*, *syriaca*, and *tedshenika*) is found south and east of the Middle East, in Middle and Central Asia and eastward to China. Our data revealed a gradual decrease in the morphological diversity in *Vormela* skulls from west to east in the distribution range. This pattern can be explained by later occupation of the eastern part of the modern species' range. The pattern of geographic variation, revealed in this study, might reflect the Pleistocene history of the species' range formation rather than relate to a gradient of climate conditions throughout the modern species' range. We assume two routes of migration of the marbled polecat from the western part of the range: 1) northern route – from southeastern Europe and Caucasus through Middle Asia and Kazakhstan territories to Mongolia and China, 2) southern route – from Asia Minor and Transcaucasia regions to the Middle East, the south of Middle Asia and Central Asia, including China.

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Pleistocene and Holocene fauna of Mustelidae around the Ural and Western Siberia

Pavel Kosintsev

The Mustelidae remains from 35 Late Pleistocene sites and 151 Holocene sites from the Urals and Western Siberia have been studied. The following species inhabited the Urals and Western Siberia throughout the Late Pleistocene (MIS 5 - 2) and Holocene (MIS 1): *Martes zibellina*, *Gulo gulo*, *Mustela erminea*, *Mustela nivalis*, and *Mustela eversmanii*. *Meles meles* and *Lutra lutra* were also present in the Urals during the Late Pleistocene interstadials. Besides the abovementioned species, *Martes martes* and *Mustela lutreola* lived there in the Eem interglacial (MIS 5e). The Holocene was characterised by the richest *Mustelidae* fauna. During this period, *Mustela sibirica* and *Mustela putorius* became part of the faunal composition, while *Martes foina* was its part only for a short time. At the onset of the Late Holocene (2500 – 1500 BP), the Asian badger (*Meles leucurus*) forced out the European badger (*Meles meles*) from the entire area of the Western Siberia, Urals and Volga-Ural region. Changes in the *Mustelidae* faunal composition occurred due to changes of the range. The ranges underwent contraction (*Mustela eversmanii*, *Meles meles*), expansion (*Mustela sibirica*, Mustela *putorius*, *Meles leucurus*), and fluctuations (*Martes martes*, *Martes foina*, *Mustela lutreola*, *Meles meles*, *Lutra lutra*). Changes in the ranges of almost all the species resulted from climatic changes. The Asian badger (*Meles leucurus*) forced out the European badger (*Meles meles*) as a result of a competitive exclusion.

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Olfactory receptor evolution shows association with dietary radiation of neotropical leaf-nosed bats

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New World leaf-nosed bats (Phyllostomidae) occupy an enormous range of dietary niches and natural selection has shaped an array of morphological and sensory adaptations to exploit these dietary niches. However, the molecular mechanisms that allowed populations to depart from their ancestral insectivorous diet and detect novel resources, such as nectar or fruit, are unknown. Phyllostomids need to find these resources while flying in the dark, and behavioral evidence has shown the sense of smell is a critical supplement to echolocation for detecting food in a cluttered environment. We hypothesised that the genetic machinery governing the detection of plant volatiles to also be shaped by natural selection. To test this, we sequenced the transcriptomes of the main olfactory epithelium and identified the olfactory receptor profiles in over 20 phyllostomids with divergent diets. We identified many duplication events unique to particular bat subfamilies with unique diets. Some of these duplications occurred within groups with increased rates of speciation, and may be related to their diversification. For example, a unique cluster of olfactory receptors in subfamily OR2/13 is present only in fig-eating phyllostomids (Stenodermatinae). Stenodermatines have a significantly higher speciation rate compared to all other bats, attributed to their ability to exploit the novel dietary niche of consuming hard-fruits. This duplication of receptors that occurred prior to the divergence of stenodermatines may be connected to the diversity of olfactory receptor ligand profiles the ancestral stenodermatines explored. Our study illuminates how the olfactory receptor evolution may have opened up novel dietary niches for bats.

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The influence of ecological and geographical context on a recent rapid radiation: A case of study in the sigmodontine rodents.

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Rodents of the subfamily Sigmodontinae (family Cricetidae), which originated in the Late Miocene, comprise one of the most diverse clades of Neotropical mammals (above 400 living species grouped into *ca.* 86 genera). Sigmodontine genera have been traditionally assembled into groups, most of which are formally recognised as tribes, which greatly differ in species richness and ecological diversity. As such, the ecological and geographical contexts are crucial to understand sigmodontine diversification. Previous studies failed to solve most relationships among tribes, remaining unknown if this is a case of almost-simultaneous cladogenesis within a rapid radiation or simple lack of sufficient data to resolve this relationship. We aimed to understand the diversification pattern, rates and drivers of this radiation. We discuss the timing of the radiation of the main sigmodontine lineages. We report that the evolution of habitat preference (considering vegetation type and elevational range) was associated with diversification rates. We propose that a overall observed diversification slowdown might be the result of ecological or geographical constraints. Lineages-per-area-through-time plots show that tropical areas accumulated more lineages than other areas. This highlights the influence of tropical lowlands -which might have acted as both a cradle and a museum of species-in the diversification of Neotropical mammals. Financial support: FONDECYT 1141055, FONDECYT-Postdoctorado 3150604.

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Comparative primate biogeography in the Neotropics

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The field of Neotropical primate biogeography has blossomed in the last decade, with the coupling of new statistical modeling methods and coordinate-based population-level sampling for genomic data sets. This talk considers both the drivers leading to the current diversity, distribution and abundance of monkeys in the Neotropics, and predicted future effects of human activity and climate change on primate biogeography. Monkeys first arrive in the Neotropics about 36 Ma, and all living Neotropical primates trace their ancestry to a single common ancestral population from the onset of the Neogene. The availability of lush Amazonian habitat, the rise of the Andes, the transition from lacustrine to riverine system in the Amazon Basin, and the intermittent connection between the Amazon and the Atlantic tropical forests each have been instrumental in how primates spread and diversified. The first Neotropical primates were pre-adapted to diurnal arboreal group living, making it possible on a continental scale to invade a range of forest niches not filled by native South American mammalian taxa. New competitors and predators emerged during a Pliocene-Pleistocene influx of North American fauna, peaking with the closing of the Isthmus of Panama. Humans, the extreme newcomers in the Neotropics, have influenced primate habitat and ecology over the last 13,000 years, with breathtaking transformations in the last 500 years as European colonisation led to rubber extraction, ranching, road-building, hydroelectric dam construction, forest fragmentation, vast land use modification for agriculture, and desertification. Human-mediated climate change is predicted to affect primates differently in different biomes.

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Survival in the snow: the first release of captive-bred mountain pygmy-possums (*Burramys parvus*) to the wild

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The mountain pygmy-possum has been the focus of active and innovative conservation over the past decade, including wild-wild translocations between populations, predator control and habitat regeneration. In 2013, we trialed the first release of this endangered species from captivity to the wild. The key objectives were to evaluate the survival rate for captive-bred possums and test whether released animals genetically augment the wild population. Eleven possums (six females and five males) bred in captivity at Healesville Sanctuary, Zoos Victoria, plus two wild-born males, were deemed genetically suitable for release to two boulder-fields at Mt Buller, south-eastern Australia, by the Mountain Pygmy-possum State Recovery Team. In captivity, possums were provided with food, habitat features and social interactions to mimic their wild environment as much as possible and were housed in temperature-controlled enclosures that promoted natural hibernation cycles. Released possums were radio-tracked for four weeks to determine survival, reproduction and habitat use. Short-term survival was extremely high, with 6/6 females and 6/7 males re-trapped one month post-release. The remaining male’s collar was found detached (without evidence of predation). Further trapping by field partners monitored the possums over time, with 85% of possums being re-trapped over the following four months. All females produced one to two litters of pouch young within four months of release, with some of their young and at least one of the released females also producing young the following year. Knowledge gained from this trial will help inform future management strategies aimed at securing this species in the wild.

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Learning how to do it right: lessons from trial translocations of Tasmanian devils

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Translocations of carnivores are notoriously difficult and the outcomes are often less than successful. Tasmanian devils, the largest remaining marsupial carnivore, are currently listed as endangered at the State and Federal level in Australia following the widespread decline of the species from Devil Facial Tumour Disease, a contagious cancer. Over the past three years we have undertaken release events to determine the best release strategy. Here we present tracking data from Tasmanian devils released into the wild in a trial to determine which devils are more successful upon release, wild-born or captive-born. Both groups of devils were released and collared with satellite-linked GPS collars. Animals were trapped regularly to check collar fit and health status. The devils were released into a 5,000 ha site; although some individuals traveled as far as 50 km from their initial release site in the first 6 weeks, most remained within 6.48 ± 5.21 km of the release site. The data from the collars has allowed us to answer important questions such as: how far do devils disperse upon release; how long does it take devils to settle after release; do bait stations act as dampening dispersal agents and help anchor devils to the release site; and importantly is there any difference in these questions between wild and captive born devils? We discuss our findings and propose a strategy for future releases of devils back into the wild

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Anti-predator training of the endangered Pacific pocket mouse (*Perognathus longimembris pacificus*) slated for reintroduction

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Reintroductions are an important management tool for recovering endangered species, but have low success rates in part due to behaviorally unequipped individuals. The inability for captive-born animals to recognize predators and/or respond with wild-type anti-predator behavior is especially problematic for small prey species. In our conservation breeding/reintroduction program for the endangered Pacific pocket mouse (*Perognathus longimembris pacificus*; PPM), results of antipredator experiments showed that captive-born individuals are less wary than wild-caught mice when presented with a terrestrial or aerial predator. We, therefore, initiated anti-predator training one month prior to the reintroduction with the goal of improving behavioral competency and release success. All mice slated for release (n = 25), and the alternates (n = 6) were exposed to a California king snake (*Lampropeltis getula californiae*) for 5 minutes pre- and post-training. The snake was contained within a Plexiglass unit with slits to allow PPM to experience olfactory as well as visual cues. Training consisted of pairing exposure to the snake with both a PPM distress call, and a physical thump under the testing arena in the event that the focal subject approached the snake. All trials were recorded, and behavior was quantified pre- and post-training to assess learning. Individuals that did not display the appropriate anti-predator response (e.g. freezing, retreating to cover, etc.) after training were removed from the release cohort, and replaced with a behaviorally competent alternate. The results of the experiment will be discussed.

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The role of human pressures in altering global macroecological patterns

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Human pressures have led to hundreds of species extinctions and have narrowed the distribution of many of the remaining species. These changes influence our understanding of global macroecological patterns, but this influence has been rarely explored. Two of these patterns, the Rapoport's rule on range size distributions and the Bergmann's rule on body mass distributions, have been largely investigated in macroecology, often under the assumption that observable patterns reflect natural processes. We assessed the extent to which humans have re-shaped the observable patterns of range size and body mass distribution in terrestrial mammals globally. We analysed the role of extrinsic (biogeography, environmental, climate, human pressure) and intrinsic (biology) variables in predicting range size of individual species, and the role of human and environmental variables in predicting body mass patterns in species assemblages. We found a dominant role of human and climatic variables over biological variables in predicting the distribution of range size in terrestrial mammals. We also found that both median and maximum body size in mammalian assemblages would be much higher if human impacts were minimal, especially in areas that are highly accessible to humans and where natural land cover has been converted. Our results provide evidence of the pervasive effects of anthropogenic impact on nature, and shows human-induced distortion of global macroecological patterns. While in the short term human pressures are causing species decline and extinction, in the long term they are causing a broad re-shaping of animal communities with yet unpredicted ecological implications.

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Extinction risk in Australasian mammals: Trends and management priorities

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Australia's mammal fauna has suffered large historical declines. Of 315 taxa of land mammals extant at the time of European arrival, at least 29 are extinct, while 27.5% of all species are either extinct or currently threatened with extinction. Recent evaluations for the Australian Mammals Action Plan and the 2015 Global Mammal Assessment show that the conservation status of Australian mammals continues to decline. Among marsupials and monotremes, 14 species moved between threat categories from 2008 to 2016, and all but one of these changes was a decline; there was a similar trend in rodents. The most pervasive threat is predation by feral cats, followed by inappropriate fire regimes, predation by red foxes, habitat loss and fragmentation, and climate change and extreme weather events. In this paper, we review the nature of these threats and their changing impacts on the mammalian fauna of Australia. We then provide an overview of current conservation research and management priorities for Australian terrestrial mammals, and evaluate prospects for mitigating threats at regional and continental scales. For most species from New Guinea there is too little information to determine changes in threat status, but it is clear that overexploitation is the predominant threat for many species. We highlight examples of community-based conservation programs that have been successful in reducing this threat.

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Pangolins on the edge: Status, threats and conservation of the world's most trafficked wild mammals

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Pangolins (Pholidota: Manidae) are the world's most trafficked wild mammals, with more than a million individuals estimated to have been poached and illegally traded in the past decade. The eight extant species of pangolin have all been assessed as threatened on the IUCN Red List (two Critically Endangered and two Endangered in Asia; four Vulnerable in Africa) on the basis of estimated population declines due primarily to over-exploitation for their meat, skin and scales. An entire mammalian order, representing 80 million years of unique evolutionary history, is at risk of extinction. This presentation will provide an overview of the status and threats facing pangolins, with particular reference to the drivers of over-exploitation and impact of use and trade on wild populations. It will also examine conservation actions undertaken to date, including a review of current attention and investment in pangolin conservation and an overview of the multi-faceted interventions needed to secure the conservation of pangolins in the future.

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The Red List status of Old World deer and matters of conservation concern

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Most deer species are distributed from Europe through mainland Asia and into Southeast Asia and the Philippine archipelago. These 51 species, including 6 species of mouse deer (*Tragulus*), fall into 3 broad categories of concern: A suite of deer species that are widespread across Europe and reaching into Asia where 5 of the species are increasing due to effective habitat and hunter management; a suite of deer throughout Asia (26 species) and the islands (9 species) that declined precipitously within the past 50 years and either their numbers have not recovered or have continued to decline; or a suite of 10 species of small deer whose genetics and population status are still being determined. At least 8 of the larger species have been established in Australia and New Zealand for hunting purposes and populations are increasing. Within several of the broadly distributed species there is concern that declines in sub-species have been masked by stability in the main distribution. An example of this are relict populations of red deer (*Cervus elaphus*) throughout central and south Asia. There is a critical need for focus on the smaller deer species, whose cryptic nature and naturally low densities prevents accurate surveys, and this lack of knowledge may be masking true declines. Recent examples of sudden declines and unknown status are the hog deer (*Axis porcinus*) and bawean deer (*Axis kuhlii*) which have not attracted international attention despite marked concern by the Deer Specialist Group.

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Conservation ecology of the Pilbara Northern Quoll: home range, distribution and future climate change impacts

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The northern quoll (*Dasyurus hallucatus*) is a nationally threatened and declining mammal species. Declines have been catastrophic, extensive and rapid due to predation on the introduced cane toad (*Rhinella marina*), habitat removal, predation by feral and domestic animals, inappropriate fire regimes and pastoralism. An emerging threat for the isolated population within the Pilbara region of Western Australia is the impact of mining, which is contributing significantly to habitat loss. To investigate the conservation ecology of the Pilbara northern quoll, we examined interactions with mining infrastructure barriers by fitting custom made GPS pinpoint 50 collars (Sirtrack) to seven individuals. We found evidence of long distance dispersal and use of road underpasses. We present data on relationships with geology and vegetation and a comparison with a study of quoll movements in undisturbed areas of the Pilbara. We undertook a comprehensive species distribution modeling exercise using bias compensation to account for a focus of survey efforts around resource projects. Under future climate change projections, northern quoll potential distributions will contract inland and cane toad distributions will shift coastwards, leading to less future conflict between the two species than has been previously predicted.

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Living on the edge of agriculture: Home range and movement patterns of the field vole *Microtus agrestis* in a fragmented agro-ecosystem

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Species living in uncultivated areas of agro-ecosystems live in a mosaic landscape with only fragments of suitable habitat available to them. These fragments differ in size, shape, diversity and resource values. Larger fragments are often far between and only occasionally connected through corridors. For small mammals such as the field vole (*Microtus agrestis*), distance between habitat fragments may pose barriers and as distance increases the probability of successful crossing become less likely. During the period 2008-2011, field voles were tracked by radio telemetry in a Danish agro-ecosystem. We analysed home ranges with autocorrelated Kernel density estimation (AKDE) to find an approximation of the range distribution, and applied the synoptic model using 10 resource covariates (ecological, temporal and between-animal-interaction) to find the best home range model fit. AKDE uses the autocorrelation inherited in any animal movement dataset thereby avoiding the crippling effect sub-sampling to independence can have. The synoptic model has been shown to be effective for calculating home ranges constrained by linear habitat features as those found in the agro-ecosystem. We compare home ranges between voles of both sexes in habitat fragments of different size and shape, and during different seasons. We find that voles would primarily stay inside habitat fragments; i.e. small habitats result in small home ranges. We expect the presence of other individuals to influence movement patterns in accordance with the individual's reproductive state and time of year (available food resources). Furthermore, we expect home ranges to change as unoccupied spaces occurs when neighbouring voles are predated.

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Inbreeding and inbreeding avoidance in wild giant pandas

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Inbreeding can have negative consequences on populations and individual fitness, which could be counteracted by inbreeding avoidance mechanisms. The giant panda, a solitary and threatened species, lives in many small populations and suffers from habitat fragmentation, both factors which may aggravate the risk of inbreeding. To evaluate inbreeding level and risk, we performed long-term observations of reproductive behavior, sampling of mother-cub pairs and large-scale genetic analyses on wild giant pandas. Moderate levels of inbreeding were found, but no high-level inbreeding occurred. More significant levels of inbreeding are avoided passively by female-biased natal dispersal rather than by breeding dispersal or active mate-choice mechanisms. The level of inbreeding in giant pandas is greater than expected for a solitary mammal and thus warrants concern for potential inbreeding depression, particularly in small populations isolated by continuing habitat fragmentation.

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Estimating hare population using thermo vision equipment in an intensive agricultural land

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Hare is a common species in Romania and inhabits most of the country, from high to very low altitude. In the last 20 years, the hare population has been dramatically decreased, particularly in the areas were intensive agriculture is practiced. Moreover, in some of the cases, legal aspects regarding small game species protection (preserving some undisturbed areas for ensuring shelter) are not respected. The evaluation method, currently implemented across the country for hare, is invasive and takes place in early spring, when beaters move across the entire hunting unit trying to scare individuals, so they will run, to count them. Thus, the actual method is based on reproduction stocks from the spring, using growth indices, not taking into consideration the natural fluctuation of environment parameters. Starting with 2014, a new method based on using thermo-vision equipment for detecting hare was used for two pilot areas (12 hunting units ~ 100000 ha), in different seasons for assessing both reproductive stock as well as offspring numbers. Our results differ significantly from those obtained with the classical method. In some hunting units, the estimation on the population was much lower, especially in those areas were agriculture is intensive and most of the refugees are lost due to that. This method is very easy to use, needs only a small number of people, the animals are not disturbed at all, and the results are much more accurate.

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Migratory livestock grazing significantly impacts rangeland vegetation and wild-ungulate population in the Indian Trans-Himalaya

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Intense livestock grazing outcompetes wild ungulates in low-productivity rangelands. This is a long-standing and highly debated conservation problem globally. We examined impacts of migratory livestock grazing on Trans-Himalayan rangeland and Asiatic ibex, a wild ungulate and primary prey of the endangered snow leopard. Vegetation and ibex were sampled in an intensely grazed (livestock density 63 sheep-goat km^{-2}) and ungrazed areas, during spring (before grazing), summer (during grazing) and autumn (after grazing). Proportionate to vegetated area, independent randomly laid 1m x 1m plots were sampled for vegetation cover and biomass estimation (Cover: $N_{Ungrazed}$=237; N_{Grazed}=127; Biomass: $N_{Ungrazed}$=119; N_{Grazed}=64). Ibex density and young:adult-female ratios were estimated by repeatedly sampling 17 trails using double-observer methods across both treatments for the three time periods and two consecutive years. Graminoid and herb biomass were significantly higher in ungrazed than grazed areas (ANOVA; Graminoid: $F_{Treatment}$=16.05; P=<0.001; Herb: $F_{Treatment}$=22.75; P=< 0.001). Overall vegetation composition was dissimilar across ungrazed and grazed areas (Morisita Index 0.18); however, palatable species composition was similar (Morisita Index 0.70). Biomass of palatable species was 2.25 times higher in ungrazed areas. Total off-take of dry forage by migratory livestock from grazed pastures (61 km^2) was 10,658 kg km^{-2} over two months of grazing. Ibex density was 1.80-7.0 times higher in ungrazed areas in 2015, while 2.45-4.7 times higher in ungrazed areas during 2016. Ibex yearling:adult-female ratio was six times higher in ungrazed areas. Significant reduction in forage availability lowered ibex density and yearling:adult-female ratios in grazed areas, suggesting migratory livestock outcompetes ibex through exploitative competition.

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Categorization and effectiveness of protected areas: Comparative study of small mammal communities in Nahuel-Huapi National Park, Argentina

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The increase in Protected Areas (PA) at a global scale during the second half of the 20th century reflects the growing concern for preserving lands in the face of biodiversity and habitat loss. However, in most cases, there is no clear evidence for PA effectiveness. Nahuel-Huapi National Park is the first and biggest Argentinian PA (750,000 ha); it hosts few large and medium size mammal species; however, the diversity of small mammals equals those found in temperate forests elsewhere. Our goal was to evaluate the conservation status of the small mammal communities in the Nahuel-Huapi protection system, accounting for the three different PA categories. To this end, we established five plots of 60x60 m in each level of protection (Strict-Natural-Reserve, National-Park, National-Reserve, outside PA), setting 50 traps per plot, over four consecutive nights monthly, during summer 2015 and 2016. Capture effort was 41,600 trap-days. We identified eight species: *Abrothrix hirta, A. olivacea, Oligoryzomys longicaudatus, Geoxus valdivianus, Chelemys macronix, Irenomys tarsalis, Loxodontomys micropus, Dromiciops gliroides*. We marked and released each individual, resulting in 727 (in 2015) and 532 (in 2016) individuals (10.2 % and 9.02% capture success respectively). We compared species richness, Shannon-Wiener diversity-index, and abundance between the four levels by ANOVA. Total abundance was higher in the highest level of protection for both seasons; however, the unequal abundance and distribution of small mammals across the 20 plots requires a more detailed study in order to elucidate if this heterogeneity is inherent to the group or to the protection system itself.

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Mice in the Anthropocene: Refuge in the built environment for the critically endangered salt marsh harvest mouse

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Worldwide, about 50% of wetlands have been lost. In the San Francisco Bay Estuary (SFBE) less than 10% of historical tidal wetlands remain, and those comprise a fragmented mosaic of natural and anthropogenically altered wetlands. Globally, only 5 species of vertebrates, and only one mammal, the endangered salt marsh harvest mouse (SMHM, *Reithrodontomys raviventris*), are restricted to coastal wetlands. SMHM is a unique wetland-adapted rodent endemic to the marshes of the SFBE. Conventional conservation practices have favored a push toward tidal restoration as a recovery action for SMHM. However, tidal wetlands are vulnerable to sea level rise and tidal restoration is slow and costly. Understanding the value of alternative habitat types can improve conservation of SMHM. We investigated the relative value of historical tidal and anthropogenic diked wetlands for SMHM. We found that both support similarly sized populations and similar numbers of reproductive females, but diked wetlands had higher densities of juveniles. Habitat use is similar between wetland types, but smaller home ranges in diked wetlands may indicate greater habitat value. Finally, preferred food plants occur at high densities in diked wetlands. This study – the first of its kind – greatly improves our understanding of the habitat requirements of SMHM. Diked wetlands have high habitat value for SMHM, possibly superior to tidal habitat; this result triples the acreage of “good” SMHM habitat in the SFBE. It also illustrates the importance of understanding the value of anthropogenic habitats for conservation of endangered mammals as historical habitat patches dwindle.

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Trends and conservation status of South American mammals

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Our planet is undergoing the sixth mass extinction of species. The accelerated change in land use coupled with other threats to biodiversity, has led to a worrying process of defaunation. For this reason, it is necessary to know the current state of those groups and species that are at greater risk of extinction or that require studies, in order to take urgent conservation measures, particularly in regions such as South America, where the loss of natural habitats is alarming. We assess the population trends and conservation status of South American mammals. We used the IUCN databases for 1197 species. Analyses were carried out at the species and order level. The results in terms of population trend indicate that of the total analysed, almost 30% are declining, and less than 1% are increasing, while there was no information of 46% of the species. The orders with most critical declining species are Carnivora, Primates, Chiroptera, Rodentia and Cetartiodactyla. In relation to the IUCN conservation status, analyses indicate that 16% of the species are under some category of risk. For example, of 44 species of carnivores, 9 have some category of danger; in the case of the primates, of the 130 species 57 are in some category of danger. This analysis shows that a third of the mammals in South America are at risk of disappearing. This percentage is likely to be higher if one takes into account that there is no information on population trends of nearly half of the species.

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Paleoenvironmental change and megafaunal extinction. Ultima Esperanza, Chile.

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Abundant Late Pleistocene bone assemblages were recovered at a number of cave sites located at Ultima Esperanza, South Chile. Some of these sites also include indications of ephemeral occupations by Late Pleistocene human foragers, particularly at Cueva del Medio and Cueva Lago Sofia 1. This evidence suggests different degrees of interaction with extinct faunas. Our excavations and dating program shows that Ultima Esperanza was occupied by extinct mammals at least since ca. 17,000 Cal BP, shortly after the retreat of the Late Pleistocene glaciers. The main species present in these sites are *Mylodon darwini*, *Hippidion saldiasi* and several extinct camelids and carnivores. Our recent work at Cueva Chica, Cueva del Medio and Cueva del Milodon uncovered evidence of Late Pleistocene periglacial/paraglacial features which suggest the presence of a very cold environment, evidence that is in agreement with recently published palynological information. Our studies of the bone assemblages suggest that Cueva del Milodon and other large caves were used as ground sloth lairs, while several endogene caves were used as carnivore lairs, particularly by *Panthera onca mesembrina*. However, most of the sites are temporal palimpsests in which a taphonomic approach was used to try to isolate the main depositional agents. The extinction of most of the taxa recovered at these sites is discussed in the light of the most recent paleoenvironmental evidence.

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Rapid climate change and megafaunal extinctions

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Improved resolution data from radiocarbon, climate and ancient DNA studies of megafauna and humans is providing the first ability to disentangle the roles of climate change and human impact in the Late Pleistocene megafaunal extinctions. We find that megafaunal populations underwent repeated local or global extinctions in association with rapid warming events on a millennial scale. The extinction events took place both before and after the presence of modern humans on the landscape. Human impacts may be through the disruption of metapopulation processes which appear to stabilise ecosystems, and may have evolved to provide resilience to rapid and frequent climate shifts in the past. Globally, we see a strong correlation between warming events at the end of the last Glacial and isotopic signatures in megafaunal bones characteristic of rapid increases in environmental moisture levels. It appears that moisture-caused fragmentation of grasslands was a key driver of the Late Glacial megafaunal extinctions, and that the constant presence of grasslands in Africa explains the relative lack of extinctions during this time. In the Americas, the rapid movement of the first Native Americans throughout both continents create a powerful and unique model system due to the opposing climate trends in each hemisphere at the time. While megafaunal extinctions were associated with warming trends in both cases, the out of phase climate patterns caused the sequence and timing of events to be mirrored, providing a unique high resolution view of the interactions of human colonisation and rapid climate change on megafaunal ecosystems.

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Why is the European bison the sole survivor of the Paleartic megafauna?

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Late Quaternary megafauna extinctions impoverished mammalian diversity worldwide, with the loss of most of the large-bodied mammals in the northern hemisphere. The relative role of climate and human impact as the drivers of megafaunal collapse is hotly debated. One of the megaherbivores that survived until modern times was the European bison, now the largest terrestrial mammal in Europe. Bison population sizes fluctuated during the Pleistocene, possibly reflecting fragmentation of its distribution range during successive glaciations, rather than southward range shifts as observed in numerous other mammalian species. This persistence in the proximity of the glacial front may have been possible due to the European bison's adaptation to colder climates, as confirmed by genome analysis. This permitted survival in latitudes less favourable for humans, and in effect allowed bison to escape the human impacts that were probably experienced by more southern megaherbivore species. Genome analysis, isotopic signatures over time and DNA-based diet analysis of modern bison show its adaptations to diverse environments and food resources. This plasticity in terms of habitat selection and foraging habits probably allowed the European bison to respond to rapid environment changes during the post-glacial period and survive, while the other large beasts have gone. Based on this hypothesis, climate extremes served to protect the European bison from humans, a substantially different perspective to that normally considered in the megafaunal extinction debate. The study was financed by the Polish National Science Centre, project no. 2013/11/B/NZ8/00914.

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Hybrid bovinae in Pleistocene Europe

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Mitochondrial introgression from *Bos* to *Bison* is predicted from three premises. (1) Extant European bison have *Bos*-like mitochondria whereas American bison are more Yak-like, (2) Female F1 from crosses of modern *Bos* x *Bison* are fertile, and (3) *Bos primigenius* and *Bison spp.* of Pleistocene Europe had considerable geographical and temporal overlap. Using mitochondrial DNA from 64 ancient bison, we identified a previously uncharacterised bison genetic clade also containing *Bos*-like mitochondria. Nuclear SNP analyses suggest the *Bos* introgression is shared by both modern European bison and the extinct clade. A dated mitochondrial tree provides a minimum age for *Bos* introgression of ~120 kya. We suggest that hybridisation, or at least outbreeding, may have been a common characteristic of bovinae in Pleistocene Europe in response to range contractions and expansions triggered by the Quaternary warming and cooling cycles. Hybridisation may have reduced inbreeding depression during range contractions, whereas wavefronts of population expansions likely radiated through many existing populations, providing genetic heterogeneity for fast adaptation to local conditions.

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Ecosystem modelling to predict ecosystem-wide outcomes of management

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Conservation interventions, such as eradicating feral invasive cats, rabbits or foxes, can lead to unintentional negative outcomes through chains of species interactions. For effective conservation management of ecosystems, we need to predict the outcomes before the intervention occurs. Modelling is a useful tool to make predictions about potential cascading outcomes and inform conservation decision-making. This can allow us to plan for potentially negative outcomes accordingly and suggest strategies to meet multi-species objectives. In this talk, I will discuss recent progress in the field and discuss applications of these methods, focusing on the effect of mammalian predators on ecosystem dynamics. In particular, I will discuss ecosystem models that estimate the impact of fox control on malleefowl populations, and how dingo and eastern quoll reintroduction could affect the recipient ecosystems.

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Exotic predators affect endangered small mammal behavior with potential for trophic cascades in island ecosystems

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Exotic predators contribute to novel ecological situations for native prey species, particularly when prey exhibit behaviors that are maladaptive in the presence of novel predators. In these instances, predators may drive selection because prey with naïve behavioral or morphological traits experience reduced survival and/or reproductive fitness. Islands are homes to many endemic species that are often exposed to exotic predation pressure from accidental or intentional predator colonisation. Many island endemics respond positively to predator eradication, but we are unaware of any examples of rapid numerical and behavioral responses to predator removal. The Key Largo woodrat (*Neotoma floridana smalli*) was historically reduced to a small population as evidenced by the rarity of their characteristic stick-nests and few captures. We monitored woodrats at supplemental nests for two years during a time when exotic predators were removed from Crocodile Lake National Wildlife Refuge. We used multi-state dynamic occupancy models to evaluate changes in woodrat distribution and stick-nest building behavior in response to predator removal. The distribution of woodrats at supplemental nests increased from < 25% to nearly 50% in the two-year period. Furthermore, woodrats commonly built stick-nests on top of supplemental nests post-predator removal, which followed a gradient away from areas with source domestic cat populations and individual pythons. We suggest that stick-nest building is maladaptive in the presence of novel predators, which has implications for trophic cascades because woodrats are ecosystem engineers, providing refugia for other species, concentrating woody vegetation for decomposition, and dispersing seeds on the island of Key Largo.

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Australia’s digging mammals: foraging beneath the surface contributes to ecosystem services

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The digging activities of mammals, although small at a local scale, are important for broader scale ecosystem services within landscapes. Australia has a large number of digging mammals that are identified as ecosystem engineers through their bioturbation of soil. Of these 29 species, approximately 70% are threatened, with mammals such as bandicoots, bilbies and bettongs having undergone substantial population and range declines within the last 200 years due to multiple threats. Our study examines how the southern brown bandicoot (*Isoodon obesulus*), a persisting marsupial in novel peri-urban environments, can alter soil nutrients and plant growth, subsequently influencing ecosystem functioning. We examined soil nutrients of foraging pits along the pit profile (in the pit, the discarded spoil heap, and undug ground) and examined seedling growth rates using soil cores collected from the same locations. The excavated spoil heap contained higher amounts of nutrients essential for plant growth (e.g. potassium). Seedlings grown in the spoil soil were the largest plants; being 1.5 times taller than seedlings grown in undug soil and double the height of seedlings grown in pit soil. The foraging actions of bandicoots alters soil nutrients, creating microhabitats that facilitate plant growth. We believe the extensive loss of Australian digging mammals is associated with a concurrent loss of ecosystem services, suggesting that the health and functioning of Australian landscapes may have drastically altered as these species declined. The reintroduction of digging mammals may therefore be essential, not only for species conservation, but also for ecosystem restoration.

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Does the loss of tree hollows contribute to the decline of arboreal mammals in northern Australia?

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The drivers of northern Australian mammal decline remain highly uncertain, but one of the main hypotheses is habitat simplification. Of the nine mammal species that have declined markedly in northern Australia, six are arboreal (including semi-arboreal and scansorial) and typically use tree hollows as daytime shelter. These species have contracted to the wetter, coastal parts of their range, where large trees happen to be most abundant. Given evidence that tree hollows are a critical limiting resource for a range of arboreal fauna in southern Australia and historical declines in the abundance of hollow-bearing trees have severely impacted populations of these species, we investigated the drivers of tree-hollow availability in the tropical savannas of northern Australia and assessed nestbox use as a potential conservation management tool. Cyclones, termites and intense fires selectively destroy large, hollow-bearing trees in tropical savanna woodlands. In a coastal refuge where mammal assemblages are still fairly intact, 41% of all nestboxes deployed were used within a one year period by threatened arboreal species, indicating the viability of nestboxes in arboreal mammal conservation efforts. The rate of nestbox use was significantly correlated with the abundance of tree hollows in the surrounding landscape. Managing fire regimes to minimise the loss of large, hollow-bearing trees at both local and landscape scales is critical to reversing arboreal mammal declines. Augmenting natural den sites with artifical nestboxes may be an effective way of boosting local populations of arboreal mammals.

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A shifting baseline: $\delta^{15}N$ analysis of individual amino acids to track ecosystem changes across the late Pleistocene extinction

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One of the likely consequences of the late Pleistocene megafauna extinction was a reorganization of mammalian communities, including trophic niche shifts of medium- and small-bodied mammals. Traditionally, nitrogen isotope ($\delta^{15}N$) analysis of bulk tissues is used as a proxy for trophic level. However, interpreting temporal or spatial changes in $\delta^{15}N$ values is complicated by potential concurrent shifts in (baseline) $\delta^{15}N$ values of primary producers. $\delta^{15}N$ analysis of individual amino acids (AAs) provides a way to simultaneously track trophic level and baseline $\delta^{15}N$ changes. ‘Source’ AAs are routed directly from diet and so their $\delta^{15}N$ values do not change with trophic level, whereas ‘trophic’ AAs show a strong relationship between trophic level and $\delta^{15}N$. Here we apply

this approach to cotton rat (*Sigmodon hispidus*) fossils from Hall's Cave in Texas, a site that spans the last 22,000 years. Cotton rats show a wide range in both carbon (~10‰) and nitrogen (~7‰) isotope values over this interval, but the only significant trend is a decline in δ^{15}N following the late Pleistocene extinction. We found a significant decline in δ^{15}N of source and trophic AAs from the mid to late-Holocene; the offset in δ^{15}N between these groups remained constant This indicates that the decline in bulk *S. hispidus* values was driven by a shift at the base of the foodweb, rather than a change in *S. hispidus* trophic position.

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Morphology and evolution of the oral shield in marsupial newborn pouch young.

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Newborn marsupials can be arranged into three grades of developmental complexity based on their external form, on their organ systems and their cytology. The dasyurids are considered the least developed at birth, while didelphids and peramelids are intermediate and macropods are the most developed. Currently there is still little information on caenolestid and microbiotherid development at birth. Developmental stages can be graded as G1, G2 and G3, with G1 being the least developed at birth, and G3 the most developed. Marsupials are also characterized by having an extremely developed craniofacial region at birth compared to therians, with the oral region varying in development between different marsupial groups at birth. The oral shield is a morphological structure observed during late embryological development and is retained until shortly after birth. Morphological variation of the oral shield can be arranged by developmental complexity from greatly developed, reduced to vestigial. In its most developed state, the lips are fused, forming together with the rhinarium, a flattened ring around the buccal opening. We observe the oral shield in newborn marsupials (dasyurids, peramelids, macropods and didelphids), including the newborn monito del monte young (*Dromiciops gliroides*). The adaptive value of the oral shield structure is reviewed and appears to be exclusively present in Marsupialia. We observe that a well-development oral shield may be related to ultra altricial development at birth, large litter size (more than 2) and is present in most species that lack a pouch or have a less developed pouch with some exceptions.

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Integration of the mammalian dentition by the inhibitory cascade

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The evolution of precise tooth occlusion in mammals was a key innovation enabling effective processing of a wide variety of foods to fuel their high metabolic rate. Such exact occlusion likely requires tight developmental control over tooth size and shape as well as the coordination between upper and lower teeth. The developmental origins of this innovation are still unclear. We examine the developmental basis of occlusion using the evolutionary-developmental rule called the inhibitory cascade. The inhibitory cascade ensures that teeth do not change in size randomly and so are integrated along the row. If both the upper and lower tooth rows were under the control of the inhibitory cascade, then relative changes in tooth size could be synchronised between the two. This coordination would result in the maintenance of occlusion during development, facilitating evolutionary change to more precise occlusion. We analysed relative tooth size in two major clades of mammals that diverged ~160 Ma, primates (including fossil hominoids and subfossil lemurs; n=65 species) and marsupials (n=70 species). Our results show that the inhibitory cascade patterning is synchronised between the upper and lower jaws as evidenced by similarities in the slope and reversal point of the inhibitory cascade. We establish that the integration of mammalian teeth is largely controlled by the inhibitory cascade, enabling more complex interdigitation required for precision chewing in mammals. This mechanism must have been present from very early in the history of mammals and is a fundamental reason for the success of mammals throughout the Cenozoic.

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Diet of brown hyaena (*Hyaena brunnea)* in the presence of a vulture restaurant

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Brown hyaena (*Hyaena brunnea*) are distributed throughout southern Africa, but owing to human population expansion, habitat fragmentation, and deliberate extermination their numbers are estimated to be less than 8000. Owing to their inefficient hunting behaviour, brown hyaenas are primarily scavengers of carcasses or opportunistic hunters of small mammals. Our study took place on Mogales Gate Biodiversity Centre, a 3060 ha reserve in the Gauteng Province of South Africa. Although no large predators such as lion (*Panthera leo*), cheetah (*Acinonyx jubatus*) or wild dog (*Lycaon pictus*) occur on Mogales Gate, there is a well-established vulture restaurant which is regularly supplied with carcasses of domestic species from surrounding farms as well as hunting left overs. Brown hyaena faecal scats were collected from the study area over 12 months and then analysed using standard techniques to identify species being fed on by the hyaena. Six dietary categories were identified from the scats, with a mean of 2.5 and 1.9 dietary categories per scat in the dry and wet season respectively. Large mammal remains were found in all analysed scats, with domestic pig being the most abundant in both the dry (92.6%) and wet season (85.4%). Our study suggests that brown hyaena on Mogales Gate incorporate at least 22 mammal species into their diet, the majority of which are large mammals supplied as carrion at the vulture restaurant.

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Altered river flow influences hippopotamus spatial use and the scale at which they alter the chemistry and biology of rivers

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In sub-Saharan Africa, many rivers are ephemeral and experience reduced hydrological flow during the dry season. The duration and intensity of these reductions in flow have been exacerbated regionally by increases in water abstraction and other anthropogenic modifications of watersheds and will be further intensified by climate change. Reduction in water availability is likely to have profound effects on the behaviour and spatial distribution of the common hippopotamus (*Hippopotamus amphibius*). *H. amphibius* is an ecologically important species because it transits between aquatic and terrestrial ecosystems and is a substantial vector of terrestrial subsidies into aquatic systems, thereby potentially promoting abundance and diversity of aquatic life. We hypothesized that in fact this role will be reversed during periods of extreme low flow and that nutrient overloading will negatively influence aquatic biodiversity. We explored effects of nutrient loading by *H. amphibius* on a historically perennial river in central Tanzania that, as a result of human modification, dries down seasonally into a series of isolated physically and hydrologically similar pools that host a wide range of densities of *H. amphibius*. Temporal patterns of abundance of *H. amphibius* as well as the chemical and biological aspects of the river ecosystem were assessed over a six-month period. GPS-collared *H. amphibius* yielded data on movement patterns of individuals as they responded to reduced flow and revealed the spatial scale over which *H. amphibius* impact the aquatic environment.

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Comparative movement ecology of four sympatric rainforest frugivores

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It is hypothesized that increased brain size and spatial cognition may lead to more efficient routing to food resources. This efficient travel behavior may have important fitness benefits for many mammal species. To address this question, we compared the travel behavior of four sympatric frugivores feeding primarily on a single fruit species. We used drone flights to create a georeferenced photo mosaic of the rainforest canopy on BCI, Panama and then identified 1402 flowering *Dipteryx panamensis* trees based on their purple color. We then tracked four species with collars set to take GPS locations at 4 min intervals. We developed a cluster analysis tool to determine if collared individuals stopped and ate at particular fruit trees. We found significant differences in the number of fruit trees visited per day, the number of trees visited per distance traveled, and inter-tree distances between our four mammal species. We also observed notable differences in home range use and travel routes between the four species. Our results are partly consistent with the hypothesis that larger brains lead to more efficient travel routes, but also reveal that species differences in locomotion and diet may exert large influences on how animals travel through their environment.

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Habitat use by the greater bilby (*Macrotis lagotis*), bridled nailtail wallaby (*Onychogalea fraenata*) and numbat (*Myrmecobius fasciatus*) ten years after release into a predator-free area of conservation fencing.

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Over the last 200 years, the distribution and abundance of critical-weight-range mammals in Australia has declined, with many species now locally extinct or confined to small isolated refuges. In 2005, the bilby (*Macrotis lagotis*), bridled Nailtail wallaby (*Onychogalea fraenata*) and numbat (*Myrmecobius fasciatus*) were reintroduced into part of their former range, a predator-free 8,000 hectare area of conservation fencing at Scotia Sanctuary in south-western New South Wales. Our study follows previous work on the habitat selection of these species conducted upon release 10 years ago (Finlayson et al. 2008). Our study examined differences in habitat selection for these species following multiple generations in a predator-free and area-restricted environment.

We used spotlighting data over 3 seasons at Scotia Sanctuary to identify habitat preferences for these species. We used a Utilization Distribution (UD) analysis to test habitat preferences within the fenced enclosure. We created kernel density estimates (KDE) from spotlighting location records for each species, taking into account detectability, the restricted area and location of the fence. We then used quasi-poisson generalized linear mixed models with the density scores for each species fitted as the response variable, and habitat type fitted as a predictor variable, with distance from spotlighting transect fitted as a random effect.

Our findings will be used to inform future translocations, fence locations and outside-the-fence releases of these species. Identifying how the habitat preferences of these species differ in the absence of key threats is critical to understanding how predator-free areas of conservation fencing can be used in a recovery and re-wilding context.

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Flexible home ranges in the agile wallaby. A bigger house only when needed.

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Despite the widespread distribution and common nature of agile wallabies, the ecology of this species remains poorly known. Only a handful of studies have explored this species' habits. The only comprehensive studies comprised their biology and reproduction in captivity, and a handful of studies concerning their diet and behaviour under very specific conditions. Here we shed some light into the species' home range, one of the most basic ecological characters of this species that, until now, was barely explored. We fitted 30 agile wallabies (15 males and 15 females) with VHF collars, in pastoral land under two different production managements (pastures under no irrigation and under irrigation). We used triangulation towers to estimate the position of each individual at 4 tracking sessions (sunrise, midday, sunset and midnight), across 4 sampling periods of 10 days, from June to August 2016. We found significantly larger home-ranges than previously reported during the dry season (31.8 ha vs 15.3 ha for females and 30.2 ha vs 24.6 ha for males), and we found no significant differences between the sexes. The only difference detected was dependent on the type of habitat the individual inhabited, with wallabies in non-irrigated pastures having home ranges twice as large as wallabies in irrigated areas (43.2 ha vs 18.8 ha). This suggests a high level of flexibility for this species that is potentially dependent on the constraints imposed by the responses available.

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Intra- and interspceific variation of skull morphology in the two species of East Asian weasels

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We investigated geographic variation in skulls of Japanese and Siberian weasels, and compared variability between the two species using multivariate analyses. In the Japanese weasel, some skull shape variables showed variation correlated with some climate variables. Cluster analysis using Mahalanobis distance showed few clustering patterns related with geographic affinity not in concordance with the clustering pattern of mitochondrial DNA sequence which consisted of two main clades: Honshu and Kyushu-Shikoku clades. In the Siberian weasel, multivariate analyses with an emphasis on insular variation revealed that the skull size of insular populations tended to be smaller than that of continental ones, but no geographic and environmental related variation was observed. In accordance with the phylogenetic pattern of mitochondrial DNA sequence, he Taiwan population is morphologically more distinct from Korean and Tsushima populations. Comparison of variability between the two species revealed that the skull morphology of the Japanese weasel is more variable than that of the Siberian weasel. It seems to be related with a genetic variation that is higher in the former species. These complicated patterns of variation in the Japanese weasel may be formed by a mixture of genetic variation related with migration history of the ancestors of this species and their adaptation to various environments of the Japanese archipelago.

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Olfactory speciation in Eurasian badgers *Meles* spp.: Diversity among Japanese and European badgers

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All carnivores are macrosmatic and use olfactory signals for intra-specific communication. Many studies have analysed the information content of these signals and speculated on their role in group-cohesion, individual recognition, and fitness advertisement, but only few studies are concerned with olfactory discrimination of closely related species. Badgers, *Meles* spp., have a large geographic range with three, partially sympatric species: *M. meles*, *M. leucurus*, and *M. anakuma*. They possess a unique subcaudal gland, that encodes reproductive status and fitness-related information, and they use its secretion for reproductive advertisement, courtship and mate-guarding. Evolutionary theory predicts that speciation should enable members of distinct species to recognise each other as ‘aliens’, whilst despite of their large geographic range, the general composition of each species’ secretion should remain similar over distance and evolutionary time to allow same-species recognition. Here, we used GC/MS to compare subcaudal gland profiles of adult badgers (n = 41) belonging to two different species ($n_{M.meles}$ = 25; $n_{M.anakuma}$ =16) trapped at 4 different locations (*M. meles*: UK = 12, Bulgaria = 13; *M. anakuma*: Tokyo = 12, Kochi = 4). *Meles* secretions contained 31.4 ± 8.3SD components, of which 10 occurred in both species, but only 4 in every sample, potentially

indicating a genus-specific scent-component. Nevertheless, *M. meles* and *M. anakuma* differed significantly in their scent-profiles, both in presence and relative abundance of components. While the two subpopulations of *M.meles* could not be distinguished statistically, *M. anakuma* scent-profiles differed significantly between the Tokyo and Kochi populations, suggesting more advanced speciation.

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Estimated seed shadow generated by martens (*Martes* spp.): Comparison with forest-dwelling animals

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To evaluate the seed shadow generated by wild Japanese martens (*Martes melampus*), we combined data on their ranging behavior obtained from the northern foot of Mt. Fuji, central Japan (7 males and 3 females) with data on gut passage time obtained from martens in Toyama Municipal Family Park Zoo (3 males and 1 female). The movement distances varied, and mean distances for 0–1, 2–3, and 4–5 h intervals were 152.4, 734.7, and 1,162.4 m, respectively, with no significant sex difference. The mean gut passage time of ingested seeds was 7.4 h (range: 0.6–51.7 h), and two-thirds were defecated within 12 h. Seeds of fleshy fruits were frequently transported 501–1,000 m, and 20% of ingested seeds were transported >1,000 m from the feeding sites. We found positive correlations between body size and home range of the animals in Japan and their seed dispersal distances. Compared to sympatric small-to middle-sized animals in forest (such as monkeys, raccoon dogs, and birds), their dispersal distances were much longer, although shorter than that of Japanese black bears. We concluded that Japanese martens are medium-range seed dispersal agents that could transport seeds from the source to open habitats, conducive for germination and/or growth, partly due to scent marking. We also would like to review corresponding data for other martens in America and Europe (*M. americana* and *M. martes*), and study the similarity and/or difference in relative importance of martens as seed dispersal agents.

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Can we use conditioned taste aversion to mitigate cane toad impacts on northern quolls?

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The invasion of toxic cane toads (*Rhinella marina*) has caused local extinctions of populations of the endangered northern quoll (*Dasyurus hallucatus*). Rather than attempting to halt the toad invasion, we trialled a novel method that used conditioned taste aversion to modify quoll behaviour. In the laboratory, we offered 'toad aversion sausages' to 25 captive northern quolls and measured their feeding responses when presented with a dead adult toad and/or a live toad metamorph the following evening. In the field, we offered toad sausages to wild quolls at bait stations in the Central Kimberley, Western Australia. Captive quolls that consumed a single toad sausage subsequently avoided dead adult cane toads and refused to attack live metamorph toads. Field trials showed that wild northern quolls readily consumed toad-aversion baits more frequently than non-target species inhabiting the study area. Through the use of Spot ID analysis software, we quantified bait uptake by individual quolls and the proportion of wild quolls that consumed baits. Furthermore, we were able to quantify non-target species activity and uptake in association with bait. Our results suggest that toad-aversion sausages can be used to train wild quolls to not eat cane toads. Further work is needed to determine whether baiting can enhance population viability. Nonetheless, our results suggest that broad-scale deployment of toad aversion sausages should be feasible, and could be used by wildlife managers to prevent quoll extinctions at a landscape scale.

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Small mammal roadkill surveys: Implications of short carcass persistence and recommendations

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Roads are important features in the landscape that can result in biodiversity loss. Roadkill surveys are a common method used to determine the vulnerability of species to roads. Surveys are done by patrolling roads in vehicles or walking, and collecting data associated with any wildlife mortality. Like any method, the validity of data collected via roadkill surveys hinges on avoiding or accounting for major biases. Carcass persistence is considered the most important factor that can bias the accuracy of roadkill estimates, and small mammals are particularly prone to bias due to their size. The purpose of this study was to test if season (winter vs. spring), land use (agricultural fields vs. forests), and placement on road (shoulder vs. middle of road) affect the detectability of small mammal roadkill. I used a variety of roads in southeastern Wisconsin, USA, that differed in the aforementioned factors to drop dead feeder rats (purchased commercially) to simulate roadkill of small mammals. I conducted surveys every 12 hours to check the detectability of the feeder rats. My results show that 90% of carcasses disappeared within 24 hours. In addition, season, land use, and position all affected the removal rates of small mammal roadkill. Anecdotal evidence suggests that many carcasses were removed by crows (*Corvus brachyrhynchos*). My results support the notion that the mortality

of small mammals may be underestimated in roadkill surveys, and precautions should be taken to minimize or account for these biases.

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Forelimb adaptations to digging in the quenda (*Isoodon obesulus fusciventer*)

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Many mammals dig, either during foraging to access sub-surface food resources, or for shelter. Digging requires large forces to be generated by muscles and transmitted to the soil via the skeletal system, and thus digging mammals tend to have characteristic adaptations that reflect their digging ability. Bandicoots (Marsupialia: Peramelidae) dig mainly for their food, searching for subterranean food items including invertebrates, seeds, and fungi (truffles). They have musculoskeletal adaptations to digging, including shortened, robust forelimb bones, large, powerful muscles, and enlarged muscle attachment areas. We investigated how these adaptations develop in the quenda (*Isoodon obesulus fusciventer*) by examining 29 males and females of a range of body size (260–1,840 g). We measured muscle mass, pennation angle, and fascicle lengths to calculate physiological cross-sectional area (PCSA), a functional estimate of maximum force, and made corresponding measures of bone architecture. Overall, we discovered total forelimb mass was significantly larger in males in absolute size, however only two individual muscles showed a significant different between the sexes. Positive allometry in muscle growth was seen in 20 of the 29 muscles, with only 9 of these having significant differences in growth rates between males and females. Muscles that were identified as digging muscles did not have significantly different growth rates compared to non-digging muscles, indicating their growth is influenced by body size rather than functionality.

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The use of non-invasive genetic sexing of echidnas from hair and scat samples for captive management and conservation

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The sex of an echidna cannot be easily determined by their appearance as they lack gender specific external features such as a scrotum. Non-invasive approaches to distinguish males from females have a number of applications in captive management and breeding programs as it removes the need for intensive handling and ultrasounds. Systematic sexing from hair and scats can also be used to address questions about sex ratios in the wild. Monotremes have an extraordinarily complex sex chromosome system, where the male echidna has 5X and 4Y chromosomes. Our systematic identification of X and Y specific sequences can be used to determine the sex of monotremes. Here, we have established a non-invasive PCR based technique using hair and scats to determine the sex of echidnas in wild and captive populations. Using as few as 10 echidna hair follicles or 300 mg of dried scat, genomic DNA was extracted followed by PCR amplification of two Y chromosome (male-specific) genes and one X chromosome gene; *Crspy*, *Amhy* and *Amhx,* respectively. Eight echidnas from the Perth Zoo breeding program were sexed using this technique, revealing a strong female bias, not uncommon for captive bred mammals. These results are aiding in the husbandry and continued breeding of this captive population. We have also successfully sexed a number of wild echidnas to begin exploring sex ratios in the wild. We are currently expanding the use of this technique in conservation, captive breeding and management of these iconic mammals throughout Australia.

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Small mammal landscape corridor usage in a fragmented grassland ecosystem in the Mpumalanga Province, South Africa

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The function of landscape corridors in terms of how characteristics such as width influence their usage by animals in a fragmented landscape has been a topic of considerable debate, restricted by lack of empirical data. This implies the need for further research, especially to generate data on mammal corridor usage, as mammals are the most sensitive to potential threats on a fragmented landscape scale. In the Mpumalanga Province in South Africa, the Mpumalanga Biodiversity Sector Plan (MBSP) was developed, containing a corridor connectivity map based on landscape features and electrical circuit theory. We aimed to resolve the lack of empirical data within the MBSP and investigated the number of mammal species and individuals that made use of these landscape corridors in a fragmented grassland ecosystem and if this was influenced by their width. Methods included ArcGIS analyses on structural corridor characteristics such as width and live trapping (using Sherman traps) of small mammals inside, outside and in the opening of corridors with widths of 100-200 m (narrow) , 200-300 m (medium) and 300-400 m (large). This research shows that the corridors in the province are actively used; significantly the most mammals were found inside the corridors. Species assemblages did not differ significantly. Preliminary results showed that corridor width is not a significant variable for either number of individuals and species. Even narrow corridors were shown to provide connectivity, but are thought to act as bottlenecks. Therefore, these corridors should be given priority for conservation planning in the developing landscape of Mpumalanga.

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Using a unique take on citizen science to conserve a unique species: Thirty years of citizen science and koala conservation in New South Wales

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Citizen science is a maturing scientific tool in which members of the community (citizens) are included in the scientific process, often with a focus on data collection. Our take on citizen science provides opportunities to look at longer temporal and broader spatial scales compared to both traditional field studies and traditional citizen science. Citizen science projects work well for studies of koalas because there is wide community interest in the species, it is instantly recognisable, sightings tend to be well remembered, and members of the public will likely have opinions on the species. Over the last 30 years, our data collection on koala populations using citizen science has included citizens directly observing koalas during a survey, recording past observations of koalas on maps, and providing perceptions regarding koala population change which can be evaluated. It is the latter two methods, focusing on the memory of citizens, rather than immediate sightings, that best allow koala citizen science projects to cover broad geographic areas and long time frames. These methods engage a broad cross section of the community, including many who would not consider themselves citizen scientists, and in doing so engender a greater sense of ownership of the results and a willingness to accept management actions to conserve koalas .While these methods rely on the iconic nature of the koala, and their application is limited in less recognizable species, conservation of charismatic species can contribute to social acceptance of biodiversity conservation in general.

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Using key wildlife species to inform conservation planning in the Cerrado and Pantanal of Brazil

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White-lipped peccaries (WLPs; *Tayassu pecari*) play a major role in their ecosystems and are increasingly susceptible to environmental threats. Their large ranges and herd sizes, plus diverse resource requirements, make them vulnerable to habitat fragmentation and degradation in the Atlantic Forest, Cerrado, and Pantanal biomes, where 89%, 50% and 20% of original vegetation cover, respectively, have been lost to deforestation. We show how WLPs are useful tools for guiding landscape-level conservation planning and protecting regional biodiversity. Camera-trap surveys of medium to large-sized mammals in Cerrado forest fragments showed that WLPs were restricted to relatively large forest fragments and had less tolerance for degraded habitat compared to other species, such as tapir, agouti, and collared peccaries, showing their value as sensitive bioindicators of intact native habitat. We also evaluated within- and between-biome impacts of deforestation and fragmentation by analysing WLP herd home ranges in pristine and relatively-disturbed areas. In both the Pantanal and Cerrado, home ranges were larger in relatively-disturbed compared to pristine regions, 51% and 54%, respectively (95% Kernel). Comparing between biomes, we found that WLP home range was 38% larger in the Pantanal. We discuss fruit diversity, abundance, and keystone species to explain this interbiome range difference. By comparing WLP ranges across biomes and between landscapes with different disturbance regimes, we assess the status of WLP populations and identify key factors contributing to population declines. We demonstrate how these data can be used for conservation planning, i.e. identifying strictly-protected reserve areas and degraded corridor areas for restoration.

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The evaluation on impact of land-use change on human-elephant conflicts in Lahad-datu since 1990's, Sabah, Malaysia

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The Asian elephant (*Elephas maximus*) is one of the most important key species for biodiversity conservation in Borneo. After logging and land-use changes on areas of natural forest during the last half century, their habitat was fragmented and degraded. As a result, human-elephant conflicts are increasing recently. People are seeking solutions and mitigation for issues, but only few basic data such as issue/damage visualised maps exist. It is necessary to build an effective strategy based on objective facts for co-existing with elephants. In this research, we evaluated the impact of land-use change on issues, using emergency handling records taken by Sabah Wildlife Department at Lahad-Datu area during 1989 to 2000. From a total of 335 records, we picked up 237 records with location information. We estimated land-use change by Landsat satellite images. We found there are four hotspots (H-1 to H-4). H-3, located near Lahad datu town, has the highest conflict frequency during this decade (31 times). Even recently the issues are still continuing. Second highest was H-2, located at 15 km west of Tabin forest reserve (FR) border. This area had big issues until 1995 but it has stopped, because the all forest was logged around this area then. In conclusion, distance from FR border had a strong impact on the frequency of issues. Since H-1 and H-3 were located between FRs, conflicts still continue today. However, H-2 and H-4 were already isolated from core habitats. We believed this result can be used for recent human-elephant countermeasures.

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Movement and landscape use by an ecosystem engineer in agricultural lands

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Pockets of native habitat embedded in agricultural lands are becoming pervasive throughout the world, and their importance to mitigate biodiversity loss is increasingly recognized. White-lipped peccaries (*Tayassu pecari,* Cetartiodactyla, hereafter WLP) are social forest ungulates that provide important services to their ecosystems. In this study, we GPS-tracked twenty white-lipped peccaries from ten herds (~two individuals/herd) in cattle ranches of the Cerrado and Pantanal, in Central Brazil. Preliminary results show that, in the Cerrado region, although only 33% of the region is covered with native forest, and mostly in patches smaller than 0.01 km^2, WLP herds continue to use predominantly the native forests (in average, 89% of locations/individual were in native forests, ranging from 74 to 96%, N = 10). Additionally, they are found mainly in larger patches. Two herds (four animals) had 94-99% of their locations in the two largest patches of the landscape (~500 and 700 km^2). Two other herds (four animals) had 98% of their locations in three patches ranging from 8, 22 and 47 km^2. Finally, two individuals living in a more fragmented portion of the landscape, had more than half of their locations in a few fragments larger than 7 km^2 and 40 km^2, respectively. Furthermore, the herds in the more fragmented portion of the landscape seemed to preferentially move from one patch to another using corridors of gallery forest. Our results indicate that large and well-connected native habitat is fundamental to ensure that these important ecosystem engineers continue to occur in agricultural lands.

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Movement and habitat use of sika deer in Japan's largest wetland

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Despite being a widespread and important ungulate in wetland ecosystems, scientifically applicable information of sika deer *Cervus nippon* do not exist in Japan. Understanding seasonal movement of deer will not only clarify habitat use, it will also lead to better management and conservation of wetland ecosystems. Kushiro Shitsugen National Park (KSNP) is the largest wetland ecosystem in Japan, located in the eastern part of the northernmost island of Japan, Hokkaido. The objectives of this study were to document fine-scale movements of female deer and determine effects of snow cover and hunting pressures on movements in KSNP. Wetland makes up 94.8% of KSNP (forests 3.4%, grassland 1.6% and urban and suburban 0.2%). Thirty-two female sika deer were equipped with GPS collars to clarify their seasonal movement and habitat use during snow cover (SC) and non-snow cover (NSC) seasons from October, 2014 to March, 2016. We calculated 50%-core home-range (LoCoH) and determined movement patterns. Deer were primarily crepuscular. We also calculated Manly's selection index, and concluded that wetland was the most-used land type, but deer preferred forest, urban and suburban, and grassland landscapes over wetland during both

SC and NSC. Over 60 % of deer used only KNSP and never migrated to outside of KSNP. About 28% of deer used KSNP only during SC and the hunting season. The study results showed KNSP was used by sika deer to avoid hunting pressure.

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Genetic diversity and population structure of white-lipped peccaries (*Tayassu pecari*) in fragmented landscapes.

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Populations of large and medium mammals in tropical rainforests have been subdivided and reduced in numbers due to habitat loss and fragmentation. Bottlenecks and restrictions to gene flow may lead to structured populations with low genetic variation, negatively affecting long-term population persistence. Here, we analysed the genetic variability and population structure of a keystone ungulate species, the white-lipped peccary (*Tayassu pecari*). This species is considered “vulnerable” in the IUCN Red List because of local extinctions and population declines throughout its distribution. We collected a total of 380 samples and genotyped 15 microsatellites from areas with different degrees of fragmentation from Pantanal, Cerrado, and Atlantic Forest in Brazil. We expected to find highly structured populations with low genetic diversity in Cerrado and Atlantic Forest because these biomes are more threatened than Pantanal. Contrary to our expectations, we found populations with weak or no signal of genetic differentiation and similar levels of genetic diversity in the three biomes. In addition, we detected no evidence of inbreeding and recent bottlenecks in all populations analysed. Recent isolation or persistence of gene flow among the sampled populations may explain our results. This study serve as a starting point for the genetic monitoring of these populations, and although no population bottleneck, inbreeding and loss of genetic diversity have been detected, the increasing threats to the biomes studied here should be considered in the species conservation and management plans.

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The influence of invasive mongoose on the genetic structure of the endangered Amami rabbit populations

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Invasive carnivores often cause heavy damage to native species on small islands. Endangered Amami rabbit (*Pentalagus furnessi*) populations have been fragmented into a north-isolated population (NI) and a south-large population (SL) caused by predation pressure from the invasive small Indian mongoose (*Herpestes auropunctatus*) on Amami Oshima Island in southern Japan. We investigated the genetic structure of these rabbit populations to determine the effects of fragmentation. We collected rabbit faeces from most of the Amami Oshima Island habitat and sequenced the mitochondrial DNA (mtDNA) control region along with its 5′-flanking region (312 bp) and genotyped eight microsatellite DNA loci. Genetic diversity was lower in the NI than that in the SL population, and F_{st} values between the two populations were significantly higher than zero in both the mtDNA and microsatellite DNA. Bayesian clustering analyses suggested some ancestral clusters of Amami rabbit, but no individual was inferred from a particular cluster. A partial Mantel test supported isolation-by-distance but not habitat fragmentation. These results suggest that the low genetic diversity in the NI population was caused by the small population size after fragmentation; however, the difference in genetic structure between the two populations was caused by isolation-by-distance and the structure has been maintained.

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Trolling the devil genome: Why conservation genomics is important to endangered species survival

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Tasmanian devil populations have declined up to 95% in parts of Tasmania due to the infectious cancer, Devil Facial Tumour Disease (DFTD). In 2003, the Save the Tasmanian Devil Program (STDP) was established to address this threat. Initial research included investigation into the disease, its transmission, latency and potential causes. Genetic research has contributed much to our current understanding of DFTD and the devil’s capability to respond to the disease. Using the Tasmanian devil genome (published in 2012) we have been able to develop species-specific genetic assays targeted to certain regions of the genome, particularly the immune region. These assays have not only been used to answer valuable disease related research questions but also for conservation management purposes. Our research has used these assays to: determine founder relationships of the insurance metapopulation and the consequences for the breeding program; reconstruct the Maria Island pedigree improving island management; genetically assess incumbent wild populations and select the most genetically appropriate individuals for

release; and develop novel methods to utilise citizen science to enhance our understanding of the different genetic diversity across Tasmania, in particular the inaccessible south-west, by asking hikers to collect scat samples. We have integrated our conservation genomic research with real-time feedback to the STDP management team who are responsible for the long-term survival of this iconic endangered species. Our approach of trolling the genome to develop tools to answer a variety of evolutionary, disease and ecological questions has direct applications to other endangered species globally.

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How does the gut microbiome of a specialist herbivore, the koala, respond to and affect translocation success?

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Anthropogenic habitat loss and resource decline as well as ecological imbalances such as overpopulation threaten many mammal populations. One practical strategy available to environmental managers to promptly alleviate these threats is to translocate animals. However, in some instances the translocated animals fail to thrive. Such translocation failures may be caused by unappreciated differences between the source and destination areas. For instance, if the diet available to the animals at the destination location is different from that at the source then translocated animals may not be able to cope with the change. This is likely to be true for specialist herbivores that rely on their gastrointestinal microbiome to digest and detoxify otherwise unpalatable material, particularly if the animals' microbiomes are unsuited to the new diet and cannot rapidly adapt. The koala is one such herbivore that has often been translocated throughout southern Australia due to their over-browsing of particular eucalypt species, leading to habitat destruction and starvation. Previous work in our laboratory has shown that koalas feeding on different species of eucalypt have functionally and compositionally different microbiomes. In the current study, we tracked how the microbiomes of 17 koalas changed over the course of a year after translocation relative to 12 control animals. We investigated whether the initial community composition of the animals' microbiomes influenced the diet, condition or survival of the koalas following translocation. This study will improve our understanding of how the gastrointestinal microbiome impacts a mammal's ability to shift diets after translocation or natural migration.

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Re-introduction of the tammar wallaby (*Macropus eugenii derbianus*) to Kalbarri National Park: Home range, habitat use and notes on survival

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Fauna translocations are a commonly used tool for improving the conservation status of threatened species. A review of translocations undertaken in Western Australia reported the success of 39% of these were unknown due to inadequate post-release monitoring**.** Global positioning system (GPS) data loggers can provide valuable information on survival, habitat use and sociality, and can be particularly useful for cryptic species and translocations in remote locations. This project reintroduced tammar wallabies to Kalbarri National Park (KNP), 600 km north of Perth. We used GPS data loggers, and VHF radio transmitters to determine survival, home range, and time spent in different vegetation types. Approximately two-thirds of collared wallabies died within one year post-release and just over half of the deceased wallabies was due to fox predation. The home range and core area estimations of male wallabies were generally larger than females, and home ranges at KNP were larger than other published studies. Wallabies utilised long undisturbed vegetation with a dense canopy cover during diurnal and crepuscular periods, and a mosaic of recently burnt and >10 years undisturbed vegetation on a variable canopy cover during the typical feeding period. Based on our initial success criteria, this reintroduction was not considered successful due to the number of wallabies that died in the first year post-release. However, the results of the monitoring provided valuable information to inform future translocations of the tammar wallaby and other species.

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Sympathy for the devil: Captive-management style did not influence survival, body mass change or diet of Tasmanian devils after wild release

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The value of captive breeding for recovery programs of endangered carnivorous mammals is often questioned because of low post-release survival reported for founder animals following translocation. The aim of this study was to test the effect of rearing method on survival, body mass, and foraging behaviour of captive-raised Tasmanian devils, *Sarcophilus harrisii*, following release on an offshore island. Twenty-eight captive-raised devils were released onto an island; 19 had been raised in intensive captive-management facilities (IC) and 9 in free-range (22 ha) enclosures (FRE). Survival and body-mass change was compared between IC and FRE for up to 440 days post-release. Devil diet was assessed via scat and stable isotope analysis. A high proportion

(96%) of the founders survived one year post-release. Pre-release captive-rearing method had no effect. Released devils gained an average of 14% of their original body mass, irrespective of captive-rearing method. There was very little difference in the diet of captive-reared devils released onto Maria Island relative to wild mainland. The intensity of captive rearing did not affect the survival of devils released onto Maria Island. This suggests that even devils held in IC facilities retain the innate behaviour required to scavenge and hunt prey. Our study provides preliminary evidence that the release of captive-raised Tasmanian devils onto off-shore islands is a viable conservation action. Captive breeding programs and captive-raised founders can play a viable and valuable role in the conservation action plans for recovery programs of endangered carnivorous mammals.

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Age-specific survival and fecundity of burrowing bettongs (*Bettongia lesueur*) on Heirisson Prong, Western Australia

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Reproduction and survival was studied in a free-ranging population of burrowing bettongs (*Bettongia lesueur*) at Heirisson Prong, Shark Bay Western Australia. A total of 189 pouch young was observed (93 male, 76 female, 20 unsexed). Age-specific survival indicated that males consistently showed a lower survival rate than females regardless of age and young at foot and sub-adults were at highest risk of mortality for both sexes. Pouch young and adult survival was high (77.8% and > 90% respectively). The age at which females gave birth to their first pouch young was estimated to be 215 days (± 10; n = 13) corresponding with sexual maturity at approximately 6.5 months of age. The average fecundity for adult females was 1.30 pouch young (± 0.07, n = 43) over six months which is below the theoretical potential of three pouch young annually.

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Population dynamics and health of self-regulating populations of the burrowing bettong within fenced exclosures in semi-arid environments

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Scotia Sanctuary, owned and managed by the Australian Wildlife Conservancy, is a 65,000 ha wildlife sanctuary in western New South Wales. Two 4,000 ha feral predator-free exclosures have been established on the site, with each supporting populations of several reintroduced locally extinct mammal species. Populations of reintroduced mammals are free-ranging within predator exclosures and entirely dependent on their own foraging for sustenance. Population size of each species is estimated annually, with many exhibiting classic boom-bust cycles. This presentation examines whether seasonal conditions, particularly rainfall, are the overriding factor behind the population dynamics and health of these reintroduced species (size of population, condition of animals, breeding rate), focusing on the burrowing bettong *Bettongia lesueur.* Management intervention of reintroduced species within large fenced exclosures is not a concern where there is evidence of self-regulation by resource limitation.

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Neotropical deer status, conservation trends and future perspectives

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Neotropical deer species have a broad geographic range in vulnerable Latino America ecosystems. Habitat destruction and over hunting have limited deer species to a portion of their former range. Our aim was to perform a review of the current situation of the neotropical deer taxa updating the taxonomy, ecological and conservation situation. Currently, there are 17 cervid species, grouped into six genera: *Blastocerus*, *Hippocamelus, Mazama*, *Odocoileus*, *Ozotoceros*, and *Pudu*. The comparative analysis of the complete *cytochrome b* gene revealed two clades with different evolutionary histories. The use of molecular genetic markers provides evidence to reconsider taxonomic issues. We found that *Mazama* and *Hippocamelus* are not monophyletic genera, having both cryptic morphological species. Particularly under the red brocket deer species need to be described at least two new species and assess geographic range and populations status. Based on the latest Red List™, and Global Mammal Assessment, 58% of the 17 species of Neotropical deer species are threatened and 18% are data deficient. This means that the currently ten species are categorised as endangered, with the updated taxonomical analysis would increase, important to develop conservation management plans for *in situ* and captive breeding programs.

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Genomic diversity and adaptation in captive tiger populations

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While natural populations of large predators decline, captive populations are increasingly being considered as potential reservoirs of genetic diversity because they may house genomic variants that are rare or extinct in the wild. However, the genome-wide effects of long-term captivity and the artificial selection of zoo breeding programs have not been extensively studied. Furthermore, captive programs have limited information on the initial genetic diversity of the individuals that contribute to the founding population, so pedigree-based analyses of inbreeding and diversity statistics may be uninformative to breeding programs. This lack of knowledge of the genetic diversity housed in captive populations inherently inhibits our predictions on the benefits and potential integration of captive populations into the wild. Here, we evaluate the accuracy of pedigree-based diversity analyses compared with those computed by low-coverage genome analyses from tiger populations in the US and India. We also investigate the genomic differences between captive and wild tigers as a first pass at how captivity affects the genomic landscape. Of the three populations kept under AZA management (Association of Zoos and Aquariums), the Amur tiger population is the largest, while the Sumatran, and Malayan populations are considerably smaller and come from smaller founding populations. The analyses from this study provide considerable evidence for using genetics as an additional management tool, in addition to a much needed evaluation of diversity of our captive tiger populations.

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Establishing a conservation evidence base for species of extreme rarity; lessons for Australia from the world’s rarest ape, the Hainan gibbon

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As the global extinction crisis escalates, an increasing number of species are declining to a state of ‘extreme rarity’, persisting as small, geographically restricted populations reduced to a handful of individuals. Conservation decision-making for such species must be rapid, as delays can mean the difference between extinction and recovery, and decisions must be grounded in evidence to succeed. Paradoxically, for species on the edge of extinction, robust data are often unavailable and their very rarity makes data collection challenging. The Critically Endangered Hainan gibbon (*Nomascus hainanus*) is the world’s rarest ape, constituting one population of approximately 25 individuals restricted to one protected area, Bawangling National Nature Reserve on Hainan Island, China. Using the case of the Hainan gibbon, I demonstrate that despite the species’ tiny population size and highly restricted distribution, by adopting a multifaceted approach to clarify key features of the ecology, behaviour, and genetic condition of the last surviving population, it is possible to develop a robust evidence base that can be used to inform conservation planning. I reveal that the Hainan gibbon has a smaller home range than previously thought, the species’ genetic diversity has declined by ~30% from historical levels, and individuals in the remaining population are closely related. Predictive models within a phylogenetic framework suggest that large, polygynous groups may be evolutionarily characteristic for the species. Together, these findings indicate that intensive, carefully planned management is essential for this species, and that an evidence-based approach to the conservation of even extremely rare species is feasible.

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Biodiversity loss of China’s terrestrial mammals during 1970 and 2010

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The Living Planet Index is an indicator of the state of global biological diversity. Based on trends in 977 population time series of 161 terrestrial mammal species, we used the LPI method to set up a population trend index for China's mammal species. The index dropped by 50% from 1970 to 2010. For further interpretation and analysis, the index was subdivided by biome. Index of population trends of forest ecosystem mammals decreased by 78% from 1970 to 2010. Index of population trends of prairie and desert ecosystem mammals increased by 26% from 1970 to 2010. Index of population trends of mammals in farmland and urban ecosystems grew rapidly in the late 1990s, before stabilising, and then started to drop early this century. The index decreased by 38% from 1970 to 2010. Animals’ survival strategies in response to the environment are also crucial factors that determine the fate of the species. The variation trend index based on 67 K-strategist mammals in China indicates that the population size continued to drop from 1970 to the end of last century, before it stabilised early this century. From 1970 to 2010, the population size of K-strategist species dropped by 64%. The variation trend index based on 87 r-strategists species in China indicates that the population size drastically continued to rise from 1970 to the early 1980s, before entering a cyclical fluctuation status. Population size has increased by 36% from 1970 to 2010.

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Using GIS and gazetteers to analyse the extirpations of large mammals under anthropogenic threats, as exemplified in south-east China during the last 500 years

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Incorporating historical data is very important for conservation biology researchers to reduce errors. We use the mammal records from 3,677 gazetteers (Difangzhi, local chronicle) to analyse the distribution change of mammals in South-East China during last 500 years. We select five kinds (in traditional folk taxonomy) of large mammals—tiger, leopard, bear, deer and primate as indicative species and incorporate human population data and farmland area data of each count as the representation of anthropogenic threats. We sort the data into 4 periods, and analyse the diachronic change of human, farmland and mammal distribution by geographic information system (GIS). The results show that: With the human population and the farmland area booming, the mammal habitats are reduced by steps; as shown in the map, the geographical reduction directions of mammal habitats were the same as the expansion directions of the anthropogenic threats; the decline rates of different mammals were different and were influenced by environment factors such as landform. Based on the appearances, we use statistical methods to analyse the relation between the mammal distribution and anthropogenic threats.

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Setting conservation and research priorities for threatened mammals in the Eastern Himalayas

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High species diversity and endemism within a vast area of intact and unexplored landscapes makes the eastern Himalayas a global biodiversity hotspot. It houses 75 globally threatened mammal species including the iconic tiger *Panthera tigris* and snow leopard *Uncia uncia*. We mapped priority areas for 255 native terrestrial mammal species in the Eastern Himalayas using current IUCN Red List spatial data, and identified centres of species richness at a spatial scale of 1×1 km using a GIS framework and the R-package 'LetsR'. To assess the degree of protection to priority areas, we calculated the percentage of a threatened species' range that fell within protected areas, and developed a comparison index to conduct gap analysis and representativeness of geophysical features (physiography, altitude, and eco-regions). Although the extent of protected areas in the eastern Himalayas has increased significantly over the last four decades, the regions' threatened mammal species are still under represented in protected areas and facing substantial anthropogenic threats from habitat loss and illegal hunting. Our results indicate skewedness in the pattern of mammal diversity, afforded level of protection, and distribution of protected areas among range countries. Despite this, Bhutan's network of protected areas and biological corridors is effective in conserving several threatened Eastern Himalayan mammal species at a finer scale. As the Eastern Himalayan landscape is shared by five countries, regional cooperation for effective transboundary research and management through collaborative efforts is necessary, and regional prioritisation of areas for biodiversity conservation is essential for preventing species extinctions.

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Treescape to moonscape: Mitigating the impact of plantation harvest on den use by threatened carnivores in Tasmania

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Under state and federal legislation, threatened Tasmanian carnivore species Tasmanian devils, eastern quolls and spotted tailed quolls must be considered when planning forest practices throughout their ranges. Management for Tasmanian devils and quolls under the Forest practices system is delivered through prescriptions designed to protect the most valuable habitat for these species; potential denning habitat. In 2014 a Tasmanian devil den was discovered within a mature pine plantation during planning for harvest. The site was investigated and management prescriptions were designed to protect the site during the harvesting operation. Infra-red remote cameras were deployed to monitor the site before, during and after harvesting. Footage showed high mammal diversity before harvesting, and after four months post-harvest. What was initially recorded as a devil den was found to be used by different mammal species each spring following 2014. Footage confirms that the same individual devils, including females with pouch young, continued to visit the den site even after harvesting when all mature trees for hundreds of metres surrounding the site had been removed. Management prescriptions implemented to preserve denning habitat for Tasmanian devils has also benefited other threatened carnivore species. The results suggest that threatened carnivores can persist in plantation landscapes even when the habitat structure is vastly altered.

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Changing migration in the Ya Ha Tinda elk population: When, where and why to migrate?

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In most temperate systems, spring migration to high elevations by ungulates is key for increasing energy intake in a variable environment. A trophic mismatch occurs if the timing of migration is not consistent with plant growth either along the migration route or on their summer ranges. Major migrations routes may change over time due to shifts in land use, predation, human disturbance, or their interactions. We used movement data from 305 elk collared on winter ranges of the Ya Ha Tinda near Banff National Park, Alberta, Canada during 2002-2015 to investigate the routes used, timing and duration of migration, and factors associated with the distributional shifts in migrating herd segments over time in a partially migratory elk herd. Timing of migration across years was most closely associated with plant phenology on summer ranges, rather than information on the winter range. Elk moving to low-elevation ranges migrated earlier and were exposed to higher green vegetation early in the calving season compared to residents or elk migrating to high elevations. Individual elk showed strong fidelity to migration routes between seasons and across years, but the proportion of elk that migrated westward to high elevation ranges declined while the proportion of migrants moving eastward to low-elevation summer ranges increased. Average exposure to bear and wolf predation risk and forest practices was similar along migration routes but not on summer ranges. Changes in forage, predation, and land use along migration routes account for distributional shifts in migrating elk over the past decade.

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Evolution of cranial development in marsupials

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Cranial ontogeny in mammals has been quantitatively studied in a number of lineages. In this report, we integrate the information of allometric growth from 15 skull variables that define shape and approximately represent (sensory, mechanical) functions of the skull. We estimated multivariate coefficients of allometry, and their resampled confidence intervals, of those 15 variables for 24 marsupial species from 10 living families, using 4 placentals as comparative outgroups. Confidence intervals were optimised in a well resolved phylogeny. Optimisations show changes in most internal nodes, although we did not detect synapomorphies either in marsupial or placental basal nodes, suggesting the conservation of an ancient therian growth pattern of Mesozoic age. Ameridelphia is defined by a growth rate increase in orbits and the height of the muzzle, and decrease in length of the coronoid process. Australidelphia is defined only by a decrease of the confidence interval of the height of the coronoid process. We detected synapomorphies in almost all subclades (except Dasyuromorpha and Phalangeridae). The variables with phylogenetic signal were those related with growth of the mandible, and marginally, breadth of the braincase and length of the upper toothrow. These results describe, from a developmental perspective, the way skull components evolved in marsupials, and show a remarkable correspondence of cranial ontogeny and marsupial lineage evolution.

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A roadmap to meaningful dingo conservation

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Many top-predators are declining and/or threatened, risking the loss of them and their important ecological roles. For these reasons, conservation efforts are a management priority for many species, but this is not presently the case for dingoes – the most closely related canid to grey wolves. There is strong support for dingo conservation from some sectors, but dingo conservation progress is slow, and is actively opposed by other sectors. Here, we evaluate the conservation status of Australian dingoes in accordance with the current Australian Government's Threatened Species Scientific Committee Guidelines for assessing the conservation status of native species according to the *Environment Protection and Biodiversity Conservation Act 1999* and *Environment Protection and Biodiversity Conservation Regulations 2000*. We also use the International Union for the Conservation of Nature (IUCN) species translocation guidelines to assess the value of translocation or reintroduction as suitable conservation action for dingoes. We further describe six socio-ecological facts about dingoes seldom considered in discourses advocating dingo conservation, and show that consideration of these guidelines and facts raises several substantial barriers to dingo conservation. Perhaps the most important barrier to dingo conservation is the lack of an accepted taxonomic definition for dingoes which, we show, ultimately determines the threatened status (or not) of dingoes and the acceptability (or not) of reintroduction as a suitable action for advancing dingo conservation objectives. We describe the actions required to overcome this barrier in an attempt to advance dingo conservation efforts from just 'talking about it' to actually 'doing something about it'.

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Conservation genomics and metagenomics of wild mammals: advance and perspective

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Along with the rapid development of sequencing technologies, conservation genomics and metagenomics have developed very fast and are now applied to non-model species, especially wild mammals, to provide new insights to properly conserve wildlife. In this talk, I will take endangered mammals, such as giant pandas, red pandas and golden monkey, as examples to summarize recent advancements in these areas and provide some perspectives for future research.

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Decline of small mammals in south east Australia: role of refuges and implications for management

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Longitudinal studies quantifying population changes are required to activate effective management and monitoring regimes. The population dynamics of small mammals in the eastern Otway region of south-east Australia were assessed across the landscape between 1975 and 2007. The aims of this paper were to evaluate the current (2013-17) population abundance of species in the region compared to historical records, to consider current threats and identify management actions. The current status of species was assessed at 40 sites, utilising live-trapping and camera trapping techniques. Trap success rate was compared to long-term data using time-series analyses to identify periods of decline for target species *Antechinus minimus*, *Rattus lutreolus* and *R. fuscipes*. Sites trapped in 2013-2017 predominantly had few or no native species present, compared to previous records of four to seven species. Most species exhibited significant declines (>95%), including two threatened species (*Antechinus minimus, Pseudomys novaehollandiae*). While significant declines were recorded in woodland, forest and estuarine habitats, higher mammal capture rates (20 - 47%) and native species richness (9) were recorded at coastal dune sites, indicating that these habitats provide important refuges for mammals. Control charts identified significant declines retrospectively, and if used routinely would have alerted authorities in a timely fashion enabling management that may have prevented extirpation at some sites. Management actions required include: prevention of further habitat fragmentation; implementation of burning regimes to protect key refuge habitat; and predator control. Effective monitoring is essential to allow an evaluation of the success of management actions.

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Partnering indigenous biocultural knowledge and science: Research and management of the threatened greater bilby on the Dampier Peninsula in the north-west of Australia

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The greater bilby (*Macrotis lagotis*) is an ecologically and culturally important marsupial that has disappeared from at least 80% of its former range. In the extreme northwest of this range, the Dampier Peninsula (approximately 1.6 million ha) represents a stronghold for bilby populations that, like many remaining wild bilby populations elsewhere, largely occur on Aboriginal owned and managed lands and on pastoral leases. The pindan woodland habitat on the Dampier Peninsula is very different to other localities where wild bilby populations are still found. The Western Australian Department of Parks and Wildlife together with Indigenous Ranger organisations have initiated research to determine the status of bilbies and their threats on the Peninsula, and to implement and determine the effects of management on bilby populations. The occupancy survey of bilbies commenced in late 2016 using a standardised sign plot tracking technique that also provides data on the occupancy of predators and herbivores, such as domestic and unmanaged stock, as well as habitat variables. Significant populations and threats will be identified during the occupancy survey, monitoring of key populations will be undertaken, and threat management will be initiated. The activities will be undertaken in partnership with Indigenous Rangers. Study outcomes will guide future management strategies to ensure the persistence of wild populations and in so doing reinforces the benefits and importance of engaging Indigenous Rangers and capturing Indigenous Biocultural Knowledge in research programs and management activities for threatened mammal species. Preliminary results from the occupancy survey will be presented.

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Evaluating detection methods for a rare small carnivore, the eastern spotted skunk, *Spilogale putorius*

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The eastern spotted skunk (*Spilogale putorius*) is an uncommon, diminutive carnivore historically distributed throughout much of the Central Great Plains, Appalachian Mountains, and peninsular Florida in the United States. While historically numerous, populations of the plains subspecies (*S. p. interrupta*) have plummeted range wide and the skunk is now being considered for listing under the U. S. Endangered Species Act. We examined the current status of the eastern spotted skunk in Texas by first producing a species distribution model based on museum specimen records. From this model, 10 counties were chosen for field surveys conducted between September 2015 and January 2017. We evaluated both non-invasive (camera traps, track plates) and invasive techniques (live traps) to detect spotted skunks using a 7-day sampling protocol with 40 of each detection device deployed at each site. Spotted skunks were detected in 4 of the 10 sites sampled and all methods detected presence of skunks. Live traps had more detections than either track plates or camera traps. Recent observations of the spotted skunk were also crowd sourced from academia, wildlife professionals, and citizen scientists. With these methods, recent verifiable observations of eastern spotted skunks were recorded in 20 additional Texas counties. With the combination of field surveys, crowd sourcing, and citizen scientists, we determined that the plains subspecies of the eastern spotted skunk is still widely distributed in Texas, although only two areas sampled had relatively high abundance.

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Characterisation of factors influencing male reproductive success in the eastern grey kangaroo (*Macropus giganteus*)

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The eastern grey kangaroo (*Macropus giganteus*) is one of the largest existing marsupials. It exhibits a polygamous mating system, established social structuring, and sexual size dimorphism. As an evolutionary response, males exhibit traits that influence their ability to successfully reproduce. In eutherian species, these can include weaponry, a larger body size and/or higher testosterone concentrations. Limited research has been performed on marsupials, impeding the development of evolutionary theories surrounding this extant mammalian lineage. The present study aimed to identify factors influencing male reproductive success in a free-ranging New South Wales eastern grey kangaroo population. Candidate male body weight, skeletal size, testes size, and testosterone and glucocorticoid concentrations were investigated as potential influential factors. Paternity was assigned to a total of 89 offspring across four breeding seasons, representing male reproductive success. As predicted, body size, indicated by body weight, leg length, testes size and testosterone, significantly influenced male reproductive success. Foot length and glucocorticoid measures had no influence. Such information contributes to the development of broad evolutionary theories across all extant mammalian lineages, as well as providing valuable information to aid the management of wild and captive populations.

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Radiocarbon dating the response of European Late Pleistocene carnivores to climate change

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During the last glacial period, several large carnivore species went extinct in Europe. Both abrupt and gradual climate changes have been blamed for these disappearances, but fossils must be precisely dated to establish whether their presence correlates with climatic events. Radiocarbon dating is a potentially powerful tool, as it directly dates faunal bone and can produce dates up to 50,000 BP. However, current radiocarbon datasets for carnivore species are small and of incomplete geographical coverage. This is partly due to the challenges of dating degraded bone collagen, which is often found in southern Europe. Furthermore, many Pleistocene radiocarbon dates likely underestimate the sample's true age, and dates often come with errors too large to match to high-resolution climatic events with confidence. In this paper, we will show that these weaknesses can be addressed by using robust pretreatment methods. In addition to ultrafiltration, routinely used in the Oxford Radiocarbon Accelerator Unit since 2000, novel compound-specific methods are being used to improve dating accuracy and expand the ability to date poorly-preserved samples. Bones of cave lion, panther, and hyena in southern Europe have been targeted for this study, as these carnivore species have few direct dates and collagen preservation in the region is problematic. When combined into a GIS model with climate records, these new results improve our understanding of how carnivores responded to climate change.

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Predicted Quaternary range shifts and interactions of the lion (*Panthera leo*) and tiger (*Panthera tigris*)

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We model the potential range shifts of lion and tiger populations over the Late Pleistocene and Holocene, to shed light on the potential competitive dynamics between these two apex predators through long-term, glacial-interglacial climate cycles. We focus on the Near East and Indian subcontinent, where both species are historically present, however the study incorporates the full distributions of both the lion and tiger throughout Africa and Eurasia. We employ species distribution models (SDMs) with bioclimatic data to model present-day idealised ranges in the absence of non-climatic, principally human, disturbance. We compare these idealised ranges with a statistically derived bioclimatic stratification layer so as to clearly describe the driving conditions behind each species' distribution. Preferred strata are then considered for time slices at the Last Glacial Maximum and mid Holocene to identify areas of optimal climate for each species. The merits of our approach are considered in relation to the practice of directly projecting models onto past climatic conditions. This novel technique of model explanation allows greater use of expert species knowledge in the evaluation of SDMs, and makes the underlying ecology of the modelling process more explicit. The modelled distributions of lions and tigers throughout the Late-Pleistocene and Holocene are discussed in relation to existing genetic and archaeological literature, to contextualise current knowledge regarding lion and tiger palaeodistributions.

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Using ancient DNA from subfossil remains to characterise past population events

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Past changes in population size, local population replacement, and admixture are difficult to detect based on fossils or genetic data from extant populations alone. Conversely, ancient DNA from subfossil remains allows us to directly observe these events tens-of-thousands of years in the past. North American bison (*Bison* sp.) have emerged as an excellent example of how ancient DNA can reveal complex population histories that are obscured by analyses of palaeontological or modern genetic data. Numerous extinct morphologically-differentiated bison species have been described from the Late Pleistocene (126 – 12 thousand years ago) of North America, including the giant long-horned bison (*Bison latifrons*). However, we have demonstrated that two unequivocal long-horned bison from Idaho possessed a mitochondrial lineage indistinguishable from other North American bison. This suggests either that the long-horned bison does not represent a genetically distinct species or that it underwent significant admixture with other bison taxa, calling into question both the validity of recognised bison taxa and the mechanisms driving the observed morphological variability among bison. Further, increased sampling of ancient bison individuals has revealed spatial/temporal structure in the distribution of their genetic diversity, suggesting that North American bison comprised a continent-wide metapopulation. This population structure – coupled with variable impacts of climate/environmental change at the regional level – may have contributed to the relatively depauperate genetic diversity of modern bison. The complex patterns and processes our results reveal are likely to be common across many taxa, and should influence our interpretation of results from other animal species.

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Extinct bison methylomes using bisulfite sequencing

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Epigenetics encompasses a suite of mechanisms for potential adaptation to rapidly changing environments. We propose that past mammal populations from the Quaternary (the current geological period characterised by dramatic climate oscillations) represent a unique model to study the epigenetic response to environmental cues, and its role in adaptation and extinction. Statistical methods have been developed recently to infer the methylation status of cytosines from ancient mammalian genome datasets, albeit at a relatively low resolution. On the other hand, experimental studies of ancient DNA methylation are impaired by a combination of pronounced DNA degradation and low levels of endogenous DNA in sub-fossil remains. Thus, empirical studies are restricted to a limited number of target loci and a small sample size. Here we present a method to perform whole-genome bisulfite sequencing of ancient DNA extracts. To demonstrate the power of this method, we characterised methylomes from extinct and modern bison from North America, spanning a time range of more than 50,000 years that include key climate cooling and warming events. In conclusion, we developed a method that improves whole-genome bisulfite sequencing data quality and quantity for modern samples, but also provides a unique opportunity to study methylomes from extinct mammals at an unprecedented level of resolution.

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Yucatan Peninsula Late Pleistocene mammal fauna.

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Yucatan Peninsula (México) is a geologically late topographic feature on Mexico´s landscape, but one that contains important faunal complexes, both modern and fossil. Those appearing during the Pleistocene are starting to provide an overall picture of just what that landscape looked like. Both dry and wet deposits have been studied, with data providing a highly diverse fauna containing at least 11 orders, 28 families, 54 genera, and 70 species. Dry caves, like Loltún Cave, have provided a very diverse faunal complex with many small and medium size animals, while wet deposits, like underwater caves, are rich in larger mammal remains, including megafauna. Hoyo Negro is a pit within an underwater cave, and is one of the richer deposits with megafauna, containing at least 12 species of extinct and extant mammals. Extinct species include the highland gomphothere (*Cuvieronius tropicalis*), three species of ground sloth (*Nothrotheriops shastensis*, a new megalonychid taxon, and a mylodontid), and sabertooth cat (*Smilodon* cf. *fatalis*). Modern species include tapir (*Tapirus*), peccary (*Tayassu*), and extralimital records like bobcat (*Lynx rufus*) and coyote (*Canis latrans*). A tremarctine bear (*Arctotherium*) also occurs in the assemblage and represents a range extension of this South American taxon. The fauna includes both Neotropical taxa (sloths, gomphotheres), taxa with Nearctic affinities (carnivores, lagomorphs) and probably some endemic animals, like the megalonychid sloth and tremarctine bear. The presence of bobcat and coyote, and the occurrence of the Shasta ground sloth, indicate a drier and cooler climate in the region during the terminal Pleistocene.

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Stakeholders' perspectives on species management: Prioritising actions to preserve our biodiversity

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While it is well-known that incorporating the perspectives and preferences of communities may lead to better conservation outcomes (i.e. long-term commitments, active participation, etc.), it is not a common practice. The literature describes several techniques to engage with the private sector, government agencies, and communities in conservation planning, but these are not applied mostly due to the challenges of achieving consensus (e.g. timeframe, existing plans, and clashing objectives). The prevalent practice often involves an individual assessment, and then a wait for managers to make decisions. In this project, we identified and incorporated the various perspectives and preferences of different stakeholders in Minjerribah-North Stradbroke Island (QLD, Australia), regarding the conservation of threatened, and culturally relevant species that are being impacted by 2 of the most successful invasive alien species in Australia: feral cats (*Felis catus*) and red foxes (*Vulpes vulpes*). We assessed the priorities and perceptions of multiple stakeholders from community groups, the private sector, and government agencies, in a spatially and temporally-explicit way. This approach reduces the gap between practitioners, the private sector, and community groups, by encouraging involvement and long-term commitment. It provides a platform for better understanding between participants, reduces management uncertainties, and facilitates the development of a unified management plan for culturally relevant, threatened, and invasive alien species in highly-vulnerable environments such as islands.

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All bark and no bite? Impacts of recolonising gray wolves on sympatric prey are primarily non-consumptive in a managed landscape of western North America

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Apex predators are increasingly recognised for the top-down impacts they can trigger by consuming and intimidating prey. These ecosystem effects have largely been demonstrated in wilderness and protected areas, however, raising questions about the extent to which they manifest in human-dominated landscapes. Accordingly, we took advantage of ongoing gray wolf (*Canis lupus*) recolonisation of a human-influenced region of the state of Washington, USA, to examine the impacts of these canid predators on survival and behavior of two sympatric prey species, mule deer (*Odocoileus hemionus*) and white-tailed deer (*O. virginianus*). Analysing data from GPS-collared deer (61 mule and 59 white-tailed deer) collected at four study sites (two with wolf packs and two wolf-free areas) over a period of four years (2012-2016), we found that the presence of wolves had little impact on survival in either prey species. Indeed, wolves inflicted only two mortalities over the course of our investigation; humans (recreational hunters) were instead the chief source of mortality. By contrast, both deer species responded behaviorally to the risk of predation, with mule deer exhibiting large-scale spatial shifts that reduced overlap with wolves and white-tailed deer manifesting fine-scale shifts to gentle terrain that facilitated their means of escape post-encounter (fleeing). Our results add to a growing literature suggesting that the effects of top predators may be dampened in human-dominated systems. They also suggest, however, that non-consumptive effects of these species (e.g., costly defensive adjustments by prey) may be more resilient to human presence than those stemming from direct predation.

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Morphometric, karyologic and mtDNA characterization of *Sciurus vulgaris* and *S. anomalus* in Turkey

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A total of 16 *Sciurus anomalus* and 10 *S. vulgaris* samples were collected from distributional areas in Turkey. Standard and geometric morphometric approaches were used to assess morphological characteristics of *S. anomalus* and *S. vulgaris*. Karyology was also studied for both species. Two mtDNA genes Cytb (959bp) and dLoop (482) were sequenced from both species to find the extent of genetic variation and the phylogenetic relationships. Standard morphological measurements were statistically tested for 26 cranial measurements and showed significant differences between the two species ($P<0.05$). A total of 13 landmarks from mandibles and 15 landmarks from the ventral side of the skull were utilized to analyze the shape variation. Based on the mandibles, the two species showed significant differences ($P=0.013$), but the ventral side of the skull did not ($P=0.069$). Karyological analyses indicated the same chromosome number ($2n=40$) but there were differences in the NF (*S. vulgaris* 76 and *S. anomalus* 80) and NFa (*S. vulgaris* 72 and *S. anomalus* 76) values. Both mtDNA gene regions separated two species into two different groups. Cytb sequences combined with the sequences obtained from Genbank and the sequences from both species were clustered with appropriate Genbank *anomalus* and *vulgaris* sequences. Two *S. vulgaris* populations in Turkey partially separated from each other. All northeast samples and the Thracian samples were separated, while the Edirne samples (from Thrace) clustered with the northeast squirrel population. The genetic distance between the two species based on dLoop sequences was $d=0.182\pm0.020$.

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Responses of mammals to thinning of regrowth in two contrasting vegetation communities

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Thinning has been proposed as a restoration tool to reduce competition between water-stressed young river red gum trees and increase structural complexity of dense cypress pine regrowth. Yet, little is known about the effects of thinning on mammalian communities. To examine this, we undertook two separate studies: 1. Chronosequence study in cypress pine communities in the Pilliga, NSW, and 2. A Before-After-Control-Impact, large-scale thinning experiment assessing short-term responses in river red gum forests along the Murray River. In both studies, we measured effects of thinning on bats, non-volant mammals, and habitat (total, dead and hollow stem density, and CWD volume). As expected, thinning significantly reduced stem (total and dead) density in both vegetation communities and this was reflected by increased bat activity and diversity, which was maintained for up to 40 years in cypress. Hollow-tree density was not affected by thinning. Bat composition was also affected by thinning in river red gum, with edge species more active in thinned sites. CWD volume increased with thinning in both vegetation communities, but was influenced by type of thinning (commercial vs non-commercial). Non-volant mammal diversity and activity was not affected by thinning in either vegetation community, though composition in river red gum shifted with less activity of common brushtail possums and foxes at thinned sites in relation to controls. Results are consistent with the view that bats respond positively to reduced vegetation density, while non-volant mammal responses were inconsistent and may be related to other habitat features (e.g., ground cover) and predator activity.

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Fenced and fragmented: Genetic management of carnivore metapopulations in South Africa

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Habitat loss and fragmentation are major drivers of biodiversity loss, with large carnivores being particularly vulnerable due to their large home ranges. These species were once widespread across the African continent but over the past 100 years their ranges have decreased by more than 75% and there is continued pressure on the remaining free-roaming populations. In South Africa (SA) the land management strategy that includes fencing of wildlife has restricted African lion (*Panthera leo*) and African wild dog (*Lycaon pictus*) to protected areas (state and private). This resulted in increasingly small, isolated population islands surrounded by a sea of anthropogenically-transformed landscapes resistant to carnivore dispersal. SA has three of the IUCN-proposed Lion Conservation Units in large Transfrontier Parks and Conservation Areas; in addition, approximately 800 lions in 47 smaller, fenced reserves also hold conservation value. Wild dog populations historically have been small and patchy but *Ne* has been further reduced and isolation increased by human impacts. Despite high mobility and long-distance dispersal, SA wild dogs are genetically differentiated from East Africa, separated by a large zone of admixture. In the late 1990's a managed

metapopulation approach was adopted to mimic natural processes and connectivity of wild dog populations. The current SA managed metapopulation comprises 19 packs in 11 reserves. A similar approach has been adopted for lions more recently. We demonstrate how inferences from genetic data provide perspectives across multiple temporal and spatial scales, to inform this managed metapopulation approach and to contribute to long-term species viability of large carnivores.

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Genomic signatures of marine mammal evolution: molecular footprints of the transition from land to sea

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Cetaceans are among the most specialized mammals and are completely dependent and adapted to the aquatic environment. The adaptation to this lifestyle has required complex changes of physiological systems, behavior and morphology. The paleontological history of 50 millions of years of evolution are well documented, but less known is the molecular trajectory behind the transition from land to sea. Identifying genes that have been subjected to selection pressure during cetacean evolution would greatly enhance our knowledge of the ways in which genetic variation in this mammalian order has been shaped by natural selection. This talk will present results from a genome-wide scan for positive selection and case-by-case analysis of candidate loci associated with adaptation to a fully aquatic life from a terrestrial life. Regarding the case-by-case analysis, we studied the molecular evolution of globin genes (hemoglobin and myoglogin) given their important role in hypoxic adaptation. Also, given the importance of hair loss in cetacean lineage to aquatic adaptation, we combined the available genomic information with phylogenetic analysis to conduct a comprehensive analysis of the evolutionary patterns of keratin gene clusters. Moreover, we investigated the molecular evolution of Hox genes in cetaceans and other aquatic mammals (pinnipeds and sirenians) once these genes are known to have important roles in establishing identity to the body parts during development. Taken together, the genome-scanning and the candidate genes analyses provide an insight into the type of biological processes that have been targets of selection in cetacean evolution.

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Generating immunogenetic resources to infer the evolution and diversity of the major histocompatibility complex of wild Suidae and Tayassuidae

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The family Suidae (pigs), mostly wild, and their closest living taxa Tayassuidae (peccaries) play important roles in their natural environment, agriculture and in emerging/zoonotic diseases. The genetics of the immune system of the domestic pig (*Sus scrofa*) in particular the major histocompatibility complex (MHC) has been extensively studied. However, there is little knowledge of the immunogenetics of wild pigs and peccaries. To address this, we used DNA capture with probes designed from the domestic pig genome to generate MHC genetic resources from 11 wild species and investigated the evolution of class Ia and Ib genes. This method shows relatively good efficiency when implemented on Suidae but was limited for Tayassuidae. As a first step, we generated consensus sequences (147 genes) from each species for comparative analyses. Our results show that: i) the repertoire of Ib and Ia genes is present in both Suidae and Tayassuidae in contrast with the previous hypothesis; ii) these genes underwent a series of duplications before these taxa diverged from the common ancestor ~35Ma; iii) all genes have evolved independently from each other after speciation; iv), there are genetic patterns of differentiation for most of the Ia and Ib genes between Eurasian and sub-Saharan Suidae; and v) balancing and purifying selection appear to have maintained the MHC diversity. These findings improve our understanding of the evolutionary history of the MHCs and provide genetic resources to further investigate the immune response of wild populations to diseases, including local adaptation of some taxa to emerging diseases.

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Genomic responses to ecological opportunity in the global invasion of Muridae

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The Muridae (old world rats, mice and gerbils) comprising 634 extant species are the most species rich mammalian family. They are exceptional colonisers with multiple transitions among continents of the eastern hemisphere, including at least ten transitions across Wallace's line to reach Sulawesi (7 colonisations), the Philippines (5 colonisations, 2 from Sulawesi), and Sahul (Australia and New Guinea; 2 colonisations, both from Sulawesi or the Philippines). Following these transitions murid rodents have adapted to a wide range of environments (e.g. rainforest, desert, alpine) and ecomorphological niches (e.g. arboreal, amphibious, saltatorial, vermivorous, folivorous). Ecological opportunity theory predicts that these ecological niches should have been filled rapidly through diversification following colonisation. In some cases, the accummulation of lineages is consistent with these predictions, particularly in species of the genus *Rattus.* In other cases, such as the shrew rats of Sulawesi and their relatives, morphological rates of evolution are consistent with early rapid evolution following colonisation. In Australia, transitions between arid and mesic biomes did not occur early but has occurred repeatedly in the phylogenetically-nested genus *Pseudomys.* Here we present rates of amino acid substitutions derived from whole exome sequencing from colonising clades of Indo-Australian rodents to test if protein evolution is consistent with rapid early rates of evolution and if a conserved set of proteins are involved in convergent evolution in morphological, dietary and ecological states.

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Genomic and ecological interactions across woodrat hybrid zones.

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Hybrid zones continue to provide unique opportunities for understanding fundamental ecological and evolutionary processes. In particular, when hybrid zones span sharp environmental gradients they provide insight into how a range of pure and admixed mammalian genomes interact with various ecological and environmental conditions. Here, we present our work on *Neotoma lepida* and *Neotoma bryanti* where these species meet and hybridise at a sharp ecotone between mesic foothill chaparral and Mohave desert scrub. Using genotype-by-sequencing approaches, we find that approximately 15% of the individuals across the ecotone are of hybrid origin, with pure parental types largely restricted to one of the habitat types. Because each taxon has access to different food plants in their respective habitat, and because woodrats are known to have locally specialised diets, we use high throughput sequencing of the *trnL* gene to gain insight into diet breadth in each habitat. The diet of each taxon is largely restricted to 1 or 2 plants that differ between the two habitat types. Further, the primary food plants used by each woodrat species are dominated by distinct toxic compounds that likely require different metabolic specialisations. We suggest that adaptation to different plant toxins may play an important role in determining species interactions at woodrat contact zones, providing a novel mammalian example of how ecological adaptation contributes to the maintenance of species boundaries.

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Post-hybridisation isolation catalyses genomic divergence and geographic structure in weasels

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Contemporary mammalian biodiversity in North America has been shaped by cycles of population isolation and divergence driven by Quaternary glacial advances, and subsequent expansion and contact during glacial retreats. As a consequence of expansion, divergent lineages from independent refugia came into secondary contact, but the extent to which intermittent admixture contributed to contemporary diversity remains poorly explored. We investigated the role of introgression in genomic evolution of a Holarctic mammal, the ermine (*Mustela erminea*) using Illumina whole-genome sequence data. We demonstrate divergence among lineages coincident with 4 distinct refugial centers: Beringia, West, East, and North Pacific Coast (NPC). We also identified multiple bouts of hybridization, including contemporary hybridization at a contact zone along the Alaska-Yukon Territory border, between East and Beringian lineages. An independent and earlier episode of admixture suggests East and Beringia lineages previously hybridised to form the NPC Island lineage, a divergent ermine that is consistent with the coastal refugia hypothesis. Isolated in a coastal refuge during the Last Glacial Maximum, the NPC Island lineage subsequently diverged, suggesting a potentially novel model of hybrid speciation: allopatric divergence after ephemeral gene flow, a process that may be more common in high latitude and insular species. While hybrid-based divergence in this coastal environment has immediate evolutionary consequences and conservation implications for ermine, it also offers an alternative lens for viewing the role of islands as engines of biological diversification.

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Intraspecific transcriptomics, differential expression and genetic divergence

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RNA-seq provides a wealth of information about the genetic makeup and physiological state of targeted tissues or organs. We provide an overview of current uses of transcriptomes to study of differential gene expression in response to environmental challenges. Differential gene expression is commonplace and multidimensional. Kidney transcriptomes across a precipitation gradient, for example, diverge in multiple genes related to water conservation, but also in genes involved in detoxification and immune responses. A special case of differential expression is the co-option of functionally relevant genes for their ectopic expression in novel organs. Associations between differential gene expression and genetic divergence can be established, but genotyping transcriptomic data present several challenges, including paralogy, alternative splicing, and differential allele expression. Our study of kidney transcriptomes shows that genetic divergence varies broadly across genes, but tends to be larger in differentially expressed genes than in the remaining loci.

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Juvenile dispersal determines population survival in the Siberian flying squirrel

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The lifetime dispersal of an individual determines the gene flow and invasion potential of the species. Linking dispersal to population growth remains a challenging task and is a major knowledge gap, for example, for conservation management. We utilized 20 year mark-recapture data on two extensive nest-box populations of Siberian flying squirrels in western Finland to analyze lifetime dispersal patterns and to study relative roles of different demographic rates behind population growth. Natal dispersal means the distance between the natal nest and the nest used the following year, whereas breeding movements refers to the nest site changes between breeding attempts. The movement distances we observed were comparable to distances reported earlier from radio telemetry studies. We observed that breeding movements did not contribute to lifetime dispersal distance. In other words, juveniles were responsible for redistributing individuals within and between populations. Based on an integrated population model, which estimated all relevant annual demographic rates (birth, local apparent survival, and immigration) as well as population growth rates, immigration was the demographic rate which showed clear correlations to annual population growth rates in both populations. That is, flying squirrels may persist in a network of uncoupled subpopulations, where dispersal between subpopulations is of critical importance. Our study supports the view that dispersal has the key role in population survival of a small forest rodent and natal dispersal is the process determining consequences of movement ecology of the species at the population level.

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Its time to move on: Preliminary insights into tiger dispersal using radio collars

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Over the last few years, we have achieved increases in tiger populations as a result of suitable protection measures. Today, tigers are dispersing across the landscape dominated by human settlements in search of habitats and mates. The aim of our research is to understand the characteristics of dispersal that may aid policy making for tiger conservation in a landscape which is developing aggressively. Five tigers were radio-collared and monitored for extensive movement across the landscape. The inter-fix intervals of the collars were 5 hours (inside PA) and 2 hours (outside PA). The radio-collared data for the 5 tigers yielded a total of 3452 fixes. Out of the total locations, 64.94% were observed in non-PAs and only 35.05% were inside PAs. We also characterized the locations based on land use patterns and found that deciduous forests were used the most (52.47%) followed by areas of double/triple cropping (16.94%). The mean step length, i.e. the distance between two consecutive locations, varied significantly inside PAs and outside PAs ($p=0.0034$) for the dispersing individuals. We tested various models, including Brownian Bridge Model, First Passage Time and Bayesian Partitioning of Markov Model, to understand movement characteristics of the animals. Fine-scale telemetry data offers exciting opportunities to study dispersing tigers (movement patterns, behaviour, food habits, etc.), especially outside PAs. Movement ecology has opened up new avenues of research in tiger ecology and holds promise for influencing policy makers to make better informed decisions about corridor management and tigers in human dominated landscapes.

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Here, there and everywhere: Spatial ecology of the red fox *Vulpes vulpes*

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Human land use changes can exert great influence on ecological systems, altering species distributions, animal behaviors, movements and survival at individual and population levels. The plasticity of the red fox and its ability to benefit from anthropogenic landscape changes, as well as changes in landscape productivity, has enabled it to exploit increasingly northern latitudes, increasing concern that the red fox is becoming a driving species directly impacting northern food webs. In response, we captured and outfitted red foxes with GPS/GSM collars, to improve understanding of red fox movement ecology. We have detailed movement data from 102 collared foxes from four study areas along a landscape gradient in Sweden and Norway. Our study highlights resident foxes using much larger areas than previously presumed and indicates that exploratory excursions are common among red foxes. Excursions were observed in all four study areas, lasting for 1-3 days and were typically less than 10 km, but could sometimes be longer than 50 km. Preliminary results further indicate that dispersal distances of foxes vary along a latitude gradient, with observed distances of 25-50 km in southern areas, while those in northern areas have reached 295 km. These spatial patterns demonstrate that red foxes can cover large areas in short time periods. The extent and potential of red fox movements may have been previously underestimated. Developing appropriate management will involve improving our understanding of how changing land use, movement ecology and dispersal patterns alter the spatial structure of red fox populations and facilitates range expansions.

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Intraspecific home range variation of African elephants *(Loxodonta africana)* in response to resource availability

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Animals utilise space and make movement decisions on the basis of interactions between multiple intrinsic (e.g. energetic and nutritional demand) and extrinsic (e.g. surface water and forage availability) factors. For species that live in highly dynamic environments, such as African elephants (*Loxodonta africana*), understanding the drivers of intraspecific variation in home range size and fidelity enables us to better predict the effects of pronounced fluctuations in resource availability on movement and space use over time (e.g. between years, within years and within seasons). Furthermore, there are currently very few studies that have considered the intraspecific variation in home range of large herbivores across different temporal scales. Consequently, our aim was to evaluate the effects of spatiotemporal variation in environmental conditions on home range fidelity of African elephants, whilst ultimately clarifying the main drivers of home range variation. In this study, we analysed home-range overlap for thirteen elephant family groups in Kruger National Park (2006-2013), across multiple temporal scales (annually, seasonally and monthly), as a function of environmental conditions (including vegetation index and rainfall data). The results from this study play an important role in determining the intra-specific responses of African elephants to resource scarcity at multiple temporal scales. An improved understanding of such individual strategies is important for predicting how elephants may respond to future environmental changes. For example, by understanding the susceptibility of this species to specific climatic variation, better-informed management practices can be implemented, ultimately aiding species conservation.

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Sable antelope display flexibility in body temperature regulation and behavioural patterns during the dry season

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The dry season is a stressful period for antelopes since reduced resource availability may exacerbate thermal stresses. Sable antelope (*Hippotragus niger*) exhibit behavioural flexibility in range extent and activity during the dry season, but it is unknown whether such behavioural flexibility completely buffers the restricted resource availability. Over an eight month period, we measured body temperature and locomotor activity using biologging and determined home and core range extent of seven free-living GPS collared sable in the semi-arid Zambezi region of Namibia, one of the more arid regions within sable's distribution range. Sable increased their home ($F_{4,6}$=8.3, p=0.0002) and core ($F_{4,6}$=6.2, p=0.0014) range extent during the dry period with ranges peaking in size (home range: 17.6±7.5km^2; core range: 1.9±0.8km^2) following rainfall. Sable decreased diurnal activity by ~58% when conditions were hot and dry ($F_{4,6}$=41.8, p<0.0001), without altering total 24-hour activity ($F_{4,6}$=1.0, p=0.4226). Despite these behavioural changes, we observed perturbations in the body temperature rhythms of sable during the dry season with a reduction in 24-hour minimum body temperature during cool-dry conditions ($F_{4,6}$=8.5, p=0.0002) and an increase in 24-hour maximum body temperature during hot-dry conditions ($F_{4,6}$=11.7, p<0.0001). Consequently, sable displayed larger 24-hour amplitudes of body temperature rhythm during resource-limited dry periods, with 24-hour body temperature amplitude reaching 4.3ºC on occasion, compared to resource-adequate periods following rainfall where sable maintained homeothermy ($F_{4,6}$=11.2, p<0.0001). This study provides initial evidence for stress-related changes in body temperature regulation of sable antelope during the dry season despite behavioural plasticity.

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Swamp wallabies living in a landscape mosaic: Movement patterns and resource selection

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Broad-scale habitat fragmentation is a visible result of human land-use throughout the world, often resulting in deleterious ecological outcomes. The ability of fauna to persist in fragmented landscapes is influenced by their capacity to move and access important resources such as food, water and shelter. When resources are depleted and spatially heterogeneous, identifying high quality habitat patches and understanding how individuals move through the landscape is critical for effective faunal conservation and management.

Phillip Island, located south of Australia, is a highly modified and fragmented landscape that contains patches of native vegetation amongst a matrix of agricultural farmland and urban developments. The island supports an abundant population of swamp wallabies (*Wallabia bicolor*), but little is known about how individuals move through this landscape. We developed and tested an inexpensive custom-made GPS wildlife tracker that sends data via the mobile phone network. High-resolution movement data gained from the trackers enabled us to highlight features that facilitate movement and others that represent barriers. Further we modeled how wallabies move both within and between landscape patches and select resources. Information about movement patterns and resource selection generated by the analysis will inform and improve the management of swamp wallabies in human-modified and fragmented landscapes and more generally enhance our understanding of the challenges faced by fauna in changing environments worldwide.

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The role of museums and natural history expertise in a fast-changing world

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Studies characterising biological variation and diversity, which are enormously valuable to science and society, have been the main use for natural history museum collections for centuries. Even with rapidly changing technologies, especially genomic techniques, traditional systematics and biogeography remain the principal collections-based disciplinary emphases for biological research programs in natural history museums. Studies relevant to modern environmental change, and biomedicine, among other major fields in the biological science, also represent important uses for museum collections, but these receive less attention within natural history museums, collections, or curator-led research programs. Very large economic and other impacts of rapidly changing environments, climates, and disease landscapes in the Anthropocene highlight a need for organized, future-focused efforts to expand natural history research programs to incorporate additional uses of collections to complement studies of systematic biology. Indeed, critical documentation of Anthropocene impacts, and the future of natural history museums, including public impressions of their relevance, may depend on it.

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Project rehabilitation of the brown woolly monkey (*Lagothrix poeppigii*) at the Yana Cocha Rescue Center: Initiations, development of biological aspects, and report of two cases, Amazonian forest and forest of Ecuador

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An analysis of the data obtained in the process of rehabilitation of two brown woolly monkeys (*Lagothrix poeppigii*) in Yana Cocha Rescue Centre was conducted. These were received during the year 2014; both individuals were kept under illegal possession in captivity as pets. With them, the rehabilitation project starts. They were admitted to the quarantine facility. During this period, they were constantly observed, detailing the activities carried out during the clinical review. After verifying the health of both, we began the process of progressive integration. It lasted approximately 6 weeks, taking place in short sessions of 5-10 minutes with a frequency of three times per week. Data for behavior, vocalizations and observable signs of distress were registered. Progressively we decreased contact with promoting human anthropic activity, overcoming dependency and recovery of the species' own habits. Data for weight gain were recorded weekly. Processes for such wildlife rehabilitation efforts require large multidisciplinary teams to be involved and determining the scope of all phases. A small percentage of individuals entering the wildlife management units may be eventually rehabilitated.

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Summary of Laurasiatheria (Mammalia) phylogeny

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Laurasiatheria is one of the richest and most diverse superorders of placental mammals. Because this group had a rapid evolutionary radiation, the phylogenetic relationships among the six orders of Laurasiatheria remain a subject of heated debate and several issues related to its phylogeny remain open. Reconstructing the true phylogenetic relationships of Laurasiatheria is a significant case study in evolutionary biology due to the diversity of this suborder and such research will have significant implications for biodiversity conservation. We review the higher-level (inter-ordinal) phylogenies of Laurasiatheria based on previous cytogenetic, morphological and molecular data, and discuss the controversies of its phylogenetic relationship. This review aims to outline future research on Laurasiatheria phylogeny and adaptive evolution.

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The role of the climatic niche in the imbalanced diversification of two sister groups

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Imbalanced diversification between closely related taxa is commonly observed, but the mechanisms remain poorly understood. We quantified the temperature and precipitation niche positions and niche breadths for 114 representative species of two closely related subfamilies of Arvicolinae and Cricetinae, and assessed the relationships among climatic niche positions, niche breadths and diversification rates. The results showed that cricetine rodents were restricted to drier environments and had narrower niche breadths than arvicoline rodents. The relationship between precipitation niche positions and niche breadths was much stronger in cricetine rodents than in arvicoline rodents. In addition, the results showed a significant positive relationship between clade level precipitation niche breadths and net diversification rates. The overlap of both niches of cricetine rodents overlapped significantly stronger than of arvicoline rodents, suggesting that aridity has acted as a filter on cricetine rodents to form a non-significant phylogenetic relationship among this clade along the precipitation gradient. Our results suggest that arid environments have strongly shaped the global speciation pattern of arid-adapted taxa by constraining those with small precipitation niche breadths. This mechanism may explain the prevalence of exclusively arid-adapted taxa and the low species richness of cricetine rodents.

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Genomic analysis of snub-nosed monkeys (*Rhinopithecus*) identifies genes and processes related to high-altitude adaptation

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The snub-nosed monkey genus *Rhinopithecus* includes five closely related species distributed across altitudinal gradients from 800 to 4,500 m. *Rhinopithecus bieti*, *Rhinopithecus roxellana*, and *Rhinopithecus strykeri* inhabit high-altitude habitats, whereas *Rhinopithecus brelichi* and *Rhinopithecus avunculus* inhabit lowland regions. We report the *de novo* whole-genome sequence of *R. bieti* and genomic sequences for the four other species. Eight shared substitutions were found in six genes related to lung function, DNA repair, and angiogenesis in the high-altitude snub-nosed monkeys. Functional assays showed that the high-altitude variant of CDT1 (Ala537Val) renders cells more resistant to UV irradiation, and the high-altitude variants of RNASE4 (Asn89Lys and Thr128Ile) confer enhanced ability to induce endothelial tube formation *in vitro*. Genomic scans in the *R. bieti* and *R. roxellana* populations identified signatures of selection between and within populations at genes involved in functions relevant to high-altitude adaptation. These results provide valuable insights into the adaptation to high altitude of the snub-nosed monkeys.

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Calling in the Eastern Indian Ocean pygmy blue whale - song variability and change

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Blue whales were heavily exploited throughout the early 20th century, with many populations hunted to near extinction. Today, a number of known sub-populations of blue whale exist, separated by geographic range and the acoustic signals they produce. The eastern Indian Ocean sub-population of pygmy blue whales is easily identified by the production of a characteristic Australian song type. Passive acoustic monitoring in the Perth Canyon, Western Australia, has allowed for long term collection of sea noise data. Analysis of individual call detections has revealed several variations to the traditional three-part Australian blue whale song type. These variations include six different song structures and two variants to the three-part song type in the form of changes to the inter-song interval. Changes to song structure are achieved through the shortening of the three-part song by the loss of components, or the combination of multiple structures into hybrid song types. All six song variants have been recorded within one year, indicating that high levels of song diversity may be attributed to individual animals producing song variants rather than population-wide processes. The mechanisms behind variability in song production are unclear though there is research to suggest that changes to vocal behaviour may be culturally driven or caused by changes in ambient noise conditions. Anthropogenic noise production by a growing industrial sector is of increasing concern for populations such as the Eastern Indian Ocean pygmy blue whale whose migratory corridors overlap with areas of importance for the shipping and mining industries.

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Do bolder woylies get fatter? Individual differences in behaviour during and post-translocation.

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An animal’s behaviour and stress level has been widely implicated in influencing its survival, fitness, reproduction and ability to obtain resources in new environments. This can have significant consequences for the management of threatened species, in particular the success of translocations of species into new or pre-occupied areas. As such, a better understanding of how individuals respond to conservation interventions, such as translocation, will assist with minimising stress, reducing risk, and improving conservation outcomes. This project is a behavioural study of the critically endangered woylie (*Bettongia penicillata ogilbyi*). The Australian Wildlife Conservancy has conducted three translocations of woylies to predator-proof enclosures, the first from Karakamia Wildlife Sanctuary to Mount Gibson Wildlife Sanctuary and two from the Upper Warren region in the southwest of Western Australia to Mount Gibson and Karakamia Wildlife Sanctuaries respectively. Behaviour of woylies during the translocations was assessed using a series of qualitative and quantitative measures, including agitation level, movement in pet packs during holding, heart rate pre- and post-processing, and behaviour at release. Faecal samples were also collected to monitor faecal glucocorticoid metabolites. Results will determine correlations between individual behavioural responses and change in body mass post-translocation. We predict that ‘bolder’ individuals will adapt more quickly to their new environment, locate resources more effectively, and show greater body mass gain. Selecting a higher proportion of such individuals for future translocations could increase survival rates, thereby improving translocation success and long-term security of the species.

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Evaluation of feral cat (*Felis catus*) management plans at Mt Dobong based on demographic status and population viability analyses

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The purpose of this study is to compare the management plan for invasive feral domestic cats (*Felis catus*) population at Mt Dobong, Seoul, Korea. This study compared the effectiveness of euthanasia and trap-neuter return (TNR) for the management of feral cats using a population viability model, based on population parameters obtained at the study site. Among three selected sampling routes (Dobong, Wondobong, Songchu), Dobong region had the highest observation frequency of cats (152 observation), followed by Wondobong (39 observation) and Songchu (26 observation). The super-population size and annual survival rate of adult cats were estimated at 79.18 and 0.61 respectively, from the capture-recapture POPAN model analyses. Annual fecundity was calculated as 2.52 kittens per female. A density-dependent matrix population model was developed to evaluate population viability of two feral cat management programs. The model predicted that the euthanasia of ≥20% or neutering of ≥30% of the effective population (fertile females) would make the population start to decrease. Furthermore, when carrying capacity of the area was higher in the model, the minimum requirement of cats was increased for the population control. However, the model showed that the feral cat population in Dobong region would reach the carrying capacity under current population control management scheme. This suggests that stronger measures of management are required to diminish feral cat populations from Mt Dobong. Since the model used in this study does not include immigration and emigration, further studies should incorporate the effect of those factors in the management of invasive feral cats.

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Status of the brown bear *Ursus arctos* in Iran: Implications for poaching and human-bear conflict

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The brown bear *Ursus arctos* is the largest carnivore species in Iran. In recent years, habitat destruction by anthropogenic activities and lack of natural foods are the main factors of high limitation for bears and makes levels human-bear conflict high. The data was collected to clarify the species' status and its conflict with humans, by news media and literature review during 2002-2016. In total, 68 brown bears were killed by shooting (n=51, 75.0%), poison (n=3, 4.4%), rail kill (n=2, 2.9%), road kill (n=7, 10.3%), sharp tools (n=2, 2.9%) and unknown factors (n=3, 4.4%) throughout Iran. Bears killed in Iranian Caucasus, Alborz, northern Zagros, central Zagros, and southern Zagros were 10, 17, 12, 17 and 12, respectively. The most killed bears by shooting occurred in central Zagros, and two rail kills happened in Alborz. Also, southern Zagros, northern Zagros and Iranian Caucasus had two road kills for per region. The brown bears killed for trade of their pelt and protection of cultivated fruits, crops, livestock and beehives were in these regions. Also, traditional uses of fat, bile powder, and meat of bears in some disease treatments are another reason for killing them in Iran. The bear is a ‘Protected Species’ by the Iranian Department of the Environment, and killing, using fat, gall-bladder and other organs of bears for traditional cure is illegal in the country. The bear is listed by IUCN Red List as ‘Vulnerable’ in the Mediterranean Region, but *U. arctos* is on edge of extinction in the Middle East.

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Toxoplasma gondii seroprevalence in endangered bridled nailtail wallabies and co-occurring alien species

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The parasite *Toxoplasma gondii* can infect any warm blooded species; however seroprevalence in most species remains largely unknown. This study examines the presence of *T. gondii* antibodies in two remaining wild populations and one captive population of endangered bridled nailtail wallabies (*Onychogalea fraenata*). Samples from cats (*Felis catus*), rabbits (*Oryctolagus cuniculus*) and dogs (*Canis lupus*) were also taken opportunistically during invasive species control. 71 wallabies, 16 feral cats, 4 rabbits and 2 dogs' blood samples were tested for *T. gondii* using a modified agglutination test. An antibody abundance of 50% (n = 8) was found in feral cats and all intermediate hosts were seronegative. This result suggests a loss of infected individuals before capture and testing, or parasite transmission being affected by Queensland's hot, dry climate.

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Differences in small mammal and habitat structures between unburned and burned pine stands subjected to two different post-fire silvicultural management practices in Korea

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This study was conducted to investigate the difference between small mammal community and habitat structure. We examined the composition of three small mammal species, Korean field mouse (*Apodemus peninsulae*), Korean red-backed vole (*Myodes regulus*), and striped field mouse (*A. agrarius*), and a habitat structure of unburned and burned stands resulting from two different post-fire silvicultural management practices (pine plantation and naturally restored stands) within a pine forest in South Korea. We captured small mammal using a live-trapping method and measured the habitat variables of different vertical layers data at each stand in June and July 2004, 2008 and 2016. The habitat structure changed dramatically depending on the post-fire silvicultural practices. Coverage of vegetation was significantly different among study areas and between years. Especially the coverage of overstory and midstory were dramatically increased in post-burned untreated stands (naturally restored). The composition of three small mammal species was different among study areas. The two silvicultural management practices showed a significant difference in small mammal compositions between years. *A. agrarius* increased in post-burned pine plantation stands and *M. regulus* increased in post-burned naturally restored stands, although the unburned stands showed a similar composition of small mammal species. The post-fire practices in burned stands should be re-evaluated because of vegetative changes according to silvicultural management may affect small mammal community by altering habitat structure. Therefore, the effects of post-fire practices and long-term experiments are needed for forest management strategies after forest fires.

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'Spot' call: an unknown great whale sound

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Underwater passive acoustic recordings in the Southern and Indian Oceans off Australia have regularly recorded a short duration (8–10 s), low frequency (22–28 Hz) tonal sound with a symmetrical bell-shaped envelope. When recorded nearby at high level the sound is often accompanied by higher frequency down sweeps (40–100 Hz) and is repeated at irregular intervals varying from 120-200 s. It is termed the 'spot' call due to its spot-like appearance on spectrograms of long time averaging. Recordings made in some parts of the Southern Ocean display a spot call chorus almost year round, with a peak in individual high intensity calls detected during the austral winter-spring. The spot call displays a decrease in fundamental frequency over years. Additionally, an almost instantaneous intra-seasonal jump in frequency from around 22 to 28 Hz was also observed in 2006. Although similar in appearance to the first unit of the Antarctic blue whale z-call, significant differences in fundamental frequency, the rate of decrease in fundamental frequency spatial and seasonal presence are seen. We present evidence to suggest the spot call is produced by another great whale species.

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How do deer achieve foraging success under intraspecific competition for food dropped by foraging macaques?

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In an warm temperate forest of Yakushima, Japan, Yaku sika deer (*Cervus nippon yakushimae*) often gather under trees to obtain food dropped by foraging Yakushima macaques (*Macaca fuscata yakui*) in the branches above. We defined areas under the food trees as macaque-food patches (MFPs). In MFPs, agonistic interactions frequently occur for food among the deer. Thus, the deer develop foraging strategies to acquire food and counter intraspecific competition in MFPs. Their ability to compete varies among the age–sex classes. In addition, the condition of the dropped foods can be classified into two types (L-type, cluster of fruits and leaves attached to a branch; S-type, individual fruit and leaf dispersed over MFPs). Therefore, we predicted that their foraging strategy changes with the age–sex class and food type. We recorded residence time, food intake, and agonistic interactions of deer in MFPs. Agonistic interactions occurred more frequently in L-type MFPs than S-type MFPs. Adult males tended to stay in L-type MFPs for a longer period, frequently attack other deer, and achieve higher food intake speed. Young males also tended to stay for a longer period; however, they were frequently attacked, and they achieved middle food intake speed. Adult and young females tended to stay for a shorter period, were frequently attacked; however, adult females also tended to attack frequently. Further, adult females achieved lower food intake speed, although young females could obtain little food. The deer in MFPs appeared to apply different foraging strategies corresponding to their age–sex classes.

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What nutrients do wild deer rely on for food selection at natural feeding stations in a warm-temperate forest?

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Although various studies have investigated food selection by herbivores, there are few observations of wild ungulates actually selecting food items from the range of alternatives available in natural situations. In addition, although many studies of ungulates have examined the effects of key food constituents (e.g. protein, carbohydrate, fiber and secondary metabolites) on food selection, consistent results have not always been obtained. For understanding mechanism of their food selection, further studies are required on feeding behavior of wild ungulates in natural situations. We observed feeding behavior of wild Yaku sika deer (*Cervus nippon yakushimae*) by following them in a natural forest of Yakushima, Japan, and collected plant samples from 59 feeding stations across seasons. Deer fed on various plant species and parts at the feeding stations, including fallen leaves and fruits of woody plants, and intact woody leaves and herbaceous plants. We analyzed the key constituents of 62 food items and other 171 available plants at the feeding stations. Content of fat, protein and total phenolics showed significant positive effects on food selection by the deer, while lignin and condensed tannin showed significant negative effects. However, soluble carbohydrate and cellulose did not show any significant effects. The higher energy content of fat, compared with sugar or starch, may make it advantageous for the small-sized deer (adult body weight 20-30 kg) that have shorter gastrointestinal tracts to select foods that are relatively rich in fat. The positive effect of total phenolics suggested that non-tannin phenolics may have some beneficial functions.

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Variability of oestrous cycles in captive southern hairy-nosed wombats (*Lasiorhinus latifrons*) as measured by urinary progesterone metabolites

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The southern hairy-nosed wombat (*Lasiorhinus latifrons*) does not breed well in captivity. To better understand the reproductive physiology of this species, eight captive females were conditioned for daily non-invasive urine sample collection between July and December 2013 and 2014. Frozen-thawed urine samples were analysed for progesterone metabolites (P4M) using an enzyme-immunoassay. Urine concentration was standardised for creatinine (Cr), and hormone concentration expressed as ng mg^{-1} Cr. Commencement of the luteal phase (LP) was defined as the first day of a sustained increase in urinary P4M above the baseline concentration determined using an iterative process. Baseline urinary P4M ranged from 1.09-4.04 ng mg^{-1} Cr. Peak urinary P4M ranged from 6.99-16.32 ng mg^{-1} Cr, and varied between cycles within females; some females exhibited higher peak urinary P4M at the beginning of the breeding season, while in others, this occurred at the end of the breeding season. Mean oestrous cycle length, defined as the end of one LP to the end of the next, was 36.1 ± 4.52 days; however, individual cycle length ranged from 23-54 days. The mean LP was 22.5 ± 4.06 days but range from 12-33 days. Females exhibited two to four cycles during each study period. These results suggest that SHNW may exhibit a variable inter-oestrous period between cycles, or abnormal or infertile cycles, which makes captive reproductive management of this species particularly challenging. Nevertheless, monitoring urinary P4M still appears to be a useful index of SHNW cyclic activity and reproductive status.

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Food preference of flying squirrels among 12 species of *Quercus* trees with different sugar and phenolic concentrations

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In the west part of Tokyo, Japan, giant flying squirrels (*Petaurista leucogenys*) eat the leaves of *Quercus* trees. In this area, there are 12 species of *Quercus* trees, including 5 deciduous and 7 evergreen species. We conducted weekly censuses of a 2 km fixed route, collecting leaf debris with feeding marks by the flying squirrels, for three years. Food availability was also estimated as the total cross-section area at the breast height of each tree species. Giant flying squirrels most preferred the leaves of *Q. acutissima* (one of the deciduous trees) during spring to summer, while they most preferred the leaves of *Q. sessilifolia* during autumn to winter when the deciduous trees were all unavailable. To examine reasons for their leaf preference, sugar and total phenolics were measured for leaves of all 12 species of *Quercus*. Sugar contents were highest in the leaves of *Q. acutissima*, suggesting that the flying squirrels prefer sweeter leaves. The total phenolic contents of leaves were positively correlated with the sugar contents among 12 *Quercus* species, so that the leaves of *Q. acutissima* included the highest total phenolics. However, the flying squirrels did not avoid eating leaves of this species. On the other hand, in autumn to winter, evergreen *Quercus* species did not include such high sugar and total phenolic contents, suggesting that factors other than sugar and total phenolics influence their tree leaf preference among the evergreen *Quercus* species.

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The effect of stereotypic pacing on maintenance behaviour of giant anteater (*myrmecophaga tridactyla*)

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Many captive giant anteaters performed stereotypic pacing and this behavior disturbed their normal behaviour. This study aims to clarify how stereotypic pacing affects the maintenance behavior that was the general basic behaviour of captive giant anteater. Nine giant anteaters kept in three zoos in Japan were investigated. We recorded each animal's 24h behaviour for 5 days using video cameras. The frequency of stereotypic pacing was recorded by 1 minute 1-0 sampling method, and maintenance behaviours (eating, drinking, resting, sleeping, exploring, moving, self-grooming, others) were recorded by a 1 minute instantaneous sampling method. The percentage of the pacing during the activity time that was excluded with sleeping and resting time from 24 hours were compared between zoos or individuals by one-way ANOVA. The correlation coefficient between the percentage of pacing and maintenance behaviour was analyzed by Pearson's and/or Spearman's test. The percentage of pacing was not different between zoos but obviously different between individuals. We observed four possible factors that would affect pacing: 1) eating, 2) sleeping, 3) locomoting, and 4) social factors. The percentage of pacing was significantly correlated with the sleeping, resting, exploring and others (social) but these correlations were different for each individual. These results suggested that the maintenance behaviours of giant anteaters would be affected by pacing and factors would be different between individuals.

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Distribution of mammals in wetlands and drylands in south-western Australia: Are wetlands important refuges for mammals?

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Climate change in Mediterranean ecosystems, including lower rainfall and extended drought, presents significant threats to vulnerable mammal species. The northern Swan Coastal Plain in south-western Australia contains conservation-significant banksia woodland remnants and has experienced increased urbanisation, and significant declines in rainfall and groundwater levels. There is evidence of associated negative impacts on the health of wetland vegetation, but little knowledge of how this impacts native mammal fauna. We investigated the distribution of mammals (~6g-9kg) around wetlands to understand the importance of these as refuges. We used a range of detection methods to characterize the presence, diversity and relative abundance of mammals within three spatial scales (0-5m, 5-150m, 150-1000m from water) across three lakes compared to surrounding dryland sites (>1000m from water). Sites close to water (<1000m) were similar in diversity and relative abundance of native mammals, such as *Rattus fuscipes* and *Hydromys chrysogaster,* to other sites within the same scale. However, there were some differences amongst wetlands in the complement of species (e.g. the presence of *Isoodon obesulus fuscivente*r at only one site). Dryland sites differed from wetland sites in the absence of native mammals (except *Tarsipes rostratus*). Introduced mammals such as *Mus musculus* showed no clear trends in relation to water. This study provides evidence that the vegetation surrounding wetlands (0-1000 m) provides an important refuge for native mammals, but also habitat for introduced mammals. Key management actions are thus needed to protect these fragile wetland habitats to maximise the persistence of native mammal fauna under climate change.

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Effects of forest management on density and survival in three forest rodent species

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Several studies have shown that small mammal communities are influenced by silvicultural activities. Investigating multiple demographic measurements is essential to understand how populations respond to forest management, nevertheless studies focusing on multiple demographic parameters are lacking. Our analyses targeted individual survival and population density, to understand the demographic mechanisms by which forest management exerts its effects on small mammals. We focused on the populations of *Apodemus flavicollis*, *A. sylvaticus* and *Myodes glareolus*, constituting the guild of forest- and ground-dwelling rodents in central Italy. Populations were monitored for three years in a continuous forest subject to different management practices. We identified four forest management types selecting 12 sampling areas. We also gathered quantitative data on the amount of trophic and cover resources in each area. For all the three species, coppicing activities had strong positive effects on population density, which were, in some cases, matched by similar effects on individual survival whereas afforestation of conifer plantations negatively affected populations of *A. flavicollis* and *M. glareolus*. We found that different types of forest management, such as the recently coppiced stands, did not create high-density sinks but, rather, enhanced the carrying capacity of the habitats by increasing the availability of cover and food resources. On the contrary, the high forest resulted to be less preferred habitat for *A. sylvaticus* and *M. glareolus,* possibility due to its lack of food and cover resources. Our analyses encompassing multiple population parameters allowed us to highlight the mechanisms by which forest management affects small mammal populations.

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Testing the efficacy of local knowledge and field surveys for assessing the status and threats of pangolins in Central Africa

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Publish consent withheld

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An invitation to publish in the journals of the American Society of Mammalogists

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The American Society of Mammalogists (ASM) publishes two peer-reviewed journals aimed at a broad, international audience. The *Journal of Mammalogy* (JM), the Society's flagship journal, publishes original research on all aspects of the biology of wild mammals, including behavior, conservation, ecology, genetics, physiology, morphology, systematics, and taxonomy. The journal, which produces six issues per year, has a 5-year impact factor of 2.30 and is the top-ranked taxonomic journal based on overall importance (eigenfactor). *Mammalian Species* (MS) publishes concise summaries (accounts) of the current state of biological knowledge of an individual mammal species. Since 1969 we have published MS accounts for 950 species (~20% of extant mammals), with approximately 20 accounts published annually. However, while accounts exist for more than 75% of North American species, we lack coverage of fauna from other continents and from some major groups, e.g., primates, tree and white-toothed shrews, most Australasian marsupials. Both journals are free to ASM members – a bargain at 55USD for regular members and 25USD for students - and accessible via the new Oxford Academic web platform, which provides a variety of enhanced features and options, including open access, advance access, color images, email content alerts, and Editor's choice articles. Although more than 60% of authors and 24% of our Editorial Boards come from outside the United States, as we approach 2019, the 100th anniversary of ASM and JM and the 50th anniversary of MS, we seek to broaden our international footprint by recruiting authors, editors, and reviewers from around the world.

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Western tree hyrax (*Dendrohyrax dorsalis)* in a changing landscape

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Understanding the influence of land use pressure on western tree hyrax populations is crucial to achieving sustainability and assists planning for the protection and conservation of arboreal mammals. Line transect surveys were used in different land use types to estimate density, distribution and response to land use. The study revealed higher distribution in primary forest and secondary forest while the species density decreased in the other areas with increase in human activities. The survey indicated that the density of hyrax across different land use patterns ranged from 6.25 km^{-2} in their core zone, 4.68 km^{-2} in the buffer zone, 2.063 km^{-2} in farm-fallow, to none in the plantation zone. The density in the core zone area was significantly related to land use pattern using one-way ANOVA z-test: x^2=4.12, p = 0.022; core vs buffer p=0.046; core vs farm-fallow p=0.065; buffer vs core different from other three areas, which were not significantly different from each other (p=0.169). Relative density was significantly higher in closed canopy forest than secondary forest and farm-fallow (z-test: core: t_{53}=15.401 p=0.001; buffer: t_{49}=9.334 p=0.001; farm-fallow: t_{17}=4.109 p=0.001). As no hyraxes were heard calling in plantations, density was not estimated. The observed differences between land use patterns are due to anthropogenic activities and changes in forest tree structure and canopy covers due to fragmentation. The results clearly revealed that the species largely depend on primary forest for survival and navigation. Thus, we call for urgent conservation concern that needs management action especially in the tropics to address habitat loss.

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Habitat availability and persistence of *Pseudomys desertor* in the southern extent of its range

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Across the rangelands of Australia, the once widespread distribution of *Pseudomys desertor* is contracting along the southern extent of its range. This change is suspected of being caused by either introduced herbivores removing areas of dense understorey, or a natural consequence of relatively low habitat variability, providing insufficient resources to sustain populations. We propose that the dominant driver will become apparent by investigating the consistency of indicator species, or their traits, identified from within critical habitats. The association between *P. desertor* and broad habitats will be examined from 2500 sites surveyed during the Biological Surveys of South Australia, and an additional 13 sites surveyed within an outlying population in the southern Flinders Ranges. Broad habitats will be defined using a cluster analysis, and key floristic and edaphic variables identified using an indicator species analysis, in PC-ORD. The abundance of captures will be used to indicate the species' relative preference for each community. We anticipate the results of these analyses to indicate the relative availability of critical habitat, and if abundant, areas where the management of total grazing pressure need to be carefully managed to prevent further declines in the range of the species.

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Can we use camera traps to estimate density of quenda (*Isoodon obesuus fusciventer*)?

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The use of camera traps in wildlife research is growing but it is generally restricted to presence-absence information or population surveys for individually recognisable animals. Using cameras to estimate the population size of nondescript, unrecognisable species would greatly increase their use but few studies have tested camera traps as surrogates for traditional fauna surveys. Therefore, the extent to which we can rely on camera traps and the resulting indices of abundance to monitor nondescript animal populations is still largely unknown. Many small to medium sized mammals in Australia do not have unique markings, such as the quenda (*Isoodon obesulus fusciventer*), but camera traps are often used to provide population information for these species. We investigated the relationship between abundance indices derived from camera trapping and robust population (program Capture) and density estimates (program Density 5) derived from live trapping for this nondescript marsupial. We trapped quenda at six sites with differing densities and compared densities derived from the capture-mark-recapture method with abundance estimates derived from camera traps. Densities ranged from 0 to 1.81 animals ha^{-1}, population estimates ranged from 0 to 71 and the number of hits per 1000 days ranged from 0 to 3842. The relationship between density and hit rate was not significant with R^2 = 0.47. By contrast, the relationship between population estimates and hit rates was significant but had a R^2 of 0.63 (P = 0.043). More work needs to be done to establish if camera traps could be used instead of live trapping to estimate population size and density for quenda.

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Taking foxes out of the system allows recovery and re-introduction of native mammals

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The Bounceback Program has undertaken 25 years of broadscale control of the feral red fox (*Vulpes vulpes*), currently covering around 700,000 ha across the semi-arid ranges of central South Australia. Fox control consists of bi-annual aerial baiting with 1080 poison meat baits, with supplementary ground baiting also occurring across reserves and partner properties, providing a quarterly control program. This has allowed sustained recovery of the nationally threatened yellow-footed rock-wallaby (*Petrogale xanthopus xanthopus*) and, more recently, the reintroduction of locally extinct species. The mammal fauna of the Flinders Ranges was hit hard by the damage to native vegetation habitats and other threatening processes following pastoral development and the introduction of new species from the 1830s onwards. This resulted in the local extinction of at least 20 species and the decline of others, including the yellow-footed rock-wallaby which is a hill country specialist, favouring rocky scree slopes and steep gorges, where deep crevices and caves provide some protection from predators. Surveys in the 1980s indicated that the range of this rock-wallaby had undergone significant contraction in the 150 years since European settlement and that remaining populations were isolated and declining. Causes of its decline included hunting, habitat degradation, fox predation and competition for resources with feral goats (*Capra hircus*). Data will be presented from a range of monitoring techniques, including aerial survey, spotlight counts and remote camera surveys that demonstrate the effectiveness of fox control and the recovery of yellow-footed rock-wallaby across the Bounceback footprint.

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On the gestation period of Indian pangolins (*Manis crassicaudata*) in captivity

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Indian pangolins (*Manis crassicaudata*), like all other pangolin species, do not breed readily in captivity. Although births have been reported throughout the year except for May and June, observations on the gestation period of Indian pangolins, are limited as mating and subsequent births are seldom observed. Here we present an isolated observation on the mating and gestation period of an Indian pangolin. We observed mating on 25-02-2014 between an adult female Indian pangolin (Microchip ID–00074D5A63, weighing 8.5 kg) and an adult male Indian pangolin (Microchip ID–98102058378, weighing 9.3 kg) at the Pangolin Conservation Breeding Center, Nandankanan Zoological Park, Odisha, India. The same female was individually housed thereafter and gave birth on 03-11-2014. In the present case, the gestation period was 251 days. We are reasonably confident about the accuracy of the gestation period during the present study as, after observation of one-time mating event on 25-02-2014, the pair was separated and the female was individually housed until the 03-11-2014 when we observed a baby pangolin attempting to crawl over the mother inside a burrow, with the umbilical cord still attached and watery discharge on mother's hind legs, as a sign of recent birth. The pangolin baby measured 25 cm nose tip to tail tip with a 10.5 cm tail and weighed 160 g. The baby was pinkish in color and with soft scales and tiny hairs. Eyes of the baby were closed at birth. It was possible to sex him from the day of birth from his prominent genitalia.

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Infraction in kidney and proliferative cystitis in an Indian pangolin

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A female Indian pangolin (*Manis crassicaudata*) aged about 5 years of Nandankanan Zoological Park, Odisha, India found with clinical signs of lateral recumbency, anaemia and passing red colored urine (haematuria) from three days before death. Post mortem examination of the pangolin revealed white necrotic patches throughout the cortical surface of the kidney, extending deep into the medulla, taking the shape of a cone suggestive of infarction. Urinary bladder revealed proliferative thickening of the mucosa. There was a presence of petechial haemorrhage and diffuse congestion at the mucosa. Histopathological examination revealed coagulation necrosis of the tubular epithelium and emptying of glomeruli with interstitial congestion. Urinary bladder mucosa revealed infiltration of neutrophils, fibrous proliferation, edema, congestion and haemorrhage. Clinico-pathological findings of the present case will be useful in better disease management of urinary disorders in Indian pangolins.

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Genetic diversity of Czech local breeds regarding their complicated history

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The Czech Republic is a small European country but it is a homeland for several dog breeds. In total, there are six Czech breeds. This is a first study that compares three of these breeds, Czechoslovakian Wolfdog (CSW), Chodsky dog (CHD) and Cesky Fousek (CF). CSW is a unique dog breed which originated from German Shepherds (GS) and Carpathian wolves (CW) in order to help protecting the Czechoslovakian borders. Experimental cross-breeding started in 1950's using two CW females and two CW males and led to the CSW breed creation in 1989. The Chodsky dog´s history reaches back to 13th century when it was used as a guarding and sheep dog; however, after World War II the breed almost disappeared. In 1985, the regeneration process started when two standard females and three standard males were used for breeding. The breed of CF is the only Czech breed of pointer and it has a very complex history. In the past, when the breeds have not yet been properly established, it was often hybridized with other wire-haired breeds. In this study, we assess genetic diversity of respective breeds regarding its history. In their genenome, we sought details of the domestication process, and the CSW breed is especially important for understanding interactions of genomes of wolves and dogs. This study was supported by Technical Agency of Czech Republic, project number TG03010020.

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Reverse zoonses and threats to wildlife health

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Spillover of zoonotic pathogens from wildlife to humans has been identified as a threat to global health. In contrast, the reverse process, zooanthroponosis, whereby pathogens move from humans into wildlife remains largely unexplored. Recent evidence has also indicated the significance of co-infection to emerging disease. We have been investigating the co-occurrence of human-associated enteric pathogens including *Cryptosporidum, Giardia* and pathogenic *E. coli* in Australian wildlife, with goal of unravelling impacts of co-infection and reverse zoonses to wildlife health. Multiloccus PCR analysis of target pathogens isolated from faecal samples of key species such as flying foxes (*Pteropus sp*), Tasmanian devils (*Sarcophilis harrisii*) and Australian fur seals (*Neophoca cinerea*) revealed strains of *Cryptosporidium, Giardia* and antimictobial resistant *E. coli frequently* associated with humans in each wildlife host. Our data indicates reverse transmission of these pathogens to wildlife undergoing rehabilitation and being bred in captivity. As our studies progress the impact of these human-associated pathogens on the health of these wildlife hosts will be defined. Our results indicate that carers and conservation staff should be aware of potential for transfer of enteric pathogens to and from wildlife in captive settings and the threats this may pose to conservation.

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Australian mammals eat seeds: Rethinking granivory in a rewilding context

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In many places, mammals are considered the dominant granivores in arid ecosystems. However, in Australia, ants are described as the dominant seed consumers and mammals as insignificant consumers. Since European settlement, many native Australian species have become rare or extinct, their declines preceding any understanding of their role in vegetation dynamics. In arid areas, native mammal decline has coincided with vegetation change. Our research explores granivory by Australia's declining mammal species. We used foraging tray experiments inside rewilded areas and in areas with depauperate mammal communities to compare granivory rates in these areas. In our foraging trays, we placed either *Acacia ligulata* or *Dodonaea viscosa* seeds. Both of these are common shrub species. We found that native mammals such as hopping mice (*Notomys alexis*) and the burrowing bettong (*Bettongia lesueur)* were the dominant predators of *Dodonaea viscosa*, and are approximately equal predators with ants for *Acacia ligulata*. We show that now rare native mammals were once important seed predators in arid Australia. The decline of omnivorous mammals across Australia may have facilitated vegetation change. Rewilding of these mammals will restore lost ecological functions to arid Australia.

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Sandhill dunnarts: Catch me if you can

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Sandhill dunnarts (*Sminthopsis psammophila*) are poorly understood, endangered marsupials. This research examined a Western Australian Great Victoria Desert (WAGVD) population. Methods comprised MaxEnt modelling, nocturnal radio- (n = 10) and GPS-tracking (n = 3), χ^2 evaluation of shelter and random Minimum Convex Polygon (MCP) quadrats, habitat preference and diet analyses. *S. psammophila* were predicted to occur over a wide area in the semi-arid southern WAGVD. 77% of diurnal shelters were burrows, 19% in spinifex and 4% in logs. Burrow entrances predominantly faced north, had uniform dimensions (but variable depth) and were often concealed under spinifex. 97% of shelters were in interdune swales or dune foot slopes, dominated by *Triodia desertorum* and *Aluta maisonneuvei*. Shelter quadrats had significantly less canopy and litter, and more sand and spinifex, though no difference in spinifex age compared with random plots. Mean foraging MCPs and 90% clusters respectively were: males - breeding, 176 ha and 64 ha, and non-breeding, 42 ha and 15 ha; females - breeding, 24 ha and 8 ha, and non-breeding, 26 ha and 11 ha. Foraging was not random; north dune foot slopes were preferred. Breeding males quickly crossed several dunes, whereas females and non-breeding males foraged close to shelter cores. Mean dusk-to-dawn foraging time was 91.3%. Diet during the non-breeding season largely comprised small insects; during breeding, scats contained bigger prey, including skinks. In conclusion, *S. psammophila* is an active, spatially organised, opportunistic insectivore and carnivore, requiring large composite dunefield habitats. Conservation priority should focus on the southern WAGVD.

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Ocelot (*Leopardus pardalis*) life histories based on a 23-year camera-trapping project in Neotropical forest in Panama

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Ocelots (*Leopardus pardalis*) are elusive mid-sized Neotropical predators that are important in a variety of ecosystems but difficult to study. At the Smithsonian Tropical Research Institute in Panama, authors JG and GW conducted a long-term (1982–2017) mammal census based on trail transect techniques to understand population variations of diurnal species. In 1994, in order to document nocturnal mammals, they started using film-cameras, camcorders, and emerging electronic remote monitoring systems. By collecting and analyzing images, they increased understanding of the ecology and behavior of wild ocelots. They established a catalog of images of individuals that could be identified by their spot patterns. Since facial recognition software tested poorly, with low reliability, the identifications were done visually, using the unique patterns of each ocelot. They documented an increase in ocelot numbers recorded over the 23 years of the study. Offspring could often be matched to their mothers through photos that showed their associations. This study provided unique insights into the lives of ocelots undisturbed in a habitat protected from human hunting. The data reveal information about ocelot ecology, including their longevity, reproduction, diet, predation, social interactions, movements, population, latrine use for communication, and more. Furthermore, the camera-trapping project revealed visits to the island by jaguars and pumas, almost never seen by resident staff and that sometimes resided for many months. The data collection method and analysis provided a foundation for further fine-scale studies by radio-tracking and prey remains and DNA from scats.

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First inner ear reconstructions of basal carnivoramorphan mammals: Implications for ecology and phylogeny

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The inner ear is a relatively small organ that provides key functions in vertebrates, such as hearing, balance, and spatial perception. Through fossilization, the soft tissues are not preserved, but the bony labyrinth, surrounding the inner ear, can be used as a proxy to investigate inner ear shape. Because of its fundamental role in coordinating movements, morphological differences of the inner ear between species and across groups could reflect locomotor specializations (whether terrestrial or arboreal, etc) and/or phylogenetic relationships. To test these hypotheses, and to investigate the evolution of this sensorial organ through time, we scanned the cranium of four extinct (~30-50 Ma) basal Carnivoramorpha species and one extinct (~50 Ma) species of Creodonta (a close relative), using high-resolution X-ray micro-CT (Computed Tomography). Succeeding, we reconstructed three-dimensional (3-D) inner ears from the bony labyrinth cavities. Our reconstructions are the first for these extinct species and of any fossil stem-carnivoramorphan. Landmarks were placed on the 3-D models and compared with a previously published dataset for extant species of Carnivoramorpha with known locomotor styles and phylogenetic relationships. Geometric morphometric analyses of both extant and extinct species reveal significant differences in inner ear shape (i.e. vestibular system) that correlate to different locomotor styles, as inferred by postcranial elements for the fossils, and phylogenetic proximity. Being able to distinguish locomotor capacities based on the inner ear shape of extant species could considerably improve insights into paleoecology and paleoenvironments. Ultimately, it also may provide crucial information on environmental changes that might have driven locomotor adaptations.

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An endemic in conflict: The nilgai antelope in a human dominated landscape of Western India

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The nilgai *(Boselaphus tragocamelus*) is Asia's largest antelope and endemic to peninsular India. The species holds a notorious reputation of being a pest due to its crop depredating habits, thus posing a major challenge for its conservation and management. This study was undertaken to understand the ecology of nilgai in a human dominated Central Saurashtra landscape, Gujarat, India. The objectives of the study were to assess the status, distribution and population ecology of the nilgai, study the habitat ecology, feeding ecology, behavioural ecology of the nilgai, assess human-nilgai conflict status, and consequently devise mitigation measures. Nilgai occur throughout the landscape with an average density of 38.24 individuals km^{-2}. Presence-absence data at different spatial scales was used in binomial regression models to understand the distribution of nilgai. Micro-histological analysis was carried out to study the food habits and the consumed plant species were analyzed for their micro-nutrient analysis. Nilgai were mixed feeders with seasonal variations in intake of different species. The crude protein level in a plant was found to be the most crucial factor governing diet selection. Focal animal sampling was carried out during three seasons, summer, winter and monsoon; circular statistics were computed for behavioural data analysis. Information on socio-economic status, agricultural practices, loss to animal depredation, preventive measures and their efficacy, attitudes towards species in conflict as well as mitigation suggestions, was collected from farmers using a structured open-ended questionnaire. The site specific mitigation measures were derived using ecological and socio-economic data of the landscape.

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Distribution modelling and conservation assessment of the pampas cat (*Leopardus colocolo*) in the Uruguayan Savannah

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The pampas cat (*Leopardus colocolo*) is a poorly known small felid that occurs in open habitats of South America. Previous studies have suggested that the disjunct pampas cat population occurring in the critically endangered Uruguayan Savannah ecoregion are a distinct 'Evolutionarily Significant Unit' (ESU), and as such should be the target of separate conservation assessment. Here, we developed spatial distribution models for this ESU, using them to estimate population size and then assess its conservation status based on IUCN criteria. We constructed two models (with and without anthropogenic variables), each of them built separately with two different algorithms (Maxent and Maxlike). All models were very similar, with strongly correlated results ($r_s > 0.88$; $P < 0.01$), consistently indicating higher suitability (or probability of occurrence [PO]) in grassland areas from sea level to 400 m of altitude. The two models incorporating anthropogenic variables provided the best fit to the data, and yielded a more restricted distribution in higher suitability and PO areas, supporting the conclusion that this pampas cat population is directly affected by human disturbance and enabling us to identify priority areas for its conservation. Using available density estimates, the population size within high suitability and PO areas would be <250 and 1,800–9,000 individuals, respectively, suggesting that this ESU may be Critically Endangered or Endangered. Very little of the high-suitability landscape is presently protected, highlighting the urgent need to expand the few existing protected areas in this region, as well as to create new ones to ensure the long-term survival of this elusive felid.

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Verifying the efficacy of passive acoustic monitoring for sika deer populations

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Considerable attention has been paid to protecting native biodiversity from the threat of cervid overpopulation, with shared challenges among various countries. Sika deer (*Cervus nippon*) is a typical cervid, which has recently expanded its distribution within its native ranges (i.e. far eastern Asia and Russia), and several introduced areas in Europe, USA, and New Zealand. With a growing demand for precautionary measures against such threats, which are mainly associated with males in the initial invasive stage, a new approach has been introduced in this study, passive acoustic monitoring (PAM), to detect males with a high sensitivity using their howl during the rut. Here, we verified the feasibility of PAM by comparing it with existing methods using spotlights and camera traps at five sites with different deer densities in the eastern mainland of Japan. For the verification experiments, we set unattended sound recorders to evaluate time and site variations in howl frequency, and measured the detection range of the howl. Consequently, PAM successfully detected males, even at sites with extremely low deer density, where the existing methods were unsuccessful. The detection zone of PAM was around 6 ha in defoliated forests, which was > 200 times higher than that for commonly used camera traps. Thus, the current findings suggest that bioacoustic methods could be beneficial for monitoring low-density populations, which are observed in the initial stage of deer invasion or in the ex-post stage following population regulation.

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Effects of beechnut production on spatiotemporal variations in mammal assemblages in cool-temperate forests of eastern Japan

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Mast production has strong effects on frugivore feeding tactics, resulting in altered behavioral patterns. Although such effects are more obvious in cool-temperate forests with less diverse nuciferous tree species, empirical research supporting such hypotheses, especially regarding entire assemblages of mammals in wide geographical distributions, has been limited. Therefore, we focused on the considerable fluctuation in the yearly production of beechnut (*Fagus crenata*), the dominant nuciferous tree species in

cool-temperate forests, and compared the spatiotemporal variations in mammal assemblages at different forest patches with diverse landscapes throughout three study sites (in total, 2,000 km^2) in northeastern Japan between 2015 (masting year) and 2016 (lean year). In each study site, we set eight 1-km^2 quadrats and provided four camera traps for each quadrat from August to November. A total of 13,201 trap-nights yielded five carnivores, two rodent, and one primate species. From this evaluation, we determined that the diurnal rhythms of several species were sensitive to beechnut production: (1) the mammal species diversity decreased during the nocturnal period in the lean year; and (2) the activity of *Ursus thibetanus* and *Sciurus lis* increased during the diurnal period in the lean year. However, these tendencies differed between study sites. Based on these findings, we discussed the ecological rationale for the shift of diel rhythms and distribution based on feeding tactics and landscape structure, respectively.

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Mammalian pollinators of *Mucuna* spp. in Asia

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Mucuna spp. are vine plants, distributed mainly in the tropics. These plants exhibit explosive opening by which the stamens and pistil are exposed from the petals of the flower during pollination. However, this step is completely dependent on animals (explosive openers). Pollen grains adhere to the explosive opener, thereby making the animal an effective pollinator. The explosive opener obtains nectar as the reward. Although most studies on the pollination system of *Mucuna* have been conducted in the Neotropics, recent studies have shown explosive openers of some Asian *Mucuna* species. In this study, we compare the characteristics of explosive openers in Asia and the Neotropics. Only nectar-eating bats are reported as mammalian explosive openers in the Neotropics and specific species of bats pollinate specific plants. Although the flowers of some Asian *Mucuna* species are opened by specific bat species, the flowers of some others are opened by both bats and non-flying mammals or only by non-flying mammals, depending on the region. The behaviors of the explosive openers also vary between Asia and the Neotropics. All the Asian explosive openers, including bats, used their forelimbs and opened flower by using their snout, except for monkeys. We believe that the ability to hover is one of the factors for determining the opening behavior because Neotropical bats can hover but Asian openers cannot. We will also discuss the differences between Asian and Neotropical explosive openers in relation to differences in the mammalian fauna of the two regions.

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Loss of diversity in the community of small mammals of Doñana National Park (SW Spain): Another effect of the local climate change?

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Doñana National Park is an important wetland located in southwest Spain, forming part of the Mediterranean Basin; it is a "biodiversity hotspot", especially vulnerable to climate change. In this study, we investigate changes in diversity and abundance occurred between 1978 and 2016 in the community of small mammals of Doñana and their relationship with local climate changes. Capture-mark-recapture methods were carried out for a total of 16 years, unevenly distributed over four decades. Our findings show a consistent loss of diversity and abundance decline in the community of small mammals. *Eliomys quercinus* and *Rattus rattus* have almost disappeared from the area and *Apodemus sylvaticus* has sharply reduced its abundance parallel to the progressive increase of *Mus spretus*. Such a process is worrying for conservation as small mammals represent, after rabbits, the most important prey for carnivores and raptors in Doñana. The detected changes could be at least partially explained by the progressive increase in local temperature observed during the study period. In line with this, the species that have suffered a greater decline are those of Eurasian origin and northern distribution as is the case for *E. quercinus* and *R. rattus* while the current dominant species, *M. spretus*, proceeds from Africa and has a Mediterranean distribution. A non-exclusive alternative is that the extreme rarefaction of rabbits may have caused a trophic cascade effect enhancing predation by carnivores and raptors towards gradually smaller species.

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Temporal reduction in the abundance of *Lynx rufus*: Evidence from camera-trapping and DNA-analysis

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Due to the elusive nature and low densities of wild felids, traditional mark-recapture methods for estimating population size are often insufficient to guide appropriate conservation actions. Furthermore, wildlife ranges are often reduced by ever-expanding urban landscapes, making it difficult to study elusive felids and maintain stable populations. Therefore, developing effective methods to assess felid populations in human-dominated landscapes is vital to understanding the future of these populations. We examined the spatial distribution and abundance of the bobcat (*Lynx rufus*) at Stanford's Jasper Ridge Biological Preserve

(JRBP), combining camera-trapping and DNA-analysis data. JRBP is a 485 hectare preserve surrounded by urban environment in Woodside, California. This study is the first to assess bobcat population in this area using both camera-trapping and DNA-analysis techniques. Initial surveys were done from 2006-2008 and 2014-2015 using mark-recapture camera-trapping methods. We conducted additional surveys in the summer and fall of 2016 employing a non-invasive, scat DNA-based capture-recapture framework, compared to concurrent camera-trapping surveys. A comparison of the three time-points shows that there has been a substantial decrease in the bobcat population, with population estimates of 25 bobcats in 2006, around half that number in 2014, and 7 in 2016. When comparing the two sampling methods (camera-trapping, scat DNA-analysis), we found higher capture rates using DNA-analysis techniques. Our genetic approach combined with traditional camera-trapping improves upon traditional mark-recapture techniques, likely providing a more reliable method for monitoring low-density wildlife populations.

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Habitat use and selection by takin in the Qinling Mountains, China

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Understanding habitat use and selection by threatened ungulates is a crucial prerequisite to prioritise management areas and for developing effective conservation strategies. Our research during 2013-2015 was to determine the habitat use and selection of takins (*Budorcas taxicolor*) in the middle range of the Qinling Mountains, China. GPS radio-tracking was used to monitor 10 collared takins to gain their location information. Habitat use and selection by takins showed obvious individual differences. At the landscape scale, all of the four most common habitat types were preferred by takins. However, all takins avoided artificially planted larch forest, and farmland and villages. Available habitats within the home ranges also mostly included the four common habitat types. At the home-range scale, all individuals had significant habitat selectivity during the entire tracking period and each season. The habitat use and selection within the home range varied obviously with season and showed sexual differences to a certain extent. Habitat selection by takins is scale-dependent. At the landscape scale, takins are most likely to occur at sites covered by forest. At both landscape and home-range scales, our results indicated that takins need more diverse forest habitats, but none of the four most common forest habitats is essential for survival of this species. Many measures such as maintaining a diversity of forest habitats, avoiding habitat alteration by invasion of exotic plants, and increasing the area of available habitats by relocating the villages from within to outside of the reserve are recommended to conserve this large species.

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Taxonomic determination of neotropical deer in zooarchaeological samples through NGS

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The aim of this study was to analyse the resolution power of the Next Generation Sequence (NGS) approach applied to the insight population genetics of archaeological cervid remains. Zooarchaeological studies of earth mounds of the eastern Uruguayan lowlands evidence the exploitation of several mammals including Neotropical deer. We analysed three specimens morphologically identified as pampas deer (*Ozotoceros bezoarticus*) dated circa 1300 years BP, recovered from the Ch2D01 archaeological site, in the San Miguel wetland of Rocha, Uruguay. We used a short fragment of the mitochondrial *D-loop* region and surprisingly they were determined to not correspond to pampas deer but were brown brocket deer (*Mazama gouazoubira*). Furthermore, the three samples contained two unique novel haplotypes. These unexpected results show the difficulty to determine these remains taxonomically by morphology, suggesting that *M. gouazoubira* is underestimated in the zooarchaeological record of the eastern Uruguay. This taxonomic adjustment is of great importance for the understanding of prehistoric animal economy because it involves the development of different exploitation strategies for each taxon. The results also show the usefulness of NGS to verify taxonomic identity derived from morphological analyses and its power to evaluate haplotype diversity on pooled samples from ancient DNA.

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Overcoming the difficulties of sending remote sensing cameras overseas

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The use of remote sensing cameras is becoming an increasingly popular method to monitor and gather data on wildlife. The success and usefulness of this technology is not in question. But one aspect of setting up a trial, which is sometimes not considered in the early stages of planning, is the difficulties which can be encountered when traveling with these cameras, especially when overseas air travel is involved. We have learnt the hard way that there are many potential pitfalls, not all of which can even be resolved with forward planning. This poster is a summary of the problems, the various regulations, and the pitfalls we have encountered. Hopefully others can learn from our adventures.

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Mass mortality of Malayan flying lemurs (*Galeopterus variegatus*) and its causal factors

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Between August and October of 2015, we found five fresh carcasses of wild Malayan flying lemurs (*Galeopterus variegatus*) in Pangandaran Nature Reserve, West Java, Indonesia. Such mass mortality of this species has never been reported though several researchers in SE Asia had reported cases of finding fresh carcasses intermittently. We tried to address causal factor(s) of the rare event. We reviewed own data on temperature, monthly rainfall (mm), plant phenology (of mature/young leaves, flowers, and mature/young fruits) and compared among 1) before, 2) during, and 3) after the mass mortality event. There were no clear relationships between temperature and the mortality event, while phenology score and rainfall during the mass mortality periods were significantly lower than those in other phases. Abnormal weather (drier environment) and/or food scarcity, therefore might be one reason for their deaths. Another likely reason of the mass mortality is recent environmental changes caused by humans. Since the development of a resort area around the study site started at the end of 2014, many tall trees, whose leaves and fruits form diets of the folivorous animals, including the flying lemurs, at the northern part of the study area were cut down. In the same period, one group of leaf monkeys started invading human settlements in search of food, and several deaths occurred. In order to test the effects of these factors, we need to conduct systematic monitoring of the environmental fluctuation in the study site.

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Estimating leopard (*Panthera pardus*) density in miombo woodlands using spatially explicit capture-recapture (SCR) modelling

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Whilst research into leopard (*Panthera pardus*) ranges and ecological requirements has been well documented in sub-Saharan Africa, large areas of the species' range lack robust scientific data and further study is needed to assess leopard populations in understudied habitats. Miombo woodlands have been identified as a habitat lacking empirical data. Furthermore, regional leopard populations are facing rising anthropogenic pressures, and therefore studies that investigate leopard habitat relationships in a context of elevated anthropogenic pressure are necessary to inform effective conservation management. This preliminary study aimed to provide the first robust leopard density estimates for miombo woodlands, in a habitat with increased anthropogenic disturbance, using spatially-explicit capture-recapture (SECR) techniques. The study was conducted in Kasungu National Park (KNP), Malawi. KNP is dominated by miombo woodland and subject to high levels of human encroachment and poaching that have severely depleted wildlife numbers. Leopard density in KNP was estimated at 3.43 (± se 1.14) adults per 100 km² from 1292 trap nights. Results from this preliminary study challenge previous assumptions that dense miombo woodlands are a highly suitable habitat for leopard and this could have implications for the effective management of the species across large portions of its range. Further research, with a higher survey effort across a wider area, is currently being carried out to understand the basic ecological requirements of leopards in this habitat and, in a wider context, their ability to adapt to large scale anthropogenic disturbance.

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Changing food preferences of ungulates in contrasting arid systems

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We explored the feeding ecology of ungulates in two contrasting arid systems in South Africa, arid savanna of the Kalahari and arid dwarf shrublands of the Nama Karoo. Historically, these arid systems of southern Africa had large migratory herds of indigenous ungulates, having a profound influence on the ecological functioning of these systems. These migratory habits have been largely disrupted, predominantly through anthropogenic disturbances. With the erection of fences and the introduction and confinement of livestock, a change in vegetation species composition has occurred. As both systems within this study consist of reclaimed farmland, improved understanding of ungulate diet requirements is needed. Fresh dung samples were collected from both systems during three seasons, early wet, late wet and dry seasons. Stable carbon isotope analysis of these dung samples was used to determine relative proportions of C_3 and C_4 plant forms within the ungulates' diet on a seasonal basis. Provisional results indicate differences in diet composition for some of the species between the two systems. Some of these differences may relate to differences in relative abundances of plant growth forms available for forage selection, and the ability of ungulates to tolerate such plant diversity within their diets.

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Evolution and extinction of the 'Siberian unicorn' *Elasmotherium sibiricum*

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Elasmotherium sibiricum, a giant, one-horned rhinoceros of the Pleistocene, was the last-surviving member of the Elasmotheriinae, one of two major radiations within the rhinoceros family. Its extinction was believed to have occurred within the Middle Pleistocene, prior to the Late Quaternary megafaunal extinction event. Here we show, by AMS radiocarbon dating of 21 individuals, including cross-validation and single amino-acid dating, that the species survived in Eastern Europe and Central Asia until at least 33,000 years ago, and was very probably extinct by the Last Glacial Maximum. Stable isotope data indicates a highly specialised dry steppe niche conforming to the species' morphology and distribution. These findings have significance for the pattern and cause of megafaunal extinctions in northern Eurasia. We further demonstrate, by the first ancient DNA sequence data obtained from a member of the Elasmotheriinae, a very deep phylogenetic split between that subfamily and the Rhinocerotiinae that includes all the living rhinos, supporting morphological evidence from fossils that the two lineages were in existence in the Eocene.

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Wild boars prefer permanently abandoned farmland in satoyama

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Why do wild boars cause agricultural damage? We analysed the behaviour of two wild boars that inhabited satoyama (agricultural woodlands and farmland) in Ohda City, Shimane Prefecture, Western Japan, to understand how such damage occurs and how to reduce it. We tracked the boars by GPS transmitter, recording their positions once per hour. Because we could not fit collars to the boars, we used a prototype vest-like garment, developed with the help of Teikoku Sen-i Co., Ltd. (Tokyo), which covered a boar from the shoulder to the chest. The boars were equipped with the devices in April 2005 and tracked for 12 and 15 days. Positional data and field surveys were used to ascertain boars' use of the land. Bamboo forest and permanently abandoned farmland with emergent scrub were intensively used. Boars can find bamboo shoots, their main food, during early spring. The farmland was abandoned in the 1980s, 20 years before the investigation; kudzu grew abundantly, serving as food, and the land became a good habitat for feeding and resting. One factor behind boar-related damage appears to be their intensive usage of permanently abandoned farmland, which may expand to adjacent productive farmlands. To reduce boar-related damage, removing crops, fruit trees, and nutrient-rich surface soil from farmland before it is abandoned and from those that are already abandoned are necessary. Increasing numbers of abandoned farmland is a problem shared by developed countries because of population decline and aging. Therefore, a farmland management plan is important for reducing friction with wildlife.

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Adenovirus in a wild population of Geoffroy's tufted-ear marmoset, *Callithrix geoffroyi* (Humboldt, 1812), in southeastern Brazil

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Understanding infectious diseases in wildlife is important in conservation as well as public health, because most infectious diseases are zoonotic. The role of many zoonoses in the chain of infection of some infectious agents is still poorly understood. Adenovirus infections have been described in fish, amphibians, reptiles, birds and mammals. Non-human primates can be reservoirs of various infectious diseases and may be important for public health when close to humans in rural and urban areas. We investigated the presence of Adenovirus in faecal samples of 50 road-killed Geoffroy's tufted-ear marmosets from suburban areas in the state of Espírito Santo, southeastern Brazil. Two samples (4%) were positive. Phylogenetic analysis show that the viruses are related to the genus *Atadenovirus* and *Mastadenovirus*. Their non-specificity suggests that these viruses are food-borne. Adenoviruses are very common in human infections, and may affect other vertebrate species. They can cause eye, gastrointestinal and respiratory infections, some of which can be fatal. This is the first record of Adenovirus in a wild population of *Callithrix geoffroyi*. The investigation of infectious diseases in free-living animals is important to determine the susceptible species to each infectious agent, and to establish the possible transmission of diseases between wild species and their zoonotic potential. Nevertheless, these studies are still uncommon due to the difficulty in obtaining samples. The use of road-killed animals in scientific studies provides access to otherwise unavailable biological material and contributes to investigation and monitoring of viral infections in the wild.

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Wild boar and Sika deer: From pests to regional resources

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Approximately 5,000 wild boars and 4,000 Sika deer are annually culled on Tsushima Island to prevent agricultural, forest, and ecosystem damages. In Japan, unlike western countries, eating wild game is not common. According to a web-based questionnaire survey on the perception of game meat, over 50% of respondents had concerns regarding the hygienic status of game meat. Wild boars ($n = 78$) and Sika deer ($n = 8$) originating from Tsushima Island were subjected to microbiological testing. The meat was evaluated for total viable count (TVC) and total coliform bacterial count (TC), *Salmonella* spp. and enterohemorrhagic *Escherichia coli* (EHEC). Pork ($n = 16$) and chicken ($n = 16$) samples obtained from retail shops were also examined for comparisons. TVC and TC of wild boar and deer meat were significantly lower than those of pork and chicken ($p < 0.01$; Steel–Dwass test). *Salmonella* spp. were detected in 50% of chicken samples and 1.28% of wild boar samples. *Salmonella* spp. were not detected in either pork or deer. EHEC was not detected in any of the study samples. Our study clarified the hygienic status of wild boar and deer meat from Tsushima Island and demonstrated that the status was comparable to that of retail meats. School lunch service centers on Tsushima island decided to provide dishes using deer and wild boar meat beginning from 2017. This decision is an important step for recognizing deer and wild boar meat as local resources.

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Ancient DNA from the North American flat-headed peccary reveals its phylogenetic position and a genetically diverse population prior to extinction

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The geographical range of extant peccaries extends from southwestern United States through Central America and into northern Argentina. However, from the Miocene until the Pleistocene now-extinct peccary species inhabited the entirety of North America - how and when peccaries moved from North to South America remains unclear. The North American flat-headed peccary (*Platygonus compressus*) became extinct at the end of the Pleistocene and is one of the most abundant subfossil taxa found in North America. Despite this extensive fossil record its phylogenetic position has not been resolved. This study is the first to present DNA data from the flat-headed peccary and full mitochondrial genome sequences of all extant peccary species. We performed a molecular phylogenetic analysis to determine the relationships among extinct and extant peccary species. Our results suggested that the flat-headed peccary is sister-taxon to a clade comprising the extant peccary species in contrast with previous hypotheses. Divergence date estimates from our molecular dating analyses suggest that if extant peccary diversification occurred in South America then their common ancestor must have dispersed from North America to South America well before the establishment of the Isthmus of Panama. We also investigated the genetic diversity of the flat-headed peccary by performing a preliminary population study on 12 specimens from Sheriden Cave, Ohio. Flat-headed peccaries from Sheriden Cave appear to be genetically diverse and show no signature of population decline prior to extinction. Future explorations of flat-headed peccary populations is likely to reveal interesting insights into Late Pleistocene life prior to extinction.

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The muscles of mastication and their related skull characteristics in the Saimaa ringed seal (*Phoca hispida saimensis*)

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As part of our research aiming to understand the genetic basis of the variation in morphological traits in ringed seals, we studied the muscles of mastication and their related skull characters of the Saimaa ringed seal (*Phoca hispida saimensis*). Six by-caught (by gill nets) Saimaa ringed seals in relatively good external condition were dissected for this study. The *musculus temporalis* muscle contributed more than half to the total jaw adductor muscle mass (mean 55.1 %). The masticatory muscle anatomy of the Saimaa ringed seal was similar to that reported for other fresh water seals but the *m. digastricus* of Saimaa ringed seal was large enough (25.2 percent of the total masticatory muscle mass) to cover the entire bulla. The skull of the Saimaa ringed seal is apparently not under significant cranial strain from any mastication muscles because they prey on small-sized fish and do not use their teeth (but claws) for scraping ice to form breathing holes. The apparently relatively high contribution of *mm. pterygoidii* of the Saimaa ringed seal to the jaw adductor muscle mass (14.5%) compared to canids (8.2 %) warrants further studies.

1. Penrose, F., Kemp, G.J. & Jeffery, N. 2016. Scaling and accommodation of jaw adductor muscles in Canidae. Anatomical Record 299: 951-966.

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Absence of an Articular Disk in the Platypus Temporomandibular Joint

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In the vast majority of mammals, the temporomandibular joint comprises an articular disk between the mandibular condyle and the mandibular fossa. However, the temporomandibular articular disk has been reported to be absent in two monotremes, the platypus and the short-beaked echidna. The aim of this study was to investigate the morphological characteristics of the temporomandibular joint in the platypus by anatomical, histological and radiological examination. Two fresh frozen platypus corpses were obtained from the School of Zoology, University of Tasmania. The right maxillofacial regions of the corpses were dissected, and the morphology of the temporomandibular joints was carefully observed by gross anatomical examination. Then, the maxillofacial region was removed and fixed with buffered formaldehyde solution. Focusing on the trabecular bone in the condyle, the left temporomandibular joints were examined by microcomputed tomography. Thereafter, the left temporomandibular joints were histologically examined. In all cases, absence of the articular disk was morphologically confirmed. Both dense and fine trabecular bone were observed in the loaded area of the condyle. Histologically, well-developed synovial membrane was present in both anterior and posterior parts of the articular cavity. We reconfirmed the absence of the articular disk in the temporomandibular joint of the platypus, first reported in 1900. Well-developed synovial membrane close to the articular surface and dense trabecular bone in the condyle might together play a role in masticatory absorption and loading of the platypus temporomandibular joint.

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Viruses associated with gastroenteritis in the crab-eating fox, *Cerdocyon thous* (Linnaeus, 1766), in the Atlantic Forest, Southeastern Brazil

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Identifying wildlife diseases is important for conservation and for public health. About 60% of diseases affecting humans are zoonotic, and so biodiversity and ecosystem conservation may influence human health. Some wildlife species, such as the crab-eating fox *Cerdocyon thous*, may be sentinels for potentially zoonotic infectious diseases because of their generalist diet and opportunistic predation strategy, being found in rural and sometimes urban areas. We investigated the presence of viruses in free-living *C. thous* in the coastal region of the state of Espírito Santo, southeastern Brazil. We analyzed kidney, liver and faecal samples of 29 road-killed foxes. Viscera were negative for viruses. Two faecal samples (7%) were positive: one for Avian Adenovirus E 8b and Equine Cyclovirus 1, and the other for Porcine Circovirus type 2. Viruses that are typically from other animal species being found in faeces of *Cerdocyon thous*, along with negative results for viruses in viscera, suggests that the foxes were not infected by the viruses. We suggest that they fed on infected material (e.g. faeces or carcasses of other animals) that in effect could be vector for the gastroenteric viruses. Thus, it is possible that they may become infected by feeding on infected material. The use of road-killed animals provides access to biological material that might otherwise be unavailable, and thereby allowing studies that would be very difficult or impossible without these specimens. Also, epidemiological surveillance of wild species may be easily carried out with road-killed animals.

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Human-macaque encounters in Ifrane National Park, Morocco: Behavioural coping strategies of the Barbary macaque (*Macaca sylvanus*)

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Wild animals in human-dominated landscapes are exposed to a range of human activities that can alter their fitness and behaviour. Many disturbance studies focus on a single stimulus, and little is known about whether different stimuli differentially affect animal responses. Encounters with shepherds/foragers, dogs, and/or tourists all have the potential to disturb primates that inhabit areas in close proximity to humans. To understand the effects of specific disturbance types on primate behaviour, we quantified the escape, affiliative, and self-directed behaviours of fifty individuals from five wild Barbary macaque (*Macaca sylvanus*) groups in Ifrane National Park, Morocco, before, during, and after five classes of disturbance. Using generalised linear mixed models we identified two broadly consistent 'response profiles'; the first in association with encounters that involved dogs, and the second with encounters that involved provisioning by humans. Encounters with tourists that did not involve provisioning elicited no significant changes in our measures of coping behaviour; however, macaques made extensive use of escape behaviours both during and after all other types of encounter. Affiliative behaviours either increased or decreased depending on encounter type, and self-directed behaviours increased in association with human provisioning and lone dog encounters. Encounters with both dogs and (provisioning) humans seem to induce stress. In the first instance because macaques experience the threat of predation, and in the second because of increased intragroup competition and increased proximity to humans. Our results highlight the importance of examining wildlife responses to multiple disturbance types when evaluating the conservation implications of human-wildlife encounters.

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Climatic, landscape and anthropogenic drivers of habitat suitability for a neotropical ecosystem engineer

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Biodiversity persistence and distribution throughout space and time are affected by increasing rates of environmental change induced by anthropogenic disturbance. We used a niche modeling approach to investigate the contribution of climate, landscape and anthropogenic disturbance as predictors of habitat suitability for the white-lipped peccary (WLP), a species that is primarily forest-dependent. WLP is the only large-herd-living Neotropical ungulate, and has been historically extirpated by over-hunting in many regions of South America, which may cause habitat alterations and cascading biodiversity loss. WLP occupancy data were reviewed for four biomes across Brazil, Atlantic forest, Cerrado, Amazonia and Pantanal. Three algorithms and two different ensemble modelling techniques were used to model the effects of six bioclimatic, five landscape and two anthropogenic predictors. Model results reflect the current conservation status of populations of this species across the biomes, and predictors had different responses in explaining habitat suitability due to a long history of land use, habitat loss, habitat fragmentation and hunting, all of which affect WLP populations in those regions. Detecting suitable areas both in terms of climate and landscape structure will be critical in defining ecological corridors and optimizing the role of protected areas for the conservation of WLP. The better comprehension of the habitat suitability of this species can also help predict how impacts of habitat loss will affect other medium and large-sized mammals at varying spatial scales.

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Distress calls in wild-living neonate Mongolian gazelles (*Procapra gutturosa*): Relationship with an open habitat, antipredatory strategy, vocal anatomy and testosterone

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In neonate ruminants, the acoustic structure of vocalizations might depend on sex, vocal anatomy, hormonal profiles, body mass and on environmental factors. In neonate Mongolian gazelles *Procapra gutturosa*, hand-captured in the Daurian steppes at the Russian-Mongolian border, we spectrographically analysed vocalizations and measured body mass of 22 (6 male, 16 female) individuals. For 20 (5 male, 15 female) of these individuals, serum testosterone levels were also analysed. In addition, we measured relevant dimensions of the vocal apparatus (larynx, vocal folds, vocal tract) in one stillborn male Mongolian gazelle specimen. Neonate vocalizations of either sex were high in maximum fundamental frequency (800-900 Hz), but the beginning and minimum fundamental frequencies were significantly lower in males than in females. Body mass was larger in males than in females. The levels of serum testosterone were marginally higher in males and did not correlate with the acoustics or body mass. We discuss that the high-frequency calls of neonate Mongolian gazelles are more typical for closed-habitat neonate ruminants, whereas other open-habitat neonate ruminants (goitred gazelle *Gazella subgutturosa*, saiga antelope *Saiga tatarica* and reindeer *Rangifer tarandus*) neonates produce low-frequency (< 200 Hz) distress calls. The proximate cause for the high fundamental frequency of distress calls of neonate Mongolian gazelles is their very short, atypical vocal folds (4 mm) compared to the 7 mm vocal folds of neonate goitred gazelles, producing distress calls as low as 120 Hz. The study was supported by the Russian Science Foundation, grant 14-14-00237.

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Evolution of sexual dimorphism in musteloid crania

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The remarkable uneven diversity in both species richness and phenotypes represent one of the more perplexing evolutionary patterns across the Tree of Life. Although an increasing number of researchers have begun to understand what drives uneven diversity between species, few researchers have examined how differences within single species can affect these broad scale evolutionary patterns. One source of variation lies in the difference between the sexes. The primary goal of this research is to build upon evolutionary theory by examining how sex differences contribute to species and phenotypic diversity. Here, we use musteloids (badgers, otters, raccoons, skunks and weasels) as a model to examine the effects of sexual dimorphism (SD) on cranial disparity at the macroevolutionary scale. Musteloids are a taxonomically rich and phenotypically disparate clade whose lineages exhibit uneven patterns of diversity. We used 3D geometric morphometrics to quantify cranial size and shape. We then quantified the rates of cranial disparity through time in males and females separately and pooled together (species means) to test the hypothesis that incorporating sex enhances the pattern of adaptive radiation. A rate shift in cranial evolution is predicted to occur just after the onset of the Mid-Miocene Climate Transition when using the pooled male and female dataset. Second, we examined an ecological basis for sexual dimorphism by testing the hypothesis that the degree of carnivory corresponds with the evolution of sexual dimorphism in cranial shape and size across Musteloidea. Hypercarnivorous musteloids are predicted to exhibit the highest degree of cranial SD.

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Diversity of alarm calls across species of Ruminantia

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Alarm calls in response to potential danger are widespread among mammals. We conduct a detailed analysis of alarm call acoustic structure in wild-living giraffe (*Giraffa camelopardalis*), sambar deer (*Rusa unicolor*) and Indian muntjac (*Muntiacus vaginalis*), and describe their vocal behaviour while mobbing people. Giraffe alarm calls represented broadband hisses of duration 0.24-1.04 s and the peak frequency at 0.69 Hz. Sambar alarm calls represented tonal barks with arc-shaped structure, the maximum fundamental frequency 0.98 kHz and the depth of frequency modulation 0.34 kHz. Muntjac alarm calls had much weaker frequency modulation, a maximum fundamental frequency 0.66 kHz and the depth of frequency modulation 0.10 kHz. Comparative data (our own and literature) suggest that ruminants have a few types of alarm calls. In giraffes, waterbucks, impala, Siberian musk deer, goitred gazelles and Western turs, the hiss, hiss-whistle and snort alarm calls are produced through the nose with an aerodynamic whistle mechanism. In sambar deer, Indian muntjacs, white-tailed gnu, greater kudus, red deer and sika deer, the bark alarm calls are produced through the open mouth and display a clear fundamental frequency. In the springbok and klipspringer, the fundamental frequencies along the aerodynamic whistle are presented. No evident relation between nasal or oral emission of the calls and animal taxonomy or habitat can be found. This suggests Ruminantia as a good model taxon for investigating the role of acoustic diversity in vigilance and alarm communication, in addition to the traditional model groups, birds, primates and ground-dwelling sciurids. Supported by RSF grant 14-14-00237 and RFBR grant 15-04-06241.

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Preliminary study of plantain squirrel (*Callosciurus notatus*) phylogeography in Southeast Asia

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Divergence patterns among some *Callosciurus* squirrel species are affected by geographic isolation by Southeast Asia's huge rivers. Currently, divergence by rivers is found within *C. prevostii*, occurring widely in Sundaland. Therefore, there may be similar biogeographical effects on *Callosciurus* species sympatric with *C. prevostii*. To test this hypothesis, we examined phylogeographical characteristics of *C. notatus* based on mitochondrial cytochrome *b* gene sequences. This squirrel is widely distributed from the Malay Peninsula to Sumatra, Borneo, Java, and adjacent small islands. It has many synonyms and subspecies. We collected specimens from the Malay Peninsula, Sumatra, and Borneo. Interestingly, specimens from Sumatra did not show monophyly, with one very closely related to specimens from Borneo. Specimens from the Malay Peninsula had diverged from the others. This phylogeographical pattern was different from that of *C. prevostii* reported previously and cannot be explained by geographical isolation from ocean or rivers. In addition to examining more specimens from many parts of Sundaland, future studies should consider the complicated effects of ocean, rivers, and other geographical structures on the phylogeography of this species.

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Food niche segregation between sympatric golden jackals and red foxes in central Bulgaria

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In Europe, the range of the golden jackal (*Canis aureus*) has expanded since the mid-twentieth century, but little is known about how it interacts with other sympatric carnivores. Among European countries, Bulgaria has the largest population of golden jackals, and jackal numbers have increased around two-fold during the past two decades, particularly in lowland habitats. Larger canids often competitively exclude, or even kill, smaller sympatric ones, especially when guild dynamics are in flux due to population re-establishment. We therefore investigated whether trophic niche segregation occurs between golden jackals and red foxes (*Vulpes vulpes*) in central Bulgaria, where both species are sympatric. Because jackals are more abundant in lowland than in upland Bulgaria, we further investigated whether habitat elevation affects the extent of trophic competition. From the analysis of stomach contents of both species, collected from lowland and upland areas during hunting seasons between 1997 and 2009, we found no significant food niche overlap, and no elevational effects on trophic interactions. In lowland habitat, golden jackals mainly scavenged carcasses of domestic animals, whereas in upland habitat they consumed mostly carcasses of wild ungulates. In contrast, red foxes predominantly and consistently predated rodents in both habitats. This suggests that trophic segregation facilitates the coexistence of these canids under these prevailing population conditions. Nevertheless, we stress that as golden jackals colonise Eastern Europe, impacts on red foxes, and consequences for ecological communities, should be monitored carefully, especially in regions with less carrion available to support jackals.

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Two new records of langurs *Trachypithecus* in Tibet, with one new record in China

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The distribution of the capped langur (*Trachypithecus pileatus*) in China is still controversial since Shortridge’s langur (*T. shortirdgei*) was upgraded to a full species. Shortridge’s langur was considered mainly distributed in west Yunnan Province, China and northeastern Myanmar. Based on our field survey, we found strong evidence for the existence of the capped langur in China and the new distribution range of Shortridge’s langur in Tibet. The capped langur is a new record for China, and Shortridge’s langur is new records for the Tibet Autonomous Region. The extended ranges of the capped and Shortridge’s langur in the southern Himalayas illustrate that the langur species of gray langurs and lutungs may have a close relationship.

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Assessing the status of koalas in forests using acoustics and an occupancy modelling framework

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Koalas are a cryptic species that are surprisingly difficult to survey, especially in tall remote forests. We are undertaking a large-scale survey of koalas in forested environments of north-east New South Wales to assess their current status and response to timber harvesting. So far, we have deployed SongMeters (SM4) at >100 sites over an extensive area, each for a period of 7 nights, to record male bellows during the breeding seasons of 2015/16. Surveys are targeting modelled moderate-high quality habitat in forests with a stratification based on time since logging and logging intensity. Recordings are scanned by Ecosounds software at QUT and then we manually checked all computer matches of koala bellows to rule out false positives. Our sample from a wide range of forests in 2015 found that koalas had a probability of detection of 0.3-0.4, indicating that low detection must be accounted for before relating occupancy to habitat type or forest successional stage. The seven nights of acoustic data are highly suitable for accounting for imperfect detection prior to occupancy modelling. Preliminary results reveal naïve occupancy levels of 50-80 % across a broad range of forests; such high detection rates were unexpected based on results from previous survey methods. Once imperfect detection is accounted for, we will estimate probability of occupancy for a range of forest types in relation to timber harvesting. Acoustic detection is proving to be a highly successful and efficient technique for recording koalas in forested areas where traditional surveys have had limited effectiveness.

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Population structure, fecundity and new born cub records for the Sunda pangolin *Manis javanica*

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The Sunda pangolin (*Manis pentadactyla*) is listed in the IUCN Red List of Threatened Species as a critically endangered species, and listed in CITES Appendices I. It is the most common illegal-trade mammal. Eighty seven live-smuggles Malayan pangolins were confiscated in China, in June, 2011. We estimated their age by their claws, scales, hair, body weight, and the relationships between mother and baby. They were divided into 4 age groups; cub (3 individuals), sub-adult (22), adult (32), and senior (27), representing 3.45%, 25.29%, 36.78% and 34.48% of the total group size, respectively. The age structure diagram was an inverse pyramid, with sex ratio 1:1.42 (male:female=36:51). The proportion of females was less than that of males, and the female proportion was the lowest in adult group (28.13%). Of the females, 7 were pregnant, a pregnancy rate of 36.10%. Among the pregnant females, one was a sub-adult whose weight was 1.95 kg. The highest fecundity (77.78%) occurred in the adult group. Morphological features of new born cubs were measured; body weight 143.3 ± 6.67 g (range 120-170 g, n=6); body length 14.7 ± 0.29 cm (range 14.8-15.4 cm, n=6); tail length 10.1±0.24 cm (range 9.5-11.2 cm, n=6). Our research indicated that the Malayan pangolin population has been largely destroyed, with severely unhealthy status in Southeast Asia. The population will continue to have a rapid decline if no effective protective measures are taken soon.

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Immune cell profile of different age-sex groups in a captive red-tailed phascogale colony (*Phascogale calura*)

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The red-tailed phascogale (*Phascogale calura*) is a small endangered Australian marsupial. Males are semelparous and disappear from the population after mating. This total male mortality has been suggested to be stress-related and associated with suppression of the immune and inflammatory reactions. In captivity, males live longer than they do in the wild but become infertile after their first breeding season. However, it remains unknown whether they also exhibit a stress response and have reduced immune functions. The aim of this study is thus to investigate the immune cell profiles of captive adult males, compared to captive juvenile males and their female counterparts. Blood and spleens were opportunistically collected from different age-sex groups (n = 6 per group) in a captive breeding colony, between December 2016 and January 2017. Preliminary haematological results reveal that captive adult males exhibit a mild lymphocytopenia and neutrophilia compared to other age-sex groups, which is consistent with a stress response. Size and cellularity of the splenic lymphoid white pulp (periarteriolar sheaths, follicles and marginal zones) are presently being evaluated through histological studies. Captive breeding colonies offer valuable opportunities to investigate wildlife health and disease, as long as captivity doesn’t interfere with normal physiology. In the case of this captive red-tailed phascogale colony, a better knowledge of the immune competence of different age-sex groups is required before further immunological studies can be designed.

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Biodiversity in a changing world: Small mammal communities in a mixed-use landscape of the Western Ghats, India

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Globally, landscapes are changing with human-induced fragmentation. The Western Ghats biodiversity hotspot in Southern India has the highest human population density in the world. Landscapes here include a mix of human-modified (tea, human settlements and abandoned plantations) and natural (rainforest and grassland) fragments. We investigated the impacts of land-use and habitat on small mammal communities in Kadumane, central Western Ghats, India. Eight species of rodents and two insectivores were represented by 268 captures of 183 individuals with a total trapping effort of 6,920 trap-nights (capture rate 3.78 %) over two seasons. Out of the 10 species captured, three were endemic to the Western Ghats. Small mammals showed distinct distribution patterns across the habitat types. Community structure, species richness, relative abundance and biomass varied across habitats, with each type having a different dominant species. *Mus booduga*, which was the most abundant species, comprising 45.90%, followed by *Mus musculus* (26.23%) and *Rattus satarae* (18.58%). The abandoned plantation supported the highest richness and biomass of small mammals, followed by forest fragments and grasslands. The grasslands were affected by seasonal fires and witnessed significant fluctuations of species abundance and hosted a unique species assemblage. Modified landscapes such as active plantations as well as built-up areas had a preponderance of commensals. Our study attempts to make predictions about biodiversity transitions in secondary and mixed-use landscapes, habitats that dominate the tropics globally.

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The biogeographic basis of Ebola-virus disease outbreaks: A model for other zoonotic diseases?

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We first determined the differential role of favorability of environmental conditions and mammalian chorotypes in explaining the presence of the Ebola virus in Africa. We then combined environmental factors and chorotypes using fuzzy logic, which better explained the distribution of Ebola virus. The core area for the virus was associated with human infections of known animal origin, with infections of unknown source detected in areas that are biogeographically more peripheral. Variation in the environmental favorability for disease outbreaks may be monitored using indices of macroclimatic oscillations. This may provide the basis for an early warning system based on the variation in macroclimatic indices and the locations where human contact with multiple animal species tend to occur. We propose to study the biogeography of zoonoses by: 1) determining the potential spatial distribution of these diseases, according to environmental factors and the biogeographic structure of animals linked to the zoonosis cycle; 2) search for relationships between disease outbreaks and global atmospheric oscillations to forecast periods of higher risk of emergence of the infectious diseases.

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Are we reaching the end for the taxonomy of mammals? A case from the revision of a most common and dominant wild rat species complex in China (Rodentia, Murinae)

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Mammals represent one of the best studied group of animals in the world; however, the taxonomy of several small-sized taxa remains lagging behind, particularly in regions that are short of extensive exploration and systematic revisions. It is worrying that the team of taxonomists largely shranked in recent years even though there are a large number of taxa remaining poorly explored and unstudied. We present one example for the necessity of a comprehensive revision on these animals. The *N. confucianus* species complex (NCSC) is one of the most common and dominant, but taxonomically ambiguous, small mammal taxa in southeast Asia and China. More than 20 species or subspecies had been described in historical literature. Based on extensive sampling and integrating information from molecular data and morphological data, we verified their distribution range and tested the genetic divergence, morphological differentiation among different species, and subspecies. Distribution of molecular voucher specimens revealed previous studies largely overestimated the distribution of *N. confucianus* with a large number of misidentifications in the literature and museum collections. Morphological analysis demonstrated significant divergence amongst genetic clades and geographical populations, highlighting quick diversification of these taxa. Taxonomic revision modified the species status of several taxa and established two new species from Tibet and China.

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Individual identity in hind and calf contact calls of Siberian wapiti *Cervus elaphus sibiricus* during separation

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Mother-offspring vocal recognition is critically important for survival of the young for many mammal taxa. Vocal identity in contact calls facilitates mothers-offspring reunions and prevents allosuckling. Hind and calf calls encode identity in many cervids, but not Siberian wapiti, *Cervus elaphus sibiricus*, an important animal farmed for velvet antlers, this information is lacking. Contact calls of mothers and 5-6 month old offspring were collected on the farm during 5 days after separation for winter keeping in December 2015. We recorded and analysed 134 oral (open-mouth) calls from 9 hinds (14-15 per individual) and 129 oral calls from 9 calves (10-15 per individual). The maximum fundamental frequency of hind calls (1.44±0.25 kHz) was as high as in calf calls (1.46±0.24 kHz; $F_{1,16}$=0.04, p=0.85). Vocal identity was well expressed in both hinds and calves; discriminant analysis based on 11 acoustic variables accurately classified individuals in 92.5% hind calls and 96.9% calf calls (chi-square test, p=0.19). Variables contributing most to vocal individuality (duration, start and maximum fundamental frequency) were the same in hind and calf calls. Distinctive to Siberian wapiti, in Iberian red deer *C. e. hispanicus*, the maximum fundamental frequency of hind calls (0.21±0.04 kHz) was significantly lower than in 4-month-old calves (0.57±0.05 kHz). In Siberian wapiti hinds and calves, vocal individuality exceeded those of Iberian red deer hinds (77.0% calls of 22 mothers) and calves (61.1% calls of 17 young). We discuss the role of individuality and differences in contact calls across subspecies of red deer. Supported by RSF, grant 14-14-00237.

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Understanding canid biology helps harness advances in non-lethal control of Australian canids

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Predation of livestock by native and introduced canids is a major source of human-wildlife conflict globally, and lethal control of canids is commonly undertaken to mitigate these impacts in human-dominated systems. However, a suite of recent Australian research activities highlight several potential benefits to emerging non-lethal control approaches. GPS-collaring studies of dingoes and maremma guardian dogs have shown that maremmas do not establish territories and exclude dingoes, but rather thwart predation events through boisterous and threatening vocalisations and behaviour towards dingoes. Within the last decade, a resurgence of pest-proof fencing across some pastoral zones has also created over 6,700 km of new fencing, inhibiting canid migration into over 39 areas totalling over 43,000 km^2 in size. Light- and sound-emitting alarm devices are being used to discourage movement of problem wildlife through open gates (roadways) along these fences. But, preliminary testing of these devices has yielded lacklustre results showing that some species habituate and completely ignore them. New predator aversion collar technologies in development also show great promise for resolving a variety of human-wildlife conflict applications worldwide. Key to harnessing the benefits of these non-lethal approaches is an understanding of canid biology. Predation of livestock and the lethal control of predators will probably continue to be common for the foreseeable future, but in many cases, advances in non-lethal control of predators are likely to provide acceptable, practical, affordable and effective alternatives.

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Mice as Stowaways? Colonization history of Danish striped field mice (*Apodemus agrarius*)

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Species belonging to cultural steppe habitats, like the striped field mouse (*Apodemus agrarius*), are believed to have colonized Northwestern Europe in the footsteps of agriculture after 6500 BP. Nonetheless, the striped field mouse is common on the two southern Danish islands, Lolland and Faster, which have been isolated from mainland Europe by the Baltic Sea since ~10,300-8000 BP. This prompts the question; are these populations early founders or later human introductions? In the fall of 2011 a population of striped field mice in Central Jutland in Denmark was discovered, highlighting once more the question of human introductions. This brought our attention to a potato sorting facility in Sweden, where several striped field mice were observed on and around the conveyor belts. Among others, the facility got its potatoes from Central Jutland. We sequenced 86 full mitochondrial genomes from the northwestern range of the striped field mouse, analysed phylogenetic relationships and estimated divergence time. The majority of evidence supported human induced colonization of Lolland and Falster <1900 BP (< 100 BC). The population in Central Jutland diverged from Falster around 200 BP (1800 AD), again favouring human introduction. The single individual we analysed from Sweden turned out to be a recent immigrant from Central Jutland, verifying that human induced colonization is not just a phenomenon of the past.

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Morphological variation of epipubic bones in didelphid marsupials: Sexual dimorphism and locomotion

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The study of skeleton morphology using linear morphometry allows us to assess the influence of size and shape in bone functions. Marsupials are one of the main vertebrate groups that possess epipubic bones. There are two hypotheses for its function; reproduction and locomotion. The aim of this work was to study the morphological variation of these bones to understand its function in Neotropical marsupials. We measured 371 skeletons (epipubic bones, pelvis, humerus, femur and tibia) of males and females of six genera and nine species with different locomotion habits to test the sexual dimorphism and its locomotion influence. We named structures of the epipubic bone that were undefined until now. We demonstrated the sexual dimorphism in size through t-tests and morphological dimorphism through qualitative osteological analysis. Females had longer and more curved epipubic bones than males in all studied species. Furthermore, a principal pomponent analysis (PCA) of epipubic bone and pelvis measurements generated groups consistent with the locomotion habits (semi-aquatic, arboreal, scansorial and cursorial), and the most important measures were the longest length and the base width of the epipubic and the pubis length, where the epipubic articulates. This differentiation in locomotion habits also occurred when we applied a PCA on the appendicular skeleton measurements, in which the more important variable was the humerus. These results support both previous hypothesis: 1) reproduction function - with a longer bone, females can have more muscle attached to support the abdomen; 2) locomotion function – specialised morphological features for each locomotor habit.

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Double trouble: Physical debilitation and allometry associated with hantavirus infection in rats

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Hantaviruses are harbored by rodents and can cause lethal diseases in humans. To elucidate allometry of infection in the main hantavirus reservoir in Brazil, 246 *Necromys lasiurus* individuals were captured, measured and tested for the presence of hantavirus antibodies in 2008-2013. Sampling was located in four Brazilian savannah areas within a hantavirus cardiopulmonary syndrome hotspot. Seroprevalence was tested by enzyme-linked immune sorbent assays. We used correlation and multivariate analysis to understand associations between sex, age, weight, standard body measurements (ear, tail and hind foot length) and presence of external wounds between infected (n=27) and non-infected rodents (n=219). Infected rodents represented a subset of the multivariate space of non-infected rodents. Infection probability did not vary with sex, but young individuals had half of the probability of subadults/adults on presenting the infection. Interestingly, there were more subadults (n=16) infected than adults (n=9), indicating that subadults are highly prone to spread the disease. Infected rodents had weaker correlation between all measurements when compared with non-infected ones, except for correlation between hind foot and ear length; it increased from +0.38 (not infected) to +0.88 in infected rodents. Injured rodents had higher probability of infection than non-injured rodents. Thus, the main attributes related to hantaviral infection in the natural-reservoir *N. lasiurus* are age and the presence of external wounds. These potential quick indicators can add up to infection diagnosis and security measures in the field. Future investigations on different species should enlighten attributes associated with effective hosts of emerging infectious diseases.

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Genital bones: Taxonomic distribution and morphological diversity

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Many female mammals have a bony baubellum within their clitorides, while males have a homologous penis bone called a baculum. Although most extant mammalian species possess os genitale, our knowledge of them is incomplete. Figures and descriptions of these bones in lipotyphlans are essentially non-existent, although comparative anatomy books routinely mention them. The literature on baubella is even more depauperate and have only been well figured and described in squirrels. In this study, the taxonomic distribution and morphology of os genitale were studied at three museums (USNM, MNHB, AMNH). All of these osteological collections contain more bacula than baubella. Bacula representing a total of 47 species of carnivorans, 17 rodents, 12 primates, 2 lipotyhlan, 1 chiropteran where found, but only one carnivoran (*Lontra*) and one rodent (*Tamias*) were found to include baubella. Very few specimens were found in main collections associated with post-crania, most were housed within special genital collections. To examine the potential preparational artefacts in osteological collections of os genitale being absent in smaller taxa, an x-ray study was conducted. A PaxScan 4030R flat panel digital radiography was used to image female and male wet lipotyphlan specimens (both whole specimens and isolated dissected genitalia). This imaging technique was robust in picking up fine skeletal detail except in whole hedgehogs, whose spines resulted in excessive background noise. A total of 79 specimens, representing 28 genera, were imaged including solenodontids, soricids, talpids and erinaceomorphs. No baubella were observed and bacula were only variably found in *Crocidura fulliginosa* and *Talpa europaea*.

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Use of camera traps as a means for mapping distribution and inferring movement in a fragmented landscape

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We examined the large mammal community in Qinling Mountains of central China and used camera trapping data, and data layers for the human and environmental landscape, to construct species occupancy models for giant panda (*Ailuropoda melanoleuca*) and six other sympatric species (takin *Budorcas taxicolor*, tufted deer *Elaphodus cephalophus*, Chinese goral *Naemorhedus griseus*, Reeve's muntjac *Muntiacus reevesi*, leopard cat *Prionailurus bengalensis*, and yellow-throated marten *Martes flavigula*). We then constructed circuit models to identify potential corridors for each species, and evaluated the effectiveness of giant panda corridors to restore the habitat connectivity for these sympatric mammals. Occupancy modeling identified the unique set of environmental variables associated with each species. We found that giant panda and all other focal species had some degree of fragmentation to their suitable habitat that required habitat corridors. Among the eight potential giant panda corridors, conservation efforts on reducing anthropogenic impacts would significantly improve the effectiveness of six corridors, while the other two corridors would require extensive topographic and vegetative alterations for improvement. The five proposed giant panda corridors had remarkable overlap with corridors proposed for other species. We suggest two giant panda corridors as a priority due to their ability to maximize the benefits to both giant panda and a broader suite of wildlife. Corridor planning in this region of China will likely continue to use the single species policy for the foreseeable future and our results highlight that not all potential giant panda corridors have equal effectiveness for other wildlife species

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Who contributed to the evolution of multiple fruits in Asian dogwoods (*Cornus*)?

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Cornus is a genus of woody plants, commonly known as dogwoods. Various species of dogwoods are native throughout much of temperate and boreal Eurasia and North America. Though most *Cornus* species produce simple fruits, which is the ancestral character, some Asian dogwoods including *C. kousa* make red multiple fruits. Flowers are separated in these species, but the separability is lost as flowers change to fruits. Eyde (1986) insists that multiple fruits have evolved via seed dispersal by Asian monkeys, who can discriminate red from green, and American dogwoods fruits remain simple because the New World monkeys, blind to red and living in warmer region, never took up foraging on them. This traditional view, however, seems to be incorrect. I monitored the number of *C. kousa* fruits on the ground and on the tree for two weeks, and found that the proportion of ripe fruits on the ground was constantly high. This shows that the fruits tended to fall off trees soon after they get ripe. On the other hand, I stayed nearby *C. kousa* trees, observed animals visiting there, and found that, though wild Japanese monkey (*Macaca fuscata*) ate many unripe fruits on the tree, they consumed few fruits on the ground even though many ripe ones still existed. When monkeys ate unripe fruits, I heard them chewing and fracturing seeds. These results suggest that terrestrial mammals other than monkeys could be the better seed dispersers of *C. kousa*, and have contributed to the evolution of multiple fruits in dogwoods.

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Phylogeny, not ecology, shapes the mammalian vomeronasal system: Evidence from *V1R*s and morphology

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In mammals, social chemical cues are primarily detected in the vomeronasal system. While vomerolfaction is well conserved due to its role in fitness-related behaviors, several mammalian groups have lost function, including Old World primates, some aquatic mammals, and most bats. These losses and gains might relate to ecological variation, such as circadian rhythm, social system, or habitat specialization, but it is unclear if these patterns are related to ecology, phylogeny, or both. We used vomeronasal genetic machinery and morphology to model the evolutionary dynamics of loss and gain vomerolfaction. Vomerolfactory cues are detected by *V1R* receptors in the vomeronasal organ (VNO), including proteins encoded *V1R* genes. Both V1Rs and VNO size and shape are highly variable among mammals. We obtained the *V1R* profiles from nearly every order of mammal, and estimated the birth and death rates of gene duplication and loss. We also quantified VNO morphology from iodine-stained soft tissue µCT-scans. Our results reveal the evolutionary history of the mammalian vomerolfaction was complex, with no clear connection to ecological explanations of loss or gain. Many mammalian orders have experienced decreased birth rates of *V1R* genes, relative to other mammals. However, many lineages with low *V1R* birth rates still possess a well-developed VNO and retain intact orthologous receptors with distantly related species, suggesting strong purifying selection in light of low diversification. Our study highlights the importance of incorporating birth-death models and phylogenetic comparative methods to understand the evolutionary history of complex traits, such as a sensory system.

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An overview on the distribution of Mustelidae (Mammalia: Carnivora) in Turkey

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Turkey has 154 land mammal species, and of them Mustelidae are represented by eight species; *Mustela nivalis*, *Mustela putorius*, *Martes martes*, *Martes foina*, *Lutra lutra*, *Meles meles, Meles canescens* and *Vormela peregusna*. Though there are a a lot of fragmented studies about these species, there are not any actual distribution maps for these species. Since a reliable distribution map for a species is crucial for a lot of ecological, conservation and management studies, here we provide these maps for mustelid species in Turkey. To prepare maps, all distribution records from the literature, press news, personal communications, some records in wildlife photography web sites in Turkey, and our original field survey and phototrap records were used. About 1350 record localities for all these species were presented and are shown in distribution maps. By combining data in literature and our experiences from the field surveys, the main threats, conflicts with people, and National Red List status for Turkey, are discussed. National Red List status for *Martes martes* was proposed as DD, for *Martes foina* as LC, for *Mustela nivalis* as LC, for *Mustela putorius* as EN, for *Lutra lutra* as NT, for *Vormela peregusna* as VU, for *Meles meles* as LC, and for *Meles canescens* as LC.

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Investigation of the present state of wild animals and the analysis of the effect by human interference using camera trapping

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Baekdudaegan is an ecological axis of the Korean peninsula, and it is home to a variety of flora and fauna including endangered wildlife. However, the development of roads and other degradation activities have led to an increase in the number of breakage of forest ecosystems, including Baekdudaegan. In addition, the number of people enjoying life vitality and healthy leisure life through mountain climbing increases the space in which use by wild animals and humans overlaps. These factors can cause a reduction in wildlife activity and habitat space. In Korea, research on the use of space in common with wildlife and humans has not been studied yet. However, there is a growing number of studies on case studies such as protection and restoration of wildlife and habitat for wildlife management. In recent years, interest in animal welfare has increased, and non-invasive research methods using camera trapping have been widely used in research of mammals. The camera trapping study carried out in this study can acquire data on the distribution status, major activity time, and species of mammals in the Baekdudaegan. Because this study analyses the relationship among wild animals emerging in the same space as mountain climbers who are in the Baekdudaegan conservation area, it can be used as basic data for countermeasures against the problems of Baekdudaegan such as the establishment of the protected area, limiting damage caused by human access, and access control.

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RAD sequencing recovers population genetic structure in desert dwelling marsupials

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Genomic level sequencing is increasingly affordable and accessible, allowing us to explore the population genetics and phylogeography of non-model taxa with previously unimaginable datasets. Population genomic studies using RAD (restriction site-associated DNA) sequencing is an alternative to traditional microsatellite and Sanger sequencing methods and has the advantage of requiring fewer individual samples whilst still producing powerful datasets. The genetic structure of most Australian desert mammals is poorly understood, in part because it is difficult to obtain enough samples for population genetic studies. Survey work in the arid Pilbara, Western Australia, in 2003-2006 provides a large repository of high quality mammal tissues held at the WA Museum suitable for RAD sequencing. In this comparative study, we sequenced the two commonly used mitochondrial genes from two endemic Pilbara planigales (Dasyuromorphia), one species a generalist that is commonly captured at most survey sites and the other restricted to cracking clay habitats. Contrary to expectations, clear genetic structure was detected in the mtDNA data for the generalist species but not for the habitat specialist. A sub-set of these individuals, selected continuously throughout the species distributions, were then used for RAD sequencing. With the more powerful RAD sequencing dataset clear population structure was evident for both species. We compare the results from the two methods and show that RAD sequencing is a useful tool for investigating the population structure of desert and rare mammals where sufficient high-quality DNA samples are available.

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Interspecific differences in tannin tolerance cause different population responses of three sympatric rodent species to acorn masting

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Acorn masting has been believed to cause positive responses in rodent population dynamics, but a considerable number of studies show that it is not always the case. Acorns are generally nutritious, but acorns of some species contain a high level of tannins, which cause negative effects on consumers. In this study, we tested the hypothesis that rodent population responses to acorn masting may vary depending on differences in tannin tolerance among rodent species, using three sympatric rodent species in Hokkaido, Japan. The effects of acorn abundance on rodent population densities were analyzed using the dataset obtained in the Uryu Experimental Forest of Hokkaido University, in which population fluctuations of the three rodent species (*Apodemus speciosus*, *A. argenteus*, and *Myodes rufocanus*) and crop of *Quercus crispula* acorns have been monitored since 1992. Population growth rates of *A. speciosus* were higher in the next year after mast years than in those after non-mast years, but this tendency was not observed in the other species. To compare tannin tolerance, an acorn feeding experiment was conducted. Test animals were fed only *Quercus crispula* acorns for 6 d after 2 wk of tannin-acclimation period. *A.speciosus* increased their body weight during this period, whereas *A. argenteus* and *M. rufocanus* lost 6.8% and 13.6% of their weight, respectively. This indicates that *A. speciosus* has higher tannin tolerance. These differences in tannin tolerance were consistent with population responses to acorn masting. This finding emphasizes the importance of evaluating tannin tolerance, to understand rodent population dynamics.

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Automatic identification of mammal genera in camera trapping pictures using support vector machines and bag of words

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Camera trappping is a non-invasive and efficient technique for monitoring terrestrial mammals. Taxonomic identification is the first step in camera trap data analysis; it requires expert knowledge and manual processing, and this process takes a long time. Pre-selecting relevant pictures for an expert review is an alternative to reduce the analysis time. The challenges to automatic identify a mammal´s genus from camera trap photographs include few examples of some genera (unbalanced classes problem), variation in light levels, constant changes in the scene, animals partially occluded, and blurred photographs. Until now there has not been a computational tool to help in the specific task of determining an animal´s genus. This work presents the use of Machine Learning Techniques, Support Vector Machine (SVM) and Bag of Words (BoW), as alternatives for labeling mammal genera. The results for a database (Andean, Caribbean and Pacific regions in Colombia) with 75,000 photographss and strong unbalance between classes are promising. It was possible to automatically identify photographs of animals and to differentiate among birds and 20 mammal genera (average accuracy 70%). Results are comparable with other theoretical works that only studied the classification problem. Our proposal includes all stages; metadata extraction, identification of images with animals, image segmentation, classification between birds and labeling the mammal genera. Currently, the tool is being tested by scientists of the Alexander von Humboldt Biological Resources Research Institute in Colombia. Technical details about the proposal, software tests and use of this computational tool will be presented.

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WomSAT – wombat survey and analysis tool

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Wombats are large herbivorous marsupials unique to Australia. The three extant species of wombat have been affected by threats associated with the advent of European settlement; however one of the major threats to the southern hairy-nosed (*Lasiorhinus latifrons*) and bare-nosed wombat (*Vombatus ursinus*) is sarcoptic mange. Mange is caused by the *Sarcoptes scabiei* mite, and is a severely debilitating disease, with affected wombats eventually succumbing to secondary infections, starvation or dehydration. Various groups have been treating wombats using treatment flaps or invasive techniques. These techniques are very labour intensive and only possible in selected areas. In the longer term, some of these strategies may lead to resistance in the mite, further endangering the wombat population. Trapping over time is also highly likely to increase stress levels in the animals, which influences their capacity to maintain appropriate levels of immunity against parasitic infections. WomSAT is a citizen science-based website, with associated iPhone and Android apps. It allows anyone to log their wombat (dead or alive, and their level of mange), and wombat burrow sightings online, in real-time. The information gathered is being used to investigate the nation-wide ecology of wombats and mange, as well identify other threats to wombat survival. In the longer term is it hoped that it will aid in the development of a nation-wide strategy to manage mange in wombat populations.

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The integration of computer assisted technology into camera trapping

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Camera trapping is used extensively across the globe for the detection of wildlife in research and monitoring programs. Numerous comparisons have been undertaken to evaluate the cost effectiveness of this method compared to historical ecological survey practices, and many papers have highlighted the benefits to conservation of using this technique. An advantage of camera trapping is that devices can be deployed for prolonged periods of time, gathering hundreds of thousands of images per deployment: a significant improvement in collecting spatial and temporal scale ecological knowledge. However, the negative side to camera trapping is the large volume of image data that must be coded and analysed. Computer assisted technology offers a number of opportunities for practitioners to further save processing time and in some cases, excludes the need for physical visitation to the deployed devices. We will outline how we are integrating computer science into camera trapping techniques to aid image library processing, and describe a prototype device we are building called Wild Dog Alert.

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Population genomics of a zoonotic disease host: The capybara as study case

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Habitat fragmentation creates open areas that could be used by generalist species as corridors among populations, allowing for gene flow, but also facilitating the spread of vector borne diseases that use these species as hosts. With the aim to understand how the genetic diversity of a zoonotic disease host is distributed along a strongly modified habitat and therefore can serve as a proxy of disease spread, we used the capybara (*Hydrochoerus hydrochaeris*) as study system. The capybara is the largest rodent and inhabits open areas along its distribution. This species also is the main host of the cayenne tick and therefore the vector of Brazilian Spotted Fever (BSF). With habitat modification for sugar cane crops in Sao Paulo state, capybara populations have increased and BSF cases have been increasing in recent years. Here we present results about i) capybara genetic variation assessed by the use of genomic tools and, ii) the population genetic structure of the species in Sao Paulo state. For our analyses, we used a reduced representation genomic library created using a RAD-seq protocol. We identified ~20,000 SNPs along the genome in 158 samples distributed along 11 populations in Sao Paulo state and two in Mato Grosso and Mato Grosso do Sul. Our results using pairwise F_{st} showed eight different populations, while clustering methods showed three different populations. These data will be of great importance for the management of populations, to avoid further spread of BSF.

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Leptospira infection in domestic dogs and wild mammals as hosts of the same serovars

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The expansion of urban areas takes humans and domestic animals into the wild environment, favoring the transmission of pathogens among species. This issue has implications for environmental conservation, since emerging infectious diseases in wild mammals can affect their populations leading to extinction. This scenario has been reported in several protected areas around the world, and here we highlight our study at Carlos Botelho State Park (CBSP), São Paulo State, Brazil. We investigate the infection by *Leptospira* in domestic dogs that live on the edge of CBSP, and move freely inside the Park without supervision of their owners. In 2015 and 2016, 10% (35/350) and 6.3% (25/396) of the animals were seropositive, respectively. Among the 252 dogs sampled in both years, six were seropositive. Of the 13 serovars tested, the most common were *L. cynopteri* (55.5%), *L. autumnalis butembo* (14.8%), and *L. grippotyphosa* (9.2%). In addition, other studies found that these three serovars also were detected in wild canids, felines, cervids, primates and marsupials in the state of São Paulo. Our investigation suggest that these infectious agents can be transmitted from these domestic dogs to wild animals of the CBSP. Knowledge of *Lepstospira* and their hosts help to understand the dynamic disease improving actions for prevention and control policies. Our results suggest that immunisation of domestic dogs and health education campaigns are the priority actions to avoid diseases on wild and domestic animals, mainly near to protected areas.

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Utilising community wisdom to determine the magnitude and causes of regional declines in the eastern grey kangaroo (*Macropus giganteus*) in south east Queensland.

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South east Queensland (SEQ) has been one of the fastest growing regions in Australia over the last two decades. The processes of urbanisation associated with this growth have resulted in rapid modification of the landscape. Much of the eastern grey kangaroo's natural habitat has been cleared or fragmented by roads and high density human settlement, raising concerns for the persistence of kangaroos in some areas. The negative impacts of urbanisation on kangaroo populations in the region, while supported by the colloquial observations of local residents and wildlife professionals, is not documented. This study therefore used a modelling approach utilising data from the general community and from official sources to address the following aims; (i) to map the current distribution of eastern grey kangaroos in SEQ, (ii) to look for trends in kangaroo abundance, and iii) to identify the anthropogenic drivers of changes in kangaroo abundance. Our results indicate that kangaroo populations have, (i) undergone an overall decline in abundance and distribution and, (ii) kangaroo declines can be anticipated in areas with high rates of human population growth and/or areas with smaller natural areas or remnant bush. This study emphasises the importance of integrated urban development over large spatial scales to mitigate impacts of urbanisation on wildlife. It also highlights how social perceptions and high visibility can obscure patterns of decline and local extinction in common species.

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Comparative three-dimensional CT image analysis of the mastication system in the giant anteater and southern tamandua

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The mastication system of the giant anteater (*Myrmecophaga tridactyla*) and the southern tamandua (*Tamandua tetradactyla*) were functional-morphologically compared by three dimensional image analysis. The anteaters medially and laterally rotate the mandibular bones to control the elongated tongue and to house the relaxing tongue. From the three-dimensional CT images of the two species, we point out that the shape and size of oral cavity can be changed by the rotated mandibular bones. The volume of the oral cavity can be bilaterally widened by the medial bending of the dorsal part of both mandibles. The masseter muscle, the superficial temporal muscle and the lateral pterygoid muscle act as main motors of the mandible rotation. These muscles contribute to the medio-lateral movements of the mandibular bones in the two species. The digastric muscle consisting of a short and thin bundle is vestigial. The dorso-ventrally lower body of mandible and the incomplete zygomatic arch avoid the collision of the mandible with the cranium during the rotation movement. The two species are commonly equipped with the elongated skull and the derived mastication mechanism. We suggest that the distribution pattern of the mastication muscles has not drastically changed in the evolutionary history within Vermilingua.

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Latrine site selection of Carnivora

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Some species of Carnivora have been thought to emit a chemical signal by placing their faeces or urine in a conspicuous manner. Although many studies suggest that animals of Carnivora select the locations of defaecation, field survey methods were biased and/or a proper statistical analysis were not applied in most studies. We investigated latrine sites with an unbiased method in a natural forest of Hokkaido. To minimize the oversight of latrine sites, three or more researchers walked the study area (153.4 ha) thoroughly in the line at 10 m intervals and observed characteristics of all latrines and latrine sites (mound, flat, and pit type topography). We also investigated the amount of available resource for latrine sites by observing characteristics of randomly selected locations in the study area. Most latrines (61, 54%) were found on mound type sites, followed by flat sites (52, 46%). No latrines were found at pit type sites. In contrast, the amount of flat type latrines (95, 84%) dominated over other types in available resources. It is therefore concluded that mound type topography was selected for latrine sites, whereas the other two types (flat and pit) were avoided.

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An improved method of capture and immobilization for medium to large size macropods

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Macropods are particularly known for their proclivity to suffer from stress related injuries and ailments as a result of capture. Over the years, several different methods for capturing macropods have been develop, but in general they can be classified in two major groups, trapping and darting. Trapping is most commonly used for small macropods that can be attracted to a baited area or traps, where they can then be caught by means of nets or by triggering of the trap mechanisms. Darting is most commonly used for large macropods, since they are more prone to suffered from stress when caught in traps. Most capturing techniques have limitations either dependent on the species habits or animal welfare implications. Here we describe a technique, partly based on the “nylon drop-net” technique described by Lentle et al. in 1997, but with substantial modifications based on commonly used capturing techniques for ungulates in Africa. We utilised this technique to successfully capture 40 agile wallabies (*Macropus agilis*), 24 females and 16 males, weighting between 6-24.1 kg. During immobilisation, a single dose of intramuscular Diazepam was administered as a muscle relaxant. No deaths occurred during or as a result of capture, or in the 8 weeks following capture.

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The Oz Mammal Genomes initiative: Mammal genomics, evolution and conservation at a continental scale

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The Australo-Papuan region has a unique mammal fauna, which faces unique threats and poses important evolutionary and ecological questions. Genomic approaches have great potential to advance our understanding of the region's terrestrial mammals and their conservation. The Oz Mammal Genomes Consortium brings together museums, researchers, data specialists and wildlife management agencies to comprehensively tackle mammal genomics at a continental scale and at three different levels of resolution. There are few published genomes for Australian marsupials. We will develop well-assembled genomes from a broadly representative range of marsupial taxa, to facilitate new insights into evolution and to provide reference data for conservation studies. Genome projects are now underway for three priority species (fat-tailed dunnart, brush-tailed rock-wallaby and eastern bettong), with several additional species to follow. Our current understanding of evolutionary relationships among many mammal taxa remains incomplete. To improve resolution of genus and species boundaries we are generating comprehensive phylogenies of all extant and recently-extinct terrestrial mammals native to the Australo-Papuan region. We are using genome scanning methods to sequence over 1000 genes from around 500 taxa, including marsupials, rodents and bats. Finally, the availability of reference genomes and phylogenies will provide a solid base for population-level studies. We will develop conservation genomic datasets for a selection of threatened mammal species. Using a genome scanning approach we will measure genetic diversity and inbreeding, determine population structures, and identify adaptive variation. Species will be prioritised so that genomic data will contribute directly to urgent conservation management decisions.

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Distribution of the Eurasian otter (*Lutra lutra*) in Gwangju Stream

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Field surveys were undertaken to estimate the spatial and seasonal distribution of the Eurasian otter on a 23 km long section of the Gwangju Stream, a first tributary of the Yeongsan River that flows through Gwangju Metropolitan City, from 2009 to 2011. The distribution of the numbers of spraints and sprainting spots as an index of otter activity were examined from upstream of the southwest valley of Mt Mudeung to downstream of the Yeongsan River confluence. The spraint markings of otters were broadly distributed along the streamline, with higher marking intensity downstream of the Yeongsan River confluence. Otter markings (which totaled 615 spraints and 169 sprainting sites over the course of the study) exhibited seasonal cycles, with a prominent peak in March and November, from the confluence of the Jeungsimsa stream to downstream of the Yeongsan River confluence. These results suggest that Eurasian otters, an endangered species in Korea, are likely to utilize the Gwangju Stream as their foraging habitat, and adapt to an urbanised environment.

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Deer and kangaroos - are they spreading weeds in their scat?

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Native kangaroos and feral deer share the same landscapes in parts of Australia. They are likely to share some similar diet items. Do the same species of plant, native and weeds, germinate from kangaroo and deer scats? We present data on germination trials from scat collected in Western Australia

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Genetic structure of the pampas cat (*Leopardus colocolo*): Defining demographic units for specie's conservation in Brazil

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Understanding the processes that guide and determine different genetic diversity patterns in wild populations is very important for conservation, because it reveals threats and possible management measures. The pampas cat, *Leopardus colocolo*, is a small felid from Neotropical region, associated to open habitats. In Brazil, the species occurs in unconnected areas in the midwestern and southern Brazil. Although the specie's taxonomy is controversial, it is known that some populations are genetically structured, as a result from long periods of isolation. We analyzed 13 microsatellite loci to characterize the genetic divergence between the two geographically disconnected Brazilian populations of pampas cat. Samples from Uruguay were included, since previous studies have indicated the existence of only one population between Uruguay and southern Brazil. Our sample comprised 23 *Leopardus colocolo* from midwestern and 22 from southern Brazil and Uruguay. The Brazilian populations showed significant genetic structure, corresponding to two genetic clusters. The gene flow between the populations is low, and apparently not sufficient to stop genetic differentiation. Therefore, we suggest these populations should be considered as different management units. The southern Brazil and Uruguay population seems to be isolated to the north by the Atlantic Forest, and to the west and south by the Paraná and Uruguay rivers. Although its genetic diversity does not seem to be reduced, this population showed levels of inbreeding and low effective population size, which can lead to the reduction in population viability and become extremely dangerous for specie's conservation in these areas.

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How can we better assess the cardiopulmonary function of large free-living mammals?

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Chemical immobilization is often necessary for the study of undomesticated animals, but can have confounding physiological effects on the data collected. We exposed sheep (O*vis aries*; n=5) and goats (C*apra hircus;* n=4) to an immobilizer (etorphine) then transitioned them onto a deeper sedative (propofol) and reversed the etorphine. The cardiopulmonary effects of these drugs were compared with data under a very mild sedative (midazolam). We hypothesized that propofol would provide better data than if animals remained on etorphine. Etorpine caused tachycardia in the sheep (110±14 to 180±7 beats min^{-1}, $P<0.001$), which abated under propofol (180±7 to 147±6 beats min^{-1}, $P<0.05$). Etorphine caused a reduced stroke volume in the sheep (53±4 to 35±6 ml, $P<0.05$), but not the goats. Overall, cardiac output was unchanged in either species. Hypoventilation was seen in the sheep under etorphine (7±2 to 3±0.3 L min^{-1}, $P<0.05$) before improving under propofol (3±0.3 to 9±2 L min^{-1}, $P<0.05$). Ventilation in the goats was unaffected. The goats were hypertensive under propofol (71±3 to 101±6 mmHg, $P<0.05$) but the sheep was unaffected. The mean pulmonary artery pressure of both species increased under etorphine (14±1 to 19±1 mmHg, $P<0.05$; 14±1 to 20±2 mmHg, $P<0.05$ respectively), before decreasing under propofol. Both species were relatively hypoxic and hypercapnic under both drugs compared to midazolam ($P<0.05$), though to a lesser degree under propofol. Many of the side effects observed in both species under etorphine were ameliorated when etorphine was reversed and the animals held under propofol. The data obtained from animals under propofol more accurately reflects the resting state.

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Applying a social-ecological system approach to influence dingo management practices

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The decline of Australia's mammal fauna is linked strongly to two exotic meso-predator species, feral cats (*Felis catus*) and European red foxes (*Vulpes vulpes*). The dingo (*Canis dingo, C. familiaris*, or *C. dingo* × *C. familiaris*), as an apex predator that may suppress smaller meso-predators, is extolled as a potential conservation tool. While the potential negative economic effects of dingo predation on sheep and cattle likely influence control practices, limited research has been applied to understand the complex socio-cultural factors that interact with economic and ecological considerations of dingo management practices. Globally, human-carnivore conflicts are ubiquitous and difficult to resolve with science or policy interventions because they tend to be value-based. Systems-based approaches recognise that humans and human constructs are integral to ecosystems, and assume that ecological problems are often as much about clashes of stakeholder values and social rules as they are about inappropriate land management. Social-ecological system (SES) models can support the testing of assumptions about the strength and direction of interactions among social, economic, and ecological components of a system and the likely efficacy of interventions. We propose a hypothetical pastoralist-dingo SES to illustrate our point.

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Mexican Late Pleistocene proboscidean diet and habitat

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During the Late Pleistocene, México was inhabited by at least five proboscidean genera pertaining to three families, two extinct ones Gomphotheriidea (*Cuvieronius* and *Stegomastodon*) and Mammutidae (*Mammut americanum*), and one extant but extirpated from the Americas Continent, Elephantidae (*Mammuthus columbi*). Coexistence of those species within the country could be explained by their different food and habitat requirements that have been studied based on their dental morphology. Mammoths had hypsodont molars that were specialized for grass feeding, inhabiting open areas like grasslands and savannas. On the contrary, gomphotheres and North American mastodons were considered as browsing specialists, living inside forests. However, the use of $\delta^{13}C$ and $\delta^{18}O$ over the last 10 years has changed understanding of the diet and habitat inferences for those animals. Carbon and oxygen isotope values for some *Cuvieronius*, inhabiting forests and grasslands, have shown either C3, mixed C3/C4, or even C4 diets, while *Stegomastodo*n living in savannas or grassland had a mixed C3/C4 diet. On the other hand, North American mastodons were exclusively feeding on C3 plants and lived in forested areas, while mammoths chose a wide variety of plants, including C4, C3, and mixed C3/C4 but mostly inhabited grassland or savannas. Overall, gomphotheres and mammoths ate a wide variety of plants, ranging from exclusive C3, C4 or mixed C3/C4 plants, as well as having variable habitats (close or open), although mammoths lived mostly in grasslands. On the other hand, mastodons were C3 diet specialists living in forest, as also inferred by molar morphology.

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Using DNA-based identification to understand diet: Giant panda and bamboo

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Next generation sequencing methods allow species identification from environmental samples, including faecal material and thus facilitate the investigation of diet and the interdependencies between predator and prey. PCR-based methods, employing a range of meta-barcodes have been widely used, but suffer from biases and limitations. Capture-based methods may reduce these biases as well as provide a means for assessing multiple barcodes and meta-barcodes simultaneously, including novel taxa-specific nuclear markers to maximise species identification. The robustness and accuracy of these methods will be tested using a range of captive animals, where the diet is known. This method will allow investigation of diet in a specialist herbivore, the giant panda (*Ailuropoda melanoleuca*). Giant panda feed almost exclusively on bamboo, yet their diet may contain hidden complexities, with over 60 bamboo species are reportedly eaten, plus occasional consumption of other plants and even animals. Many bamboo species are difficult to distinguish, especially following digestion, restricting our understanding of the precise bamboo species giant pandas rely on. Standard ‘universal’ plant barcodes have limited resolution in bamboo due to low rates of molecular evolution, and even whole chloroplast sequencing shows limited differences. Using existing genomic data from bamboos and other grasses to develop nuclear DNA species diagnostic markers that can be incorporated into a capture-based approach, we will be able to increase the reliability of bamboo identification in the diet. In addition, information from standard ‘universal’ meta-barcodes will also be incorporated to provide a complete overview of both bamboo and non-bamboo species consumed by giant panda.

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Developing a next generation genomic toolkit for management of the koala, *Phascolarctos cinereus*: From pedigrees to population genomics

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The koala (*Phascolarctos cinereus*) is an iconic Australian species with complex management requirements, from halting declines to dealing with overabundance. The discrepancy in population trends across their distribution means that broad scale management of koalas is not ideal. Instead, management often occurs at local scales (in local government areas or on regional populations) with little reference to the broader Australian context. Previous population genetic studies of koalas have been carried out using a range of different marker sets. These are useful in isolation, but are often not comparable across studies. This study uses next generation sequencing methods (targeted exon capture) to develop a single nucleotide polymorphism (SNP) assay for use in koala population genetic studies at a range of scales, from individualization within local and captive populations to broad scale population genetics. Identified neutral and functional SNPs will allow us to investigate gene flow and neutral genetic diversity across the koala's distribution as well as through time with both contemporary and historic museum samples to be analyzed. Additionally, as part of the Koala Genome Consortium, these SNPs have been mapped to the koala genome, providing unprecedented power to investigate a range of questions involving traits under selection, linkage, and much more. It is our hope that these markers may be utilised in future population studies, and by other researchers and management bodies to facilitate more consistent and comparable data collection for conservation management of this species.

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Bloody and the beast: Invasion of blood sucking nematodes in European bison - contributory factors and consequences

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The appearance and spread of new parasitic invasions in populations of wild animals are rarely observed. We investigated invasion of the blood-sucking nematode *Ashworthius sidemi* in European bison from its initial phase, and analysed factors affecting infection severity. The study showed the rapid spread of a new parasite in a bison population (100% prevalence after four years), fast increase in the infection intensity to the mean level of 8,000 nematodes per bison (maximum 44,310), and the strong immune response in animals with severe infection. Factors influencing infection intensity were time since the appearance of the parasite, herd size, bison age and sex. The highest number of parasites was found in sub-adult bison. Adult females were more infected than males. The increase in herd size was followed by an increase in the infection intensity with *A. sidemi*; the greater when the parasite was present longer in the bison population. Measures aimed at reducing the winter aggregation of bison in supplementary feeding sites reduced the parasitic load. High infection levels led to a decrease in red blood cell parameters and an increase in the level of gamma-globulins. Moreover, increasing intensity of *A. sidemi* infection significantly increased the probability of occurrence of other parasites. This study allowed a better understanding of the mechanisms of biological invasions in populations of wild animals and the protective immune response of the host. It also showed that adaptive management can effectively lower rates of parasitic infections. The study was financed by the National Science Centre, project No. 2012/07/B/NZ8/00066.

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Site selection for musk deer monitoring based on similarity analysis

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Musk deer (*Moschus moschiferus*) are endangered by anthropogenic threats and they are included in CITES appendix II. They are very rarely observed in the mountainous region of the northeastern part of Korea. This study attempted to find sites similar to those in which they had appeared to determine monitoring sites for musk deer. For this, similarity analysis and spatial analysis of GIS were used. The study area is Hwacheon-gun and Inje-gun located in the northeastern part of Korea. The spatial unit of analysis is a 5 × 5 km regular grid and the study area consists of 138 grids. Twenty-five points where musk deer were observed were used to define the environment in which they were observed and to determine similar areas. Thirteen points were used for the experiment and twelve points were used for the verification. The similarity analysis method was Minkowski Distance (MD), and 12 factors of three categories such as climate, terrain, and land cover were used as environmental factors in MD analysis. In the results, the mean, maximum, minimum, and standard deviation of MD at the grid where musk deer appeared was 56.3, 69.1, 19.4, and 17.4, respectively. The probability of detection of musk deer was divided into five stages: a) MD <= 20: very high; b) 20 < MD <= 40: high; c) 40 < MD <= 60: medium; d) 60 < MD <= 80: low; e) 80 < MD: very low. The monitoring sites were selected as clustered areas with high probability grids.

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Deciphering wolf howls

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Howling evolved in wolves to communicate with other group members and to demarcate their territories. Howls can travel large distances owing to their high amplitudes and narrow frequency ranges. Howl modulation is not arbitrary; therefore, it can be used to distinguish one population from another. My objective is to use howling as a tool to identify individual wolves and investigate its use as a population estimation tool for wolves. Howls recorded from the captive wolves were played in the field during early morning and evening hours, expecting a response. A 50 second long howl was played five times in a session, at an interval of 3 minutes with increasing amplitude. If a response was received, the session was repeated after an interval of 15-20 minutes to enhance possibility of recording a better howl. Fundamental frequency, the lowest frequency of periodic wave form, of each howl was identified and data on thirteen main parameters of the sound were extracted to identify individual wolves. The method was validated by using 54 howls of known wolves (n = 4) from captivity as well as from the wild. Data was analysed using discriminant function analysis (DFA). During validation of the method from the howls of known individuals, we achieved 94.0% accuracy. From this study, it was inferred that howling has a high potential to be used as a tool to monitor population of wolves. The application of this techniques as a tool to monitor free ranging populations in human dominated landscape will be discussed.

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Habitat use and home range of neotropical cats in Brazilian Cerrado.

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The majority of neotropical cats are sympatric in almost all Brazilian biomes. The aim of this study was to determine the habitat use and home range of three neotropical cat species in Brazilian Cerrado. Two *Leopardus guttulus* (males), two *Puma yagouaroundi* (male and female) and one *Leopardus pardalis* (male) were monitored by radio-tracking. All animals' demonstrated preference for gallery forest, with a mean of 83.5%. *L. guttulus* had the largest preference for open areas (30%) compared with other species. *L. guttulus* had the smallest home range by Minimum Convex Polygon (MCP 100%) of 4.67–4.93 km^2 and Harmonic Mean (HM 95%) of 4.83–5.45 km^2. *P. yagouaroundi* home range was 17.97 for female and 25.32 km^2 for male by MCP and by HM 95%. We observed the formation of two home ranges per animal (female 6.22 km^2 and 15.44km^2; male 11.90 km^2 and 20.25 km^2). The home range of *L. pardalis* was 19.21 km^2 by MCP and the two home ranges observed by HM 95% were 8.42 km^2 and 15.11 km^2. *L. guttulus* core area (HM 75%) varied 46.6 to 60% of the home range. The core area of *P. yagouaroundi* was 5.3% of small and 39% of large female home range, and 16% and 23% of male home range, respectively. *L. pardalis* core area was 22% of small and 53.6% of large home range. This study provides basic information about the ecology of these species in Cerrado.

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Effects of sika deer on understory vegetation, seedlings and saplings in Akan National Park, northern Japan.

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Overabundant deer populations often cause habitat degradation, for example disappearance of seedling and sapling in forests or soil erosion. Few studies have reported the response of vegetation to deer foraging pressure when deer density decreases; on the other hand, many studies have indicated the changes of vegetation when deer density increases. Sika deer *Cervus nippon* population has irrupted during the 1980s and 1990s in eastern Hokkaido, northern Japan, and causes severe damage to forest vegetation. Thereafter the population has decreased by artificial control by the Hokkaido Prefectural Government based on a management plan. The estimated deer density in Akan National Park (ANP) was 27.1 ± 10.7 deer km^{-2} in 1993, and significantly decreased to 9.5 ± 2.5 deer km^{-2} in 2009. Our objective in this study is to identify the response of forest vegetation to the variation of deer density. We established seven sets of an exclosure sites and a control site in 1995 in ANP and have sampled by the quadrat method from 1995 to 2011. We analyzed the 15 palatable herb species and 2 unpalatable species, and found the cover and maximum height of *Sasa senanensis* and *Trillium* spp. on the former increased and *Senecio cannabifolius* on the latter decreased in the control sites. We also determined the impact of the deer fence and relative photon density on the seedling and sapling's density and survival. We suggested that herbaceous plants were recovering because of reduction of deer density, but it was still high for survival of seedlings and saplings.

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Sika deer(*Cervus nippon*) identify hunting zones in Kushiro, Japan?

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Sika deer (*Cervus nippon*) move to wildlife refuges during the hunting season. In Kushiro, located in the eastern part of Japan's northern-most island Hokkaido, Sika deer density increases during the hunting season. While sika deer behavior is affected by hunting pressure, there are only a few studies where the relationship between hunting pressure and Sika deer behavior is identified, using detailed movement with GPS collars in Japan. This study investigated whether sika deer move to wildlife refuges to avoid hunting pressure. Differences in behavior between the hunting season and the closed (non-hunting) season was evaluated for 20 sika deer equipped with GPS collars (Lotek Iridium M2D), over a period of 365 days with, location data received every three hours. We calculated 95% home ranges (ha) for each month using the a-LoCoH method and the areas where home ranges and wildlife refuges overlap were designated as the protected home range (PHR). PHR use between the hunting season and the closed season was compared and analyzed using a generalized linear mixed model (GLMM). Our results showed that there was no difference in PHR use between the hunting season and the closed season in Kushiro ($p = 0.79$). Furthermore, the results showed that sika deer did not identify and use wildlife refuges selectively as a form of predation avoidance during the hunting season.

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Aerial detection of the presence of a burrowing marsupial, the greater bilby, using remotely piloted aircraft.

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Remotely piloted aircraft (RPA), also known as drones or UAVs, are fast becoming a cost-effective, alternative technology for the purposes of fauna survey and monitoring. RPAs can provide access to remote areas and enable the survey of large areas more rapidly. The greater bilby (*Macrotis lagotis*) was once found across most of arid and semi-arid Australia; however, since European colonisation bilbies have disappeared from at least 80% of their former range. Bilbies dig for food and burrow extensively, and have been described as ecosystem engineers. They are cryptic and not easily observed or trapped, are sparsely distributed across large areas, and populations can move across the landscape, therefore, detection has relied on sign, such as tracks, scats, diggings and burrows. We tested the ability to detect bilby diggings and burrows using video imagery captured by a commercially available multi-rotor drone. Transects were flown using combinations of altitude, speed and camera angle to compare detectability, then ground-truthed. With the rapid development of RPA technology, drones have the potential to become a useful tool in detecting the presence of species, particularly burrowing mammals, in remote locations or across large areas.

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Risk factors of illegal killing in legally harvested wolf (*Canis lupus*) populations

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Illegal harvesting of wildlife is a global issue. Illegal killing is the major threat to recolonizing wolf (*Canis lupus*) populations. In Northern Europe, poaching is focused on wolves that have the biggest conflicts with human. Poaching is largely a hidden criminality and is difficult to measure. The wolf population in Finland has fluctuated between 100-300 during the past 20 years with no known reason. We examined the role of poaching on wolf population changes. We created different scenarios to detect the effect of poaching on population level. Data consisted data of 130 tagged wolves from the period 1998-2014. Illegal killing and legal hunting were the most common causes of mortality. Social status of the wolf had a significant relation to their fate. Breeding adults had the highest risk of being killed illegally. Poaching risk had a clear seasonal trend and survival dropped steeply in mid-winter. Poaching rate varied considerably between the years. Further, we modeled the predictors of illegality of a wolf kill using data from 76 GPS-collared wolves on two spatial scales. According to our results, poaching has regulated the Finnish wolf population that is simultaneously legally harvested. Legal hunting on local and country-wide scales decreases poaching risk, whereas an increasing trend in quota and detectability increase poaching risk. Legal hunting seems to decrease poaching in the short run but does not increase the tolerance as such. Our results provide useful knowledge for conservation, management and law enforcement.

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Automatic transponder readers: A new tool for studying activity, movement and mortality of mammals

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Passive implanted transponders (PIT tags) are currently widely use for identification of individuals in animal studies, and have successfully replaced most of the older marking methods. The advantage of this technique is an automatic registration of animal's presence and storage of collected data. However, the main limitation of the automatic systems is high power consumption. Thus, to reduce the energy loss, energy-efficient motion detectors were applied. Newly implemented detectors turn on the power supply only when initiated by animal presence. Combination of transponder readers with camera-traps was used in order to estimate the proportion of marked and unmarked individuals in the population. In addition, this design enables application of capture-mark-recapture (CMR) statistical models. In comparison with traditional methods, the new technique is by far more cost-effective and is particularly suitable for long-term data collection. To demonstrate the usefulness of Automatic Transponder Readers, we present data on activity, movement and mortality of small and medium-sized mammals (mice, voles, dormice, weasels and martens).

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Simulation tests for the sex-biased dispersal hypothesis explaining distinct differences between nuclear DNA-based and mitochondrial DNA-based population structures in the Hokkaido vole.

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Spatial genetic structure of populations, on the ecological time scale, is thought to be shaped by the balance between genetic drift and gene flow. Different patterns have been identified between nuclear DNA-based (nDNA) and mitochondrial DNA-based (mtDNA) structures in various mammalian species. A mechanism generating the differences, however, has not been elucidated. In this study, we aim to evaluate the effect of sex-biased dispersal on the genetic structure of populations of the Hokkaido vole on the island scale from 10 km to 400 km. To observe empirical patterns, we compared genetic distances for all pairs of local populations using microsatellite loci of nDNA and the control region of mtDNA. Most pairwise genetic distances based on mtDNA were significantly differentiated, whereas most genetic distances based on nDNA were not significantly higher than zero; these proportions were significantly different (Fisher's exact test, $p = 0.0045$). These results indicate that nDNA-based structure was larger than mtDNA-based structure. On the basis of simulation analyses with the individual-based model, we will discuss the effect of male-biased dispersal on the observed genetic patterns.

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Phylogenetic analysis of the Bonin flying fox using mitochondrial 12S rRNA and cytb sequences

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The Bonin flying fox (*Pteropus pselaphon*) is endemic to, and the only native mammal on, the Ogasawara Islands, a collection of small oceanic islands in the Pacific Ocean. The species inhabits only five small islands, and the population is currently estimated to comprise a total of 200–300 individuals. Because of these conditions, the species is categorised as critically endangered (IUCN, 2013). Results of our previous molecular study suggest the migration ability of the species is low, as each island population is genetically unique. The Ogasawara Islands are distant from any other extant habitat of *Pteropus* species: >500 km from the Mariana Islands (*P. mariannus*) and, >1,000 km from the Ryukyu Islands (*P. dasymallus*). Therefore, how the species has evolved is always a question. Here we conducted phylogenetic analyses using mitochondrial 12S rRNA and cytb gene sequences to show the relationships of *P. pselaphon* with the other *Pteropus* species. In spite of our expectations, *P. pselaphon* was close not to *P. mariannus*, but to Asian species such as *P. pumilus*. Additionally, the genetic distances between *P. pselaphon* and any other species included were comparatively long. These results suggest the south-eastern Asian ancestor of *P. pselaphon* should have colonized Ogasawara, though the process is unclear, and the species has long history of isolation.

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A cryptic species model from Turkey: *Allactaga* (Mammalia: Rodentia)

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Genus *Allactaga*, also known as the jerboa, is represented by 3 cryptic species as *A. williamsi*, *A. elater* and *A. euphratica* in Turkey. Although the relationships among these species were identified morphologically, the validity of the species and sub-species of this genus have not been precisely clarified by molecular data. The aim of the present study is to survey the genetic structure and the validity of *Allactaga* populations distributed in Turkey inferred from 1049 bp of the mitochondrial DNA cytochrome *b* (Cyt*b*) gene and 430 bp of 12SrRNA. Bayesian tree and the median-joining method reveal the existence of 3 species of *Allactaga* in Turkey. Divergence time analysis prove the speciation of the genus *Allactaga* was in the Pleistocene, namely *A. euphratica* was most like *A. williamsi*, supported by fossil molar measurements. On the other hand, sub-species of *A. williamsi* (*A. w. shmidti, A. w. laticeps, A. w. williamsi*) are not clear and are connected to the same node. Also, *A. w. shmidti* grouped both *A. w. williamsi* and *A. w. laticeps*. Thus, the validity of *shmidti* has become problematic and might be denied.

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Gene-flow with male dispersal in the Qinling Mountains of China

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Habitat fragmentation restricts the exchange of individuals and genes between populations, reduces the genetic diversity, aggravates the genetic differentiation and influences the survival of species. Due to the limitation of analysis methods and the difficulty of genetic sampling, previous studies tried to explain the phylogeographic structure of species by long isolation times or wide spatial ranges, which can hardly be applied to endangered species restricted into a narrow habitat. This study planned to extensively collect genetic samples from habitats in both southern and northern slope of the Qinling Mountains, and measure mechanism on the dispersal of individuals in the AMB had an effect on the gene-flow between different herds in Qinling Mountains of China. We recorded the dispersal events of each member in the AMB and investigated genetic diversities of the AMB and four breeding bands. We used microsatellite profiles to investigate the genetic diversity, population structure, gene flow and population assignment of the golden snub-nosed monkey *R. roxellana.* We found a relatively high level of genetic diversity, and we detected three distinct genetic lineages among the five bands. The result was also further supported by the Migrate analysis, that the male's dispersal promoted the gene-flow between different bands. It is said that the monkeys could find adaptive changes to reproduce and sustain highly gene diversities to avoid their population extinction.

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Chinese fan palms as important food source for the Daito flying-fox (*Pteropus dasymallus daitoensis*) on Daito Islands, Japan

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The Daito flying-fox *Pteropus dasymallus daitoensis* is a subspecies of the Ryukyu flying-fox, endemic to Daito Islands in the Ryukyu Archipelago, Japan. The Chinese fan palm *Livistona chinensis* dominates the natural forests of the oceanic Daito Islands, and plays an important role in the ecosystem of these islands. Daito flying-foxes feed on inflorescences of this palm. In this study, we aimed to investigate the importance of Chinese fan palms as food source for Daito flying-foxes. The flowering/fruiting phenology of this palm and other food plants, and the feeding behaviors of flying-foxes were investigated in 2013, 2015, and 2016. In 2013, the feeding frequency of flying-foxes increased with increasing number of flowering palms; however, it remained low in 2015 and 2016. The fruiting periods of *Calophyllum inophyllum* and *Terminalia catappa*, two major food plants for flying-foxes, overlapped with most of the flowering period of the Chinese fan palms; flying-foxes fed on these fruits. As these species are abundantly planted as windbreak and garden trees, flying-foxes can normally utilize these plants more frequently during the flowering period of the Chinese fan palms. In 2013, many flowers and fruits on the islands dropped or withered because of two strong typhoons. The flowers could recover from the damage more quickly than fruits, which might explain the increased feeding frequency of flying-foxes observed that year. These findings suggest that the Chinese fan palms are an important food source for the Daito flying-foxes, to compensate for the food shortage caused by typhoons.

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Community disassembly in carcasses: Metacommunity persistence in an ephemeral habitat

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Ecologists have long highlighted how a community's assembly sequence can shape its future assemblage. However, in ephemeral ecosystems, communities repeatedly disassemble. Community disassembly is the non-random process of progressive species declines and losses, and is usually studied in the context of how communities lose species to different forces (disturbance, habitat fragmentation, unnatural/anthropogenic stressors, etc.). However, in ephemeral/temporary ecosystems, disassembly is a natural and repeated process. While most ephemeral ecosystem research has been done in aquatic systems, the sequence of disassembly in terrestrial habitats can have an equally strong effect on the future community. Common terrestrial ephemeral habitats are carcasses. They have distinct communities, and these communities persist long-term through meta-community processes. We set out to test how carcass communities responded to disassembly, specifically how the meta-community responded to distance between each community patch. We laid out rat carcasses in a grid with a variety of distances between each carcass. We observed the presence/absence of different scavengers (insects, coyotes, crows, etc) through direct observation and camera trapping. We expected carcasses that were close to each other to have a higher diversity and more slowly disassemble. We found that diversity was higher at the carcasses close to each other, but the rescue effect was not that strong, which could be partly due to the presence of other carcasses naturally in the environment. Overall, disassembly is an important part of the ecology of ephemeral ecosystems. Learning about this fundamental ecological process teaches us about a key part of the life cycle of ephemeral ecosystems.

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Large carnivore management in Romania

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Pan-Carpathian populations of large carnivores still exist in considerable numbers. There is a great difference in density and number between countries. Romania and Slovakia harbor the largest populations, Poland and Ukraine have medium populations, while the Czech Republic and Hungary have the smallest populations. In the Romanian Carpathians, the estimated populations of large carnivores are 6000 brown bear, 2800 grey wolf and 1400 lynx. In Romania, people's attitude is still positive, although in areas where the density of bears and wolves is large, they annually produce heavy damages in the livestock sector (officially 1300 cases recorded in 2016) and bear produce direct conflicts with humans (in last 10 years, bears killed 12 people and seriously injured 140 people). Important threats for carnivore conservation in some countries are recent changes in hunting systems (too small size of hunting units), unfavorable attitude of hunters and wildlife managers, and low levels of law enforcement. In Romania, all activities with potential negative impacts for large carnivores have to be done after a careful analysis with mitigation measures if they can't be avoided. The management of large carnivore populations directly involves the hunting associations and game managers, the Ministry of Environment and local environmental protection agencies, and indirectly administrators of protected areas, research institutes, universities, enviromental NGOs, local communities and other local authorities. The goal of large carnivores' management in Romania is to maintain, in coexistence with people, viable populations of large carnivores as an integral part of functional ecosystems and landscapes, across the Carpathians.

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The role of photoperiod in the biology of a desert didelphid: Reproduction and energetics of male *Thylamys pallidior*

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Reproduction implies high energetic cost to animals; therefore, it should be synchronized with the most favorable season of the year. Photoperiod could act as a cue for regulation of reproduction in mammals from seasonal habitats. *Thylamys pallidior* is a marsupial inhabiting the Monte desert of Argentina; it reproduces once in its life time, synchronizing with high food resource seasons. However, only those individuals able to cope with winter conditions will reproduce. Our objective was to investigate the role of photoperiod as a potential cue for the onset of reproduction and its effect on metabolism as an indicator of energetic performance. Male *T. pallidior* were captured in the Monte Desert; five were maintained under natural photoperiod (NP) and five under constant LD 12:12 and 10:14 (winter; CP) for 12 months. We recorded body weight, tail and scrotal width, testes pigmentation and spermathorroea. Metabolic rate and changes in body temperature were measured for individuals from each treatment at different temperatures (5-38°C). We found no difference in scrotal-related variables between treatments, individuals from NP showed spermathorroea 2 months earlier than CP. We found different patterns of tail width variation between treatments. No statistical differences were found for metabolic rates and body weight loss. However, NP animals showed decreases in body temperature and metabolic rate at the end of trials compared to CP. These tendencies seem to indicate some effect of photoperiod in regulating reproduction and in performance of animals under low temperatures. Further studies are necessary to explore and confirm these results.

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Comparison of renal gene expression profiles of the South American olive mouse *Abrothrix olivacea* in natural and controlled conditions

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The olive mouse *Abrothrix olivacea* has a large distribution in southern South America. It occupies a variety of contrasting environments, in particular in terms of water availability and vegetation cover (e.g. humid Valdivian forests and Mediterranean scrublands in central Chile, arid steppes in Patagonia). With an RNA-seq approach, we assessed renal gene expression profiles as a way to understand how the olive mouse faces this environmental variability. After showing that expression profiles vary in natural populations facing distinct environmental conditions, our interest is to evaluate if the olive mouse can modulate or not gene expression profiles. Here we present results of comparisons of gene expression profiles occurring in natural (i.e. tissues collected in the field) and controlled (i.e. tissues from acclimated specimens) conditions. Genes with significant differential expression among treatments are involved in biological regulation and distinct metabolic processes. Financial support: FONDECYT 1141055.

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The ecology of stress: Linking life-history traits with physiological control mechanisms in free-living guanacos

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In vertebrates, a key response to life's challenges is the activation of the stress (HPA) and gonadal (HPG) axes. Much of the interest in stress ecology is motivated by the desire to understand the physiological mechanisms by which the environment affects fitness. In both social and non-social animals, the frequency and type of interaction with conspecifics, as well as the status in social species, can affect HPA axis activity, resulting in changes in the reproductive success of animals. We predict that social environment can affect both guanaco axes by increasing the secretion of testosterone (T) and glucocorticoids (GCs) in response to individual social interactions and the energetic demands of breeding. Assuming that prolonged elevated levels of GCs over time can be harmful to individuals, it is predicted that the HPA axis suppresses the HPG axis and causes T levels to decrease, as GCs increase. All of the data for individuals were collected by non-invasive methods (faecal samples) to address hormonal activities. As expected, there was a marked adrenal and gonadal response due to seasonal variation in *Lama guanicoe*. The marked endocrine and gonadal response due to seasonal variation in male guanaco individuals highlights the individual's energetic demands according to life-history strategies. Finally, the dataset was used to build a reactive scope model for guanacos. Guanacos cope with the trade-off between sociability and reproductive benefits and costs, by regulating their GCs and T levels on a seasonal basis, suggesting an adaptive role of both axes to different habitat pressures.

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Social networks, friendships, and aggressions in yearling wild boars (*Sus scrofa*)

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Pigs are a highly social and intelligent species. However, studies investigating behavioural questions are usually limited to the domestic pig, while the wild boar is far less well studied. Especially studies investigating the formation and stability of groups in more detail are rare. Here we investigated, via visual observations, social networks, friendships and aggressions among 110 yearling wild boar females kept in an enclosure in Austria. The females were separated from their natal group (four different origins) at the age of approximately 6 months and transferred into two new neighbouring breeding enclosures (33 ha, 19 ha). Densities were ~2 females ha^{-1} in both enclosures. We observed that the yearling females already formed stable groups with sizes between 16 and 22 individuals. We did not observe a strong linear hierarchy within the groups. Socio-positive interactions occurred more frequently within a group and therefore defined the group. Especially heavy females attacked females outside the group. Interestingly, heavier females seem to support more friendships within the group than lighter group-mates. Our results provide new insights into the social structure of yearling wild boar groups, which seem to occur more frequently under conditions of high hunting pressure in the field. Even young animals without the presence of a leading, old female are able to from stable groups. Females started to reproduce at the age of ~2 years (after this study).

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Above-ground nests provide alternative shelter for nine-banded armadillos (*Dasypus novemcintus*).

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Nine-banded armadillos (*Dasypus novemcinctus*) are known to modify habitats by constructing burrows throughout their distribution. In addition, this species has been reported to build above-ground nests in habitats with poorly drained soils when burrows are flooded during heavy rains. Published reports of these nests have been limited to palmetto and palm habitats in south Florida and Belize. During a survey of burrows in South Georgia, we found 29 above-ground nests in a 13 ha pine forest with well-drained soils. 100% of the nests were surrounded by thick tangles of thorny vines of Blackberry (genus *Rubus*) and/or Smilax (genus *Smilax*), and 69% had small oaks, large pines or fallen logs < 0.5 m away. Construction consisted of an entrance tunnel leading to a circular dugout depression (averaging 28 cm in diameter and 17 cm deep) that was lined and covered with pine needles. The total mound of needles had average dimensions (72 cm by 48 cm by 37 cm high), similar to those previously found in south Florida. Walls of the mound were about 10 cm thick and so dense that water did not penetrate all the way through. Some nests even survived a controlled burn. Compass directions of nest entrances were randomly distributed. Preliminary distribution analysis suggests that the nests are not randomly distributed in space but may be aggregated in areas where heavy brush occurred. Preliminary temperature data suggests the nests provide a buffer from heat and may provide alternative shelter from burrow conditions.

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No magnetic alignment of form direction in European hares (*Lepus europaeus*)

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Mammals show a directional response to the geomagnetic field. This magnetic alignment represents a spontaneous, fixed directional response in which mammals align their bodies along or perpendicular to the magnetic field lines. We tested the potential effect of the geomagnetic field on the position of forms used by European hares (*Lepus europaeus*) in an arable landscape in Lower Austria. For 400 forms, we determined their direction to the nearest 5° and classified them into the categories N, NE, E, SE, S, SW, W, NW. The statistical analysis revealed no significantly preferred direction but a rather uniform alignment (Rayleigh test $p = 0.4798$, Chi-square $p = 0.05877$). There is no evidence for dependence of form direction on vegetation height, ground cover or main wind direction in our study site. Effects of agricultural land orientation on form alignment could only be explored in cropland with cereal grain only. We suggest hares adjust form alignment on small-scale structures like machine tracks or plow furrow and on prevalent environmental conditions. To sum up, magnetic alignment in European hares seems to be negligible under natural conditions and largely suppressed by numerous other orientation determining factors.

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The dingo menace: An early account of farmer interactions with dingoes from surveys by N. W. G. Macintosh

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In the 1950s, Professor N. W. G. Macintosh conducted the first national public survey on dingoes. Essentially a citizen science project, the survey was a call for information on dingo biology from farmers and doggers, with 23 categories ranging from reproduction to domestication, and from hunting behaviour to the effectiveness of management methods. The surveys contained 202 open-ended questions, which were delivered by mail, primarily via the Graziers' Federal Council of Australia, with a 19.6% response rate (141 completed responses received). However, analysis of the results was never completed so we seek to finish the project. In addition to biological information, the surveys provide an account of farmers' attitudes towards dingoes. Of particular interest are experiences with and attitudes towards management methods, with overwhelmingly negative responses towards aerial baiting, which had just begun to be implemented and now forms a major component of Australian dingo management. By considering the historical context under which this survey was conducted, we analyse how social and environmental factors shape values and decisions in wildlife management and discuss how such analysis can be applied to today's dingo management.

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Cryptic male choice: Experimental evidence of sperm sex ratio and seminal fluid adjustment in relation to coital rate

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The differential allocation hypothesis suggests that a mother should adjust the sex of her offspring in relation to her mate's attractiveness, thereby increasing future reproductive fitness when her sons inherit the attractive traits. More attractive males

have been shown to sire more sons, but it is possible that the sex ratio skew could be a result of paternal rather than maternal manipulation, which would be a more parsimonious explanation. Sex allocation research in mammals has focused almost exclusively on mothers under the assumption that the male contribution is genetically determined during meiosis and therefore not under adaptive control. However, we have recently challenged this assumption and shown variation under conditions where you would not expect it. Here we manipulated coital rate (an indicator of attractiveness) in laboratory mice and showed that males that mate more often have higher levels of glucose in their semen despite lower blood glucose levels. Since peri-conceptual glucose levels *in utero* increase male conceptus survival, this could result in male-biased sex ratios. The males that mated most also had more remaining X-chromosome-bearing-spermatozoa, suggesting depletion of Y-chromosome-bearing-spermatozoa during mating. We hypothesise that males may alter both seminal fluids and X:Y ratios in an ejaculate to influence subsequent sex ratios. Our results further support a paternal role in sex allocation.

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Species diversity of mammalian carnivores in the Chihuahuan Desert.

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Mammalian carnivores are important predators as they provide particular dynamics to ecosystems. Our objective was to investigate the diversity and distribution of mammals of the Order Carnivora in the Chihuahuan Desert from specimens deposited in scientific collections. Species information was gathered from electronic databases of national and international scientific collections, geographic coordinates of each locality where the species were recorded were superimposed on digital map layers of Mexican political division, Chihuahua desert borders from the terrestrial ecoregions and Natural Protected Areas (NPA) obtained from electronic portal of the National Commission for the Knowledge and Use of Biodiversity (CONABIO in Spanish) and visualized with GIS ArcMap 9.3. Number of species and number of records for each one was analyzed. A total of 1464 records were obtained, 298 in Mexico and 926 in the United States. Fourteen species of carnivores were found, from 13 genera and 5 families. Skunks *M. mephitis* (388), cacomixtles *B. astutus* (259), cougars *P. concolor* (240) and raccoons *P. lotor* (198) show highest number of records, weasels *Mustela frenata* (13) and the desert foxes *Vulpes macrotis* (20) have lowest number. Twenty animals were recorded inside a NPA, five species were found in NPA and 6 NPA have at least one species of carnivores. The analysis show that skunks are the best represented carnivore in the Chihuahuan Desert with very few records of weasels and foxes. This information gave an overview about the knowledge of the predators in Chihuahuan Desert as a starting point for future studies related to these organisms.

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Chilean foxes exhibit a Type IV functional response in response to changes in abundance of a social prey species.

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The per capita behavioral responses of predators to variation in prey species abundance is characterized as the functional response (FR). Most vertebrates exhibit either Type II (consumption increases to a plateau with increasing prey abundance) or Type III (sigmoidal, reflecting prey switching as prey increases from low to modest abundance) FR. A Type IV FR is similar to a Type II or Type III except that per capita consumption declines at very high prey abundance. Type IV FR are best known among invertebrates but were originally postulated for vertebrates foraging on group-living prey such as schooling fish. Reflecting this, many prey species capitalize on group living or group foraging to increase proportional vigilance. The degu (*Octodon degus*) is a social hystricomorph rodent that has been subject to extensive behavioral research. Degus foraging in large groups detect predators more rapidly than those in smaller groups, suggesting that predation rates should decline at high degu densities. A key predator of degus is the culpeo fox (*Lycalopex culpaeus*), which is characterised as a generalist rodent predator that exhibits numerical but no FR. We monitored degu and culpeo numbers over two decades, and we characterized culpeo diet with traditional scat analysis. Using 23 years of observations, our data show a clear Type II FR for rodents in general, but for the highly social degu the per-capita consumption clearly declines at the highest degu density. To our knowledge this is the first demonstration of a Type IV FR for a mammalian predator.

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Evaluation of body mass and body size as an ecological indicator of population changes in sika deer (*Cervus nippon*)

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To evaluate the utility of body mass and body size (hind foot length and jaw length) as an ecological indicator in sika deer, we analyzed the time-series data of the measurements in three populations on Shiretoko Peninsula, Hokkaido, Japan, where density levels were different. We used GAMM and GLMM to detect changes in body mass at the capture year and hind foot length and jaw length at the birth year (cohort) reflecting density effects. After two populations reached a carrying capacity (K), they have been maintained at a low density by intensive culling, while a population has been maintained below K by long-term culling. For the population below K, the body mass for all sex-age classes, hind foot length for fawns, and jaw length for adult males decreased. For two population that reached K, the body mass for fawns and adult males, hind foot and jaw length of adults (male and female) decreased, while hind foot and jaw length for fawns increased after culling. These findings suggested the rank order of responses to density as follows; fawn> adult males> adult females and body mass> hind foot length or jaw length. Hind foot length for fawns is an important ecological indicator for detecting early stage of population increase in sika deer because it is sensitive to changes in density and could be accurately and easily measured in the field. In addition, understanding the rank order in a series of ecological indicators is useful in evaluating the population condition.

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Behavioral control of sika deer (*Cervus nippon*) by capsaicin repellent

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Sika deer (*Cervus nippon*) can severely affect natural vegetation and ecosystems. Wire fencing has been used to prevent damage, but this is generally unsuitable aesthetically for natural parks and landscaped grounds. Therefore, fenceless prevention methods are also required. We investigated the specific effect of capsaicin by using mimetic repellent non-capsaicin (experiment. 1), also the effects of different quantities of capsaicin repellent dispersion on deer (experiment 2). Five deer were used in these experiments. In experiment 1, four treatments were tested: for a control, the deer were fed from a feeding box containing hay cubes (HC); for the non-capsaicin treatment, mimetic pellets were mixed with HC in the feeding box; for the repellent treatment, repellent was mixed with HC in two quantities. The average amount of HC eaten was significantly greater for the control and non-capsaicin treatment (Holm test, $P < 0.05$) than capsaicin treatments. In experiment 2, six treatments were tested: the control was the same as experiment 1, HC; for the repellent treatments, repellent was mixed with HC in the feeding box in four different quantities; for the repellent-smell treatment, repellent was placed at the bottom of box and covered with wire under HC. The average amount of HC eaten was significantly greater in the control and repellent-smell (Holm test, $P < 0.01$) than the others. Our results showed that stimulus of capsaicin had an effect on eating behaviour of deer, and capsaicin repellent is effective when deer touch the product with their snouts.

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Paleoecological reconstruction of Late Pleistocene deer from the Ryukyu Islands, Japan: Evolution and extinction on islands

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The Ryukyu Islands (Amami Islands, Okinawa Islands and Sakishima Islands) form an island arch situated at the southern end of the Japanese Archipelago. In this area, there are numerous fossiliferous localities estimated to date from the end of the Pleistocene, which have yielded abundant vertebrate fossil remains. Among the excavated fossils of terrestrial vertebrates, two extinct deer species, *Cervus astylodon* and Muntiacinae gen. et sp. indet., are representative of the Late Pleistocene fauna of the Okinawa Islands. However, their ecological characteristics have been largely unknown to date. In the present study, we reconstructed the paleoecology of the deer species excavated from the Hananda-Gama Cave, Okinawa Island. By mesowear analysis and stable isotope analysis of the fossil deer molars, it was estimated that both deer predominantly consumed C3 browse under the climatological/environmental condition similar to the current Ryukyu Islands. Additionally, using tooth wear model of extant sika deer population with a similar diet, the age of *C. astylodon* was estimated. The fossil deer were estimated to have lived up to 26 years, which was surprisingly long for their small body size. Life history of *C. astylodon* was considered to follow a K-selection strategy (or slow life history), which might have evolved under predator-free insular environment. This life history trait made them vulnerable to human exploitation, because animals with a K-selection strategy are represented by lower population recruitment. Human hunting might have a considerable impact on the fossil deer populations, and be responsible for their extinction at the end of Pleistocene.

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Reintroduction success of collared peccaries (*Pecari tajacu*) in the Ibera Natural Reserve, Argentina

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The collared peccary (*Pecari tajacu*) is distributed from southern USA to northern Argentina; however, in some Argentinean localities it went extinct over 50 years ago. As part of a rewilding project, two peccary herds (one captive-breed family group and one mixed group of rescued or zoo individuals) were reintroduced to the Ibera Natural Reserve, northeastern Argentina. We evaluated initial reintroduction success by assessing survival rates, site fidelity, and behavioral changes to provide recommendations for future reintroductions. After quarantine time, 10 individuals (3 males and 7 females) were brought to a pen for a soft-release in June, 2015, and each individual was fitted with a VHF collar. A second herd (2 males and 4 females) was released following the same protocol in May, 2016. We monitored post-release movements of all the individuals to obtain GPS locations every 100 min. Also scan sampling was used every 5 min to determine activity budget right after release and changes through time. The first group had monthly survival rates from 0.87 to 1 and all surviving individuals remained within the study area. For the second group, high dispersal distances yield low monthly survival rates from 0.66 to 1 with two individuals remaining within the study area. The first group showed a behavioral change from 30% to 52% foraging time and 20% to 15% traveling time, for 2015 and 2016, respectively. Our results indicate a successful reintroduction of peccaries in Argentina and future reintroductions should consider only releasing cohesive family groups to reduce mortality and dispersal.

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Using sensor cameras to inform management strategies for a rare macropodid, the spectacled hare-wallaby, on the Yawuru Indigenous Protected Area

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The spectacled hare-wallaby (*Lagorchestes conspicillatus*) is a medium-sized macropodid whose range formally occupied half of the Australian continent. Today, however, the distribution of *L. conspicillatus* is extremely patchy. In particular, *L. conspicillatus* has suffered a substantial decline in the Kimberley region of Western Australia where it is now considered very rare. As a specialist of dense tussock grasslands, *L. conspicillatus* is likely threatened by altered fire regimes and grazing by introduced livestock as well as by introduced predators such as foxes and feral cats. In 2014 and 2015, Yawuru Country Managers with the Nyamba Buru Yawuru (NBY) Land and Sea program together with WWF-Australia researchers conducted surveys for *L. conspicillatus* on the recently dedicated Yawuru Indigenous Protected Area (IPA). Prior to these surveys, *L. conspicillatus* had not been recorded for 9 years, with speculation they had become locally extinct. Although these 2014/2015 surveys confirmed the presence of *L. conspicillatus*, they could only answer limited questions relating to the occurrence and distribution of this species on the Yawuru IPA. The NBY Land and Sea program with assistance from WWF is currently conducting a more intensive survey for *L. conspicillatus* using a network of sensor cameras across the Yawuru IPA. These surveys are intended to answer more specific questions regarding the distribution of *L. conspicillatus* in relation to habitat characteristics, fire history, cattle grazing and the occurrence of invasive predators. The results of this survey will help inform management strategies to protect and recover populations of *L. conspicillatus* on the Yawuru IPA.

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Seasonal patterns and habitat use of urban sika deer in Sapporo, Japan

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Urban and suburban wildlife have been a problem all over the world. As in Japan, major threats such as deer-vehicle collisions are concerning due to overabundant sika deer (*Cervus nippon*). Sapporo metropolitan area is the fifth-largest city in Japan with the population over 2.5 million people. The area is surrounded by mountains, forests, and farmlands where urban wildlife is a major threat to citizens. However, preceding studies about urban and suburban deer are very few. The purpose of this study was to observe the seasonal patterns and habitat use of sika deer in Sapporo metropolitan area by spotlight counts and radio-telemetry tracking. We conducted spotlight counts twice a month from 2009 and monitored four deer with VHF or GPS collars. As a result, deer counted by spotlight counts increased each year but decreased in 2013 and then increased again from 2015. Deer were counted the most in April and November, but January to March and June were least counted. Seasonal migration was monitored in all collared deer. Three of the collared deer crossed the railroad to move to their summer home-ranges. Our results suggested that urban deer used farmlands in the summer to gain food and recreational forests in the winter to avoid snow and hunting. In addition, urban deer skillfully utilised small patches of forests and farmlands to move to their seasonal habitats.

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Is the Brazilian environmental law positive for ocelot (*Leopardus pardalis*) occurrence?

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Wildlife corridors might represent additional habitat, apart from improving connection between remaining isolated populations of native species. In Brazil, the riverine Areas of Permanent Protection (APP) are recognized as wildlife corridors. However, these areas had suffered reduction in their extent due to recent changes in the Brazilian Native Vegetation Protection Law, which protects native vegetation in private lands. Given these changes, and the growing demand for agricultural and biofuel production, it is important to assess the role of APPs in their current configuration. We did this by analysing ocelot occurrence in three Cerrado landscapes dominated by sugar cane and silviculture. We collected detection/non-detection data with camera-trapping during two dry seasons (April to September of 2013 and 2014) at 208 stations (6606 camera days). We estimated ocelot detection and mean relative abundance (lambda) using single-species/single-season occupancy models with heterogeneous detection probability induced by variation in abundance (Poisson distribution) using the package Unmarked in R. The amount of native forest, silviculture and sugarcane were, in this order, the covariates with higher explanatory weight; silviculture and sugarcane had a negative effect and native forests a positive effect on the relative abundance of ocelots. Furthermore, location relative to APP and degree of protection also had a positive effect on ocelot relative abundance since these cats were more abundant inside APP than outside it, which reinforces the importance of wildlife corridors. Our results demonstrate that landscape composition was determinant of ocelot relative abundance, corroborating the importance of native vegetation protected by law in private lands.

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Influence of ecological factors on burrowing of the specialized red viscacha rat *Tympanoctomys barrerae* in the Monte desert biome, Mendoza, Argentina

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Arid ecosystems represent heterogeneous scenarios in the distribution of resources and species. The red viscacha rat is an octodontid rodent endemic to the aridlands of Argentina. It lives in burrows built on mounds associated with salt basins. The aim of this study is to characterize the associated factors on the burrowing activity of *Tympanoctomys barrerae* in the Monte desert. We conducted fieldwork in the locality of Huanacache, Mendoza province, from August to January. For the characterization of burrows systems, we measure different ecological data, as orientation and variations of entrances per mound, soil hardness data at 3 and 9 m from burrows, vegetation cover, and biomass. We used live-trapping and radiotelemetry to estimate activity patterns. We found 49 active burrows with a mean distance of 12 m between them. Burrows have length and a maximum height of 4.68 m and 0.45 m; 40% of burrow entrances were facing N and 15% facing E. We find differences in soil hardness at different burrow distances. At a microhabitat level, active burrows were positively associated with vegetative cover (> 53%) and dry biomass (> 24 g). Activity pattern was greater during nighttime than daytime, and the distance moved was around 25 m. These results provide the first microhabitat data associated with the burrowing activity of *T. barrerae*. The present study highlights the importance of ecological factors (i.e. soil hardness, vegetative cover, and biomass) as drivers for dispersal, colonization and activity patterns of red viscacha rat.

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Research informing practice: Mitigating impacts of forest practices on threatened mammals

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Tasmania's forests provide habitat for an array of mammals, including four threatened species, the Tasmanian devil, spotted tailed quoll, eastern quoll, eastern barred bandicoot and New Holland mouse. Formal reserves contribute to the conservation of these species at the landscape-scale, but such reserves are limited in extent and distribution. Furthermore, reliance on a 'set-aside' approach alone can result in intensification of land-use activities outside reserves and subsequent loss and fragmentation of habitat. Complementary measures are needed to conserve habitat for these species in areas outside reserves. Under state and federal legislation, threatened species must be considered when planning forest practices in Tasmania. Research on the ecology of the species has been used to inform the development of measures to mitigate the impacts of forestry practices. A decision support system provides forest planners with a way to assess the risk and obtain information on practical ways to reduce any impacts of the proposed operation on listed species. Both coupe-level and landscape-scale measures are recommended. Ongoing monitoring and review, involving both forest planners and threatened species specialists, has resulted in a practical and useful tool for planning. Habitat descriptions, potential range boundaries and a planning framework have also been developed to facilitate landscape-scale planning. Taking a multi-scaled approach to the conservation of habitats for wide-ranging threatened

species is not easy. The ongoing success of such an approach depends on a high level of commitment to monitoring and adaptive management.

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The effects of hydroelectric dam filling on home range and habitat suitability of jaguars (*Panthera onca*) (Carnivora: Felidae) on Upper Paraná River, Atlantic Forest, Brazil.

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The construction of hydroelectric power plants results in habitat destruction and fragmentation, and this destruction is the major cause of the decline of endangered species, especially large mammals and especially carnivores. Brazil's energy matrix is based on approximately 70% hydroelectricity. Jaguar (*Panthera onca*) populations have been reduced or extinguished by human pressure. In Brazil, it is considered a vulnerable species and it is critically endangered in the Atlantic Forest. In the Upper Paraná River (UPR), the reservoir filling of the Porto Primavera Hydroelectric plant (PPH) began in 1998, and flooded an area of approximately 2250 km^2. We evaluated the effects of the PPH reservoir filling on the jaguar population, spatial distribution and habitat suitability. We monitored 11 jaguars using radio telemetry over two periods (1992-1995 and 1998-2002). Jaguars' home ranges increased significantly after reservoir filling (females: 78 km ^{2} before [n = 8], 197 km ^{2} after [n = 5]; male [n = 1]: 111 km ^{2} before, 149 km ^{2} after). The PPH filling suppressed approximately half of their suitable area and most jaguars were killed in retaliation for cattle predation as they commenced to occupy the most degraded areas. The remaining area of the UPR still holds approximately 50 adult jaguars. Therefore, the long-term species conservation depends on the preservation of the adjacent wetlands and on the restoration of forest patches. Our results can subsidize jaguar conservation and management plans in the UPR and show that habitat suitability modeling can be a useful tool for assessing environmental impacts.

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Roles for the dingo in Australian food webs reviewed: Where do they fit?

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The dingo is the largest of Australia's non-human, mammalian predators, often considered to be an apex predator, if only by default. However, the ecological roles of dingoes remain controversial and sometimes differing arguments are exacerbated by comparisons to the enigmatic grey wolf or colored by emotional considerations. In the minds of many it functions as an apex predator, regulating systems as a top-down driver; for others, the dingo's roles are unclear. We hypothesized that because, the dingo is medium-sized in relation to other canids, it may have evolved with similar ecological roles to other medium-sized canids. We reviewed the literature and compared the occurrence, diet, behavioral ecology and presumed functions that similar sized canids play in food webs. We conclude that direct comparisons to the grey wolf are not always appropriate. Rather, the dingo's ecology is more in line with other medium-sized canids like jackals and coyotes. The dingo's ecology as a mesopredator is likely facilitating its success in Australia. Similar to characteristics of other medium-sized mesopredators, the dingo shows flexibility in social structure and habitat as well as a generalist and opportunistic diet. These characteristics have allowed the dingo to adapt and thrive in an anthropogenic landscape. There is sufficient doubt about the dingo's role as an apex predator and top-down driver to warrant more research into its true ecological roles. This should lead to better conservation and management strategies.

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Mitochondrial DNA diversity of the Arabian oryx from Oman

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The Arabian oryx (*Oryx leucoryx*) is an endangered ungulate that became extinct in the wild in 1972, but conservation plans are underway to save this species. This includes a program in Oman involving captive breeding for reintroduction into the wild using a few captive populations from around the world. However, there is limited knowledge of the actual genetic diversity of the breeding populations from Oman. As a first step to address this, we investigate the mitochondrial DNA (mtDNA) of 114 individuals

from three groups held at the Omani Al Wusta Wildlife Reserve (originally from Oman; sourced from the United Arab Emirates; and a mixed group which are the result of preliminary breeding between the former two groups) as well as 24 historical samples from private collections. We identified 9 haplotypes out of the 18 previously identified globally in the Arabian oryx founder population for the Omani conservation initiative. The results indicate that genetic variability among the three groups held in this reserve is slightly below the observed average found in other Arabian oryx populations. Our findings improve knowledge of the current status of the genetic diversity of the oryx and support the future strategy of translocation and genetic management of reintroduced populations. This data provides a preliminary tool to inform the management of this conservation program allowing adequate selection of breeding pairs to preserve mtDNA variability. Population genomic analyses using dd-RAD sequencing are underway to better understand the genetic make-up of the Arabian oryx.

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Difference in small mammal and forest structures between primary and secondary forest subjected to two different post-fire management practices in the Phou Khao Khauy National Protected Area, Lao PDR

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This study was conducted to clarify differences between small mammal community and habitat structure. Small mammals were captured ten consecutive nights from nine study plots in each of the three different stands in Phou Khao Khauy National Protected Area, Lao PDR. We used a capture-mark and release, using live-trapping method. In addition, the data collected for nine factors were related to the forest structure of the study plots. Five species and 456 individuals of small mammals were captured in the rainy season and the dry season. Total number of individuals captured from the natural forest stand area was the highest. The number of individuals captured from the post-burned rubber plantation stand was the lowest. This result showed that the post-burned rubber plantation stand can have negatives effect on habitat condition for small mammal communities. The home range size of the individuals captured in the nature forest stand was smaller than that in the post-burned rice field stands. The home range size of individuals captured in the post-burned rubber plantation stand was the smallest. The home range size was larger in the rainy season and smaller in the dry season. It showed that in the dry season, food quantity and quality are suitable than in rainy season. In the forest, variables were significant in relationships between the numbers of small mammal individuals. This result showed that forest composition has an influence on small mammal communities and variations in small mammal species require different forest values for communities.

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Diversity and origins of wild pigs from Madagascar

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Madagascar was settled by Austronesians (proto-Malagasy) ~1500–2000 years ago and immediately after that by native East African groups. Bushpigs of the genus *Potamochoerus* are suggested to have been introduced to Madagascar from eastern mainland Africa and/or offshore islands. The earliest archaeological evidence for bushpigs in Madagascar dates to the 10th-13th centuries and possibly on the Comoro Islands to the 9th-10th centuries. Although the circumstances of the translocation are unclear, it has been proposed that pigs introduced to this island were of sub-Saharan African origin, which could have been transported directly across the Mozambique Channel or through a corridor via the neighbouring islands by early sea navigators who settled in Madagascar. Furthermore, two subspecies/populations of Malagasy bushpigs have been nominated from eastern and western Madagascar. However, genetic evidence to make definitive conclusions on the taxonomic status and geographical origins of these Malagasy wild bushpigs is currently not available. To contribute to this debate, we investigate the level of differentiation within Malagasy bushpigs (n=62) and their phylogenetic position in relation to other species of African and Eurasian Suidae using mitochondrial and nuclear DNA. Our preliminary results show little genetic differentiation between Malagasy bushpigs from western and eastern Madagascar and that they cluster within the genus *Potamochoerus*. Analyses of further samples from mainland Africa are underway to better pinpoint the evolutionary relationships of Malagasy bushpigs with the recognised species of this genus and the geographical source of the populations.

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The swamp wallaby (*Wallabia bicolor*): A common mycophagous species yet potentially important for maintaining the diversity of Australian fungi.

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Swamp wallabies (*Wallabia bicolor*) are a common mycophagous (fungus-eating) species found along the east coast of Australia. Unlike many mycophagous mammals, such as bettongs (*Bettongia*) and bandicoots (*Isoodon*), swamp wallabies are not threatened by the presence of introduced predators such as feral cats (*Felis catus*) and red foxes (*Vulpes vulpes*). Mycophagous mammals, such as the swamp wallaby, play an important role in maintaining ecosystem function by part-taking in mammal-ectomycorrhizal fungal interactions, consuming and dispersing the spores of these fungi. The foraging behaviour of swamp wallabies, may be important for understanding their role in this interaction; however, it has not been the focus of research studies in previous years. Using motion-sensitive camera traps deployed at Mount Duval in New South Wales, it was observed that swamp wallabies actively forage for buried food items, such as artificial truffles which mimic the buried state of ectomycorrhizal fungi ('truffles'). Swamp wallabies were successful at excavating buried food items in 66% of trials, spending on average 5 seconds excavating each artificial truffle. These observations support the data gathered from diet samples collected in two 12 month sampling periods, set 10 years apart, which showed 28 taxa of ectomycorrhizal fungi, found in the New England Tablelands, are regularly consumed by swamp wallabies. Evidence collected during this study has shown that swamp wallabies actively part take in excavating buried food items while consuming a large diversity of ectomycorrhizal fungi. This has provided a greater understanding of their role in the dispersal ectomycorrhizal spores throughout a forest remnant ecosystem.

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Who's afraid of the big bad fossa?

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The fossa (*Cryptoprocta ferox*) is the top terrestrial predator in Madagascar and a known threat to lemurs. To reduce the risk of predation, lemurs may rely on chemical cues (scents) left by fossa in the environment in order to accurately evaluate their immediate endangerment. We used camera traps to study predator-prey interactions, focusing on the scent-marking behavior of the fossa and subsequent responses of lemurs to those scent-mark sites in Maromizaha, an eastern rainforest in Madagascar. Our data showed that the fossa is active day and night. Lemurs, of diurnal or nocturnal habit, also visited the scent-mark sites during both day and night. Several species of lemur, such as indri (*Indri indri*), diademed sifaka (*Propithecus diadema*), brown lemur (*Eulemur fulvus*), eastern lesser bamboo lemur (*Hapalemur griseus*), eastern woolly lemur (*Avahi laniger*), and small-toothed sportive lemur (*Lepilemur microdon*), did not avoid the scent-mark sites. Quite to the contrary, individual lemurs were observed to feed, rest, play and even sniff and scent-mark over the mark of the fossa. Because the home range of the fossa is large relative to that of sympatric lemur species, it is likely that only one fossa overlaps the range of a group or an individual of a particular lemur species. Because the volatiles of fossa scent may communicate an individual's identity, our results suggest that, although risky, assessing these scent marks may provide resident lemurs with information essential for the spatial/temporal use of their home range.

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Social network structure of the African woodland dormouse *Graphiurus murinus*

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We investigated the social structure of a free-living population of African woodland dormice *Graphiurus murinus* using association indices from, and social network analysis of, dyadic sleeping associations. The locations of 28 adult males, 31 adult females, and 21 juveniles were recorded over a 30 month period, using radio-tracking and 80 nest boxes. A total of 3238 locations (average = 40 per individual) were collected. Sixty-eight (85%) of the 80 dormice formed sleeping associations. A total of 496 sleeping associations between 112 dyads were recorded. The average Association Index (AI) was 15.05%. Male-male dyads (17.31%) had a significantly higher AI than male-female (11.72%) and female-female dyads (7.33%). AI was significantly negatively correlated with the number of simultaneous locations in male-female dyads, but not in female-female dyads, indicating that the latter were temporally more stable. Males (median 1.00; range 0–6) and females (1.00; 0–3) had a similar number of adult opposite-sex sleeping partners, and this number increased monotonically with the number of locations and the monitoring period. Social network analysis revealed a complex web (density = 5%; median degree ± interquartile range = 3.00 ± 4.00) of relatively even associations (edges) between adult males and females, with no significant intersexual difference in the five network metrics studied. Sleeping associations and the social network structure mirrored the social tendencies of African woodland dormice as well as the strong affinities between certain individuals. These affinities were sex-specific, likely relating to communal breeding, social huddling and the putative promiscuous mating strategies of the species.

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Periodic movement patterns by a specialist herbivore, the koala, in a patchy landscape

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As animals move across the landscape to satisfy their nutritional needs, movement patterns emerge, painting a picture of the areas they visit. In some species, these movement patterns may be repeated temporal scales. Specialised herbivores have been argued to be ritualistic, and from a foraging perspective this could be manifest in periodic movement patterns with animals moving regularly and predictably through their landscape to harvest food. We aimed to test this prediction for a specialist herbivore, the koala (*Phascolarctos cinereus*), across different temporal scales within a patchy landscape. Associated with efficient foraging, we also predicted koalas would revisit large and clustered foraging patches more frequently than small isolated patches. Our study sites were on highly fragmented eucalypt woodland in the Liverpool Plains, New South Wales, Australia. We tracked 20 koalas for five months with GPS collars from 2015-2016. We used biased random bridges to determine foraging patches frequently visited by koalas. Then we used Fourier transforms to determine the periodicities of revisits and wavelet analysis to determine whether those periods were consistent across the time series. The results of our analysis showed that koalas periodically revisited foraging patches every 14 days and that larger foraging patches were revisited between 5 to 6 days. These findings provide an insight into periodic space use by foragers, and support the hypothesis of ritualised feeding patterns by a specialist herbivore. The next step is to determine why animals revisit food patches at a particular periodicity.

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Yellow sandplain mammals of the Great Victoria Desert

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Across a decade of sampling, 14 small (<200g), ground-dwelling mammals were recorded from the yellow sandplains of the Great Victoria Desert. The assemblage was derived from four complimentary survey techniques, trapping (12 species detected), motion-sensitive cameras (11 species), the identification of trace evidence (6 species) and the material present in predator scats (7 species). Three species consistently dominated the assemblage trapped; *Ningaui* sp. (49% of captures), *Notomys alexis* (18%) and *Pseudomys hermansburgensis* (13%). The assemblage varied between sampling periods, attributable to factors such as temperature, rainfall and fire history. The identification of remains within predator scats (feral cat, fox and dingo) revealed the presence of cryptic species (e.g. *Notoryctes typhlops*) and highlighted the threat of predation to many native mammals, including the threatened *Sminthopsis psammophila*. While most small mammals were highly detectable, three species, *Dasycercus blythi*, *Sminthopsis psammophila* and *Cercartetus concinnus,* were rarely recorded and appear to be sparsely distributed across the landscape (*Cercartetus concinnus* was trapped only once over 9,720 trap nights). The study area lies in a biogeographic interzone with several temperate-adapted species occurring in small populations near their known range limits (e.g. *Cercartetus concinnus*). As some populations are patchy, additional species were added to the known assemblage during years nine and ten of sampling, revealing significant effort can be required to fully document the mammal assemblage of a site. Detection of small mammals was greatly improved using motion-sensitive cameras. Techniques used to identify several species are displayed below.

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Can some burrowing mammals be keystone species in the Brazilian Cerrado?

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Some burrowing mammals have been considered ecosystem engineers since they build potential microhabitats for vertebrates and invertebrates. Thus, these species may function as keystone species in their communities, because they may be beneficial to several other species. In this study, we tested the possible influence of the burrow density of *Clyomys bishopi* and armadillos (*Cabassous unicinctus* and *Euphractus sexcinctus*) on the diversity (richness) of terrestrial vertebrates (frogs, lizards and small mammals) in a savanna (Cerrado) area in southeastern Brazil. Ten areas of grassland with scattered shrubs (“campo sujo”) were sampled from August 2007 to January 2008 at Itirapina Ecological Station. In general, the burrow density seems to have a positive effect on the richness of terrestrial vertebrates (frogs, lizards and small mammals). However, armadillos are apparently the most important burrowers in this ecosystem, because they, unlike *Clyomys bishopi*, dig burrows not only for sheltering, but also for feeding, thereby increasing the probability of their use by other species. These results support the hypothesis that these burrowing mammals may function as possible ecosystem engineers or keystone species in this community.

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A day in the life of a bandicoot: analysing behaviour using accelerometry data

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Determining how mammals use different habitats is important for understanding the ecology of a species. However, it is rarely feasible to physically monitor a study individual for twenty-four hours a day. Furthermore, the constant human presence may adversely affect natural behaviours. The development of accelerometer technology for wildlife applications has provided a new opportunity to quantify animal movement and behaviour remotely. Here we assess tracker-attachment methods and the ability to use accelerometry data to differentiate behaviours exhibited by captive southern brown bandicoots (*Isoodon obesulus fuscivent*er). Bandicoots are recognised as important keystone species for their role in the bioturbation of soil for a healthy, functioning ecosystem. As one of the few marsupial species persisting within metropolitan areas of Western Australia, adding to the knowledge of how bandicoots behave as they move through the human-modified environment has important management implications. Successful captive trials will allow for future deployment of accelerometers on wild bandicoots within a suburban area to study how they move through the urban matrix. Bandicoots are notoriously difficult to collar, so alternate attachment methods such as tail mounting and fur adhesives are tested. The collection of high-resolution accelerometry data gives distinct patterns which we can use to distinguish when bandicoots are digging or running, foraging or at rest. This behaviour data, in combination with GPS movement patterns, will allow for detailed spatial and temporal accounts of how mammals utilize their environment.

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Predator-prey activity patterns in the urban landscape: The case of the quenda vs the cat

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Populations of quenda (southern brown bandicoot, *Isoodon obesulus fuscivente*r) in Western Australia appear to be quite adapted to surviving in the urban landscape. Quenda are primarily nocturnal omnivores, and are common in bushland reserves and backyards in the City of Mandurah (70 km south of Perth, Western Australia). It is thought that domestic free-roaming cats may pose a threat to quenda in urban areas. It is therefore of interest to know whether spatial and temporal overlap exists between quenda and cats in the urban landscape. Remote cameras were deployed in four urban habitat types within our study area (City of Mandurah). Habitat types included 1) remnant fragments of natural vegetation, 2) narrow corridors of remnant vegetation, 3) highly modified road reserve vegetation strips, and 4) urban backyards. Detection rates of each species were used to compare the spatial and temporal activity patterns of urban quenda and cats. Understanding the patterns of temporal and/or spatial overlap between these two species will provide important information regarding the impact of domestic cats on urban quenda. This will inform management considerations and policy regarding urban wildlife.

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Different seasonal migration patterns between Japanese macaques and sika deer in the summit area in Yakushima Island

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In the mountains, differences in the use of vegetation by animals in higher elevation may reflect their adjustments to harsh environments. Yakushima Island has a mountain with an elevation of 1,936m above sea level and its vegetation changes vertically. Above the forest vegetation, the summit area of Yakushima Island, at more than 1,700m a.s.l., is the sasa grassland, mostly covered with a species of sasa bamboo (*Pseudosasa owatarii*). We studied the use of vegetation at the highest area of Yakushima Island by two mammal species: Japanese macaques (*Macaca fuscata yakui*) and sika deer (*Cervus nippon yakushimae*). This study was conducted from August 2015 to November 2016. We monitored the phenology of some parts of the sasa bamboos and collected location data and food items of two mammal species. We found that mature leaves of sasa bamboos existed throughout all seasons, while buds and shoots of sasa bamboos were present from spring to autumn. Japanese macaques seemed to exhibit seasonal migration to the area; they used the area from spring to autumn to feed on sasa bamboos only when they were available. However, contrary to the monkeys, sika deer seemed to use the area throughout all seasons to feed on both immature and mature leaves of sasa bamboos. Generally, sika deer, which are ruminants, can eat more fiber-rich foods than Japanese macaques, which are monogastric animals. Both species' distinct digestive systems may contribute to their different seasonal migration patterns to the high altitude sasa grassland.

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Cryptic diversity revealed in a golden mole assemblage from south-eastern Africa

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The Chrysochloridae (golden moles) is a family of highly threatened fossorial small mammals endemic to sub-Saharan Africa. Research concerning these enigmatic animals has been limited, and there is a general dearth of biological information for most species. Clarifying the taxonomy of this afrotherian family is needed to inform conservation prioritization. *Amblysomus hottentotus* (Least Concern, IUCN 2016) is one of only two geographically widespread chrysochlorids, and one of five golden mole species endemic to the Greater Maputaland-Pondoland-Albany (GMPA) region of vertebrate endemism. We collected samples from 50 sites across the distribution range of *Amblysomus*, with emphasis on *A. hottentotus*, to test for cryptic diversity and to better understand diversification within the genus. Phylogeographic analyses using mitochondrial DNA and nuclear intron data revealed that *A. hottentotus* comprises several distinct lineages, or evolutionarily significant units (ESUs), some with restricted geographic ranges and thus worthy of conservation attention. Molecular dating suggests early-Pliocene divergence of the major lineages, with later radiations during the late-Pliocene to early-Pleistocene. *Amblysomus hottentotus* appears to represent a species complex, highlighting the need for a taxonomic revision of the genus. In a pilot study using ddRAD-Seq, we demonstrate the utility of this reduced-representation genome sequencing method for assessing phylogeographic structure in *Amblysomus*. The distinctiveness of some A. *hottentotus* lineages is confirmed, but there is also evidence of some incomplete lineage sorting or ongoing gene flow between two of the newly discovered ESUs. Finer-scale analyses are required to elucidate speciation and population genetic structure in this potentially speciose genus.

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Gut microbiome profile of an extinct caprine (*Myotragus balearicus*) from the Balearic Islands

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Myotragus balearicus was a small-sized caprine that lived in the Balearic Islands (Western Mediterranean Sea), and that became extinct around 4000 years ago. We extracted DNA from a Holocene coprolite (fossilized feces) from *M. balearicus*, and prepared double-stranded (DSL) and single-stranded (SSL) DNA libraries. Then we performed shotgun sequencing on the two library types DSL and SSL. To minimise DNA contamination, experiments were conducted in a laboratory dedicated to ancient DNA research, and strict filtering of the metagenomic data was performed using extraction blank controls and environmental data (soil, freshwater and air). Results show that the gut microbiome of *M. balearicus* is dominated by *Actinobacteria*, *Firmicutes* and *Proteobacteria*. Typical gut dwellers of ruminants, including *Ruminococcus*, *Runimiclostridium*, and methanogenic archaea, are also found in the coprolite. Before filtering, a significant increase in salt-tolerant and environmental microbes is found in SSL data when compared to DSL. However, we do not observe any difference in diversity and abundance between DSL and SSL datasets after filtering and normalisation. Thus, SSL may not be an ideal approach for maximising the sequencing effort in paleo-metagenomic studies due to the potentially higher risk of capturing environmental DNA contaminants.

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Review of contemporary records reveal new insights into the distribution and habitat for the threatened Carpentarian pseudantechinus (*Pseudantechinus mimulus*): More widespread than we thought?

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The Carpentarian pseudantechinus (*Pseudantechinus mimulus*) is a small, saxicoline marsupial found in the Northwest Highlands (NWH) bioregion of Queensland, and the adjacent Northern Territory (NT) and offshore islands. For a long period, it was only known from the type specimen collected in 1905 at an imprecise location on ‘Alexandria’ station in the north-east area of NT, and from the Pellew Islands in the Gulf of Carpentaria region of NT in rocky habitats dominated by a sandstone geology. Over the last 20 years, there has been a sporadic increase in records of this nationally threatened species and it is now known from at least 92 locations in the NWH, and in the north-east NT both on the mainland and offshore islands. These new records increase the known extent of occurrence of *P. mimulus* to approximately 57,000 km² and reveal that the species occurs on a diverse range of rock types and vegetation communities within its range. Extrapolation by Queensland Herbarium Regional Ecosystem mapping suggests that habitat for the species occurs even more widely than currently known and will be the target for future surveys.

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The nuchal ligaments in Carnivora: Speculative relations with sniff trail behavior

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It is widely known that the nuchal ligaments are well developed in some species of perissodactyls and artiodactyls. This ligament connects the caudal edge of the skull and thoracic vertebra to support the head weight without interfering the ability to lower the neck during feeding. This ligament is also present in dogs. However, the existence of this ligament has not been well studied in other mammals. Cadavers of several carnivorans including dog, Japanese raccoon dog, red fox, raccoon, Japanese badger, masked palm civet, cat, lion, tiger and Asiatic black bear were dissected to confirm the presence/absence of the nuchal ligament. It was found in all canids dissected (dog, raccoon dog and fox) but not in any other carnivorans. This ligament connects the tip of the first thoracic spinous process and the caudal edge of the spinous process of axis with abundant elasticity. In contrast to horse and cow, only the funicular part exists and laminar part was not found. The nuchal ligament was not only found in adults but also in fetal stages of felids. Among carnivorans, most canids are engaged in the so-called “sniff-trail behavior” when chasing prey. We speculate that the nuchal ligament works as an elastic support that continuously supports the head; this is beneficial for sniffing the ground over a long period to follow an invisible prey.

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Phylogenetic study of extinct Korean leopards in South Korea using mitochondrial DNA from old hides

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The leopard, *Panthera pardus*, is a threatened species in the world. Although there have been high densities of leopard populations in the Korean Peninsula historically, they became extirpated in South Korea by 1970, leaving almost no genetic specimens. The sub-specific classification of Korean leopards remains obscure even though they have been traditionally classified as *Panthera pardus orientalis.* Therefore, we attempted to do first the genetic study of South Korean leopards using an old hide of a leopard captured in Jirisan, South Korea in the 1930s. DNA was extracted from the old leopard hide and a total 727 bp of mitochondrial DNA, including NADH5 (611 bp) and D-loop (116 bp) regions, was amplified by PCR. The phylogenetic analysis of the sequence in comparison with the sequences of nine leopard subspecies from Genbank showed that the extirpated Korean leopard belonged to the same clade as the Amur leopard (*Panthera pardus orientalis*) on the phylogenetic tree. This result indicates that the leopard inhabiting South Korea in the past was the same sub-species as the Amur leopard population currently inhabiting the trans-boundary region with Russia, China and North Korea. The results emphasise the importance of conserving the endangered wild Amur leopard population, estimated to be about 60-80 individuals, because this population could be the source for the restoration of leopards in the Korean Peninsula in the future.

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Flutter detection by bats using different echolocation strategies

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Echolocating bats separate calls and echoes in time using low duty cycle (LDC) echolocation, or in frequency using high duty cycle (HDC) echolocation to avoid self-deafening. HDC echolocation is well suited for detecting fluttering targets (flying insects) in cluttered environments. It is also known that some LDC bats, e.g. *Coelops frithii*, Muriniae and Kerivoulinae, could detect fluttering targets, although the reason is not clear. In this study, we tested whether the flutter detection of these LDC bats could be explained by the similarity of their call design, and predicted Muriniae/Kerivoulinae, like *C. frithii*, would detect fluttering target more frequently than other LDC bats. We presented bats a mechanical fluttering target, consisting of a piece of paper (6 x 11 mm) mounted on the 20 cm metal spindle of a 12 V motor, in a flight tent and the field. We recorded sound and flying behaviour from 96 individuals (16 species) in tents, including (1) *C. frithii*, (2) Muriniae/Kerivoulinae, (3) other LDC and (4) HDC species. We showed the four groups of bats detected and approached the fluttering target with similar approach rates. In addition to approaching to the fluttering target, some *Murina*, *Kerivoula* and *Myotis* species also attacked the target with the paper removed, indicating these bats detected the prey from cues other than echoes reflected from fluttering wings. Two HDC and five LDC bat species were recorded in the field, and the HDC bat, *Rhinolophus monoceros*, was recorded most often and showed the highest approach rate of 58%.

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Reproductive behavior of the Asiatic wild ass (*Equus hemionus hemionus*) in Central Inner Mongolia

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The Asiatic wild ass belongs to Equidae and *Equus* Linnaeus. It is an endangered species according to the International Union for Conservation of Nature (IUCN) and one of the highest class of protected animal species in China. For the purpose of studying the regularity of reproductive behavior, we have observed the Asiatic wild ass's reproductive behaviors in central Inner Mongolia from February 2004 through November 2016. This is the first study to define and record estrus and mating, parturition and sexual behavior of the Asiatic wild ass in the wild. In the breeding season, there is a difference in terms of the ratios of time for the aforementioned behaviors between mature male and female Asiatic wild asses. The behaviors of a decreasing ratios of time are feeding (40.75%), standing and gazing (23.16%), resting (16.78%), moving (14.72%), sexual behavior (2.55%) and others (2.04%) for mature male Asiatic wild asses and feeding (53.99%), resting (28.35%), moving (6.91%), standing and gazing (6.06%), others (3.02%) and sexual behavior (1.67%) for mature female Asiatic wild asses. It is obvious that the feeding behavior takes the most time for both genders, which can be explained by poor local plants in terms of the amount and the nutrition. In the breeding period, most of members in a population of Asiatic wild asses behave regularly and consistently, with alternating behaviours of resting and activity.

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Mammalian reproductive investment strategies: An emergent property of the interplay between maternal body size and environmental productivity?

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Compared to other animal groups, mammals invest substantial amounts of energy in their offspring via gestation and lactation. Despite this unifying characteristic, strategies of maternal investment – i.e., reproductive energetics – differ considerably across species. Indicators of maternal investment strategies include gestation time, fetal and offspring growth rates, birth mass, litter size, lactation time, and weaning mass. While these indicators scale to some degree with maternal body size, comparisons among groups indicate investment strategies may differ between terrestrial and aquatic mammals. In this study, we synthesized multiple datasets from the scientific literature of approximately 3000 placental mammals, with the specific aim of comparing maternal investment indicators between marine and terrestrial groups. Our results show that (1) the effects of maternal body size on investment indicators differ between aquatic and terrestrial mammals such that (2) investment indicators tend to be higher in marine mammals than terrestrial mammals of similar size. For marine mammals, these include faster fetal and offspring growth rates, as well as larger birth and weaning masses, despite shorter gestation and lactation times. These results indicate that marine mammals invest a larger amount of energy in their offspring, and more quickly, compared to their terrestrial counterparts. We posit these differences to be driven by the very different characteristics of their respective environments, whereby the greater environmental productivity of the marine environment promotes large investments of energy in offspring while, simultaneously, the sheer scale of the spatiotemporal dynamics of seasonal migrations between feeding and breeding grounds constrains aquatic mammals to do so quickly.

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Conservation units of African bovid species: Conserving evolutionary and ecological processes

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Due to anthropogenic and natural impacts (environmental changes and disease outbreaks) many formerly widespread bovid species now exist only as managed populations on private land and in isolated formally protected areas, especially in South Africa. Natural ecological processes, such as migration (and consequent gene flow), and evolutionary processes, such as local adaptation and reinforcement of differentiation, currently occur on a limited scale. Instead managers need to mimic natural migration through translocations and the re-establishment of dispersal corridors between isolated areas. Due to changes in the distribution patterns of populations, subspecies and species, local adaptation is broken down due to outcrossing and outbreeding, or due to other changes in selection regimes. Varied management strategies across different conservation areas and on private lands further exacerbate the situation. We are using studies of genetic variation, based on markers that provide resolution across different time scales, to infer the evolutionary and ecological processes that have operated across populations of large and small antelope species. These insights can be used by managers to identify the most feasible options for maintaining the short- and long-term benefits of these processes that ultimately contribute to species persistence. Our research also questions previous subspecies and species descriptions and what we know about distribution records.

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Consequences of exposure to leprosy in wild nine-banded armadillos

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We used data from a six-year (2005-2010) study of a nine-banded armadillo (*Dasypus novemcinctus*) population in Mississippi, USA, to examine patterns and consequences of exposure to *Mycobacterium leprae*, the causative agent in producing leprosy. No juveniles or yearlings tested seropositive, implying there was no vertical transmission of infection. Older adults were more likely to be seropositive than younger adults and, in some years, females were more likely to be seropositive than males. Prevalence of infection varied from year to year but there was no spatial clustering of seropositive individuals. The latter result suggests transmission of infection was via some form of homogeneous mixing process (e.g. contaminated soil). Population modeling of host and pathogen dynamics showed that leprosy reduced annual survival of adult armadillos by ~15% and population growth rate by ~13%. The probability that a non-leprous adult armadillo would become seropositive from one year to the next was 0.18, with no possibility of recovery. The net reproductive number (R_0) was estimated to be 1.36, which suggests a 36% increase in seroprevalence per leprosy generation. Assuming a leprosy generation time of 3-5 years, we predict that *M. leprae* will spread within the population at the rate of 7-12% per year. Nine-banded armadillos are the only known non-human animal hosts of leprosy in the Western Hemisphere, and current evidence indicates likely zoonotic transmission. Thus, our results are important not just for understanding the dynamics of disease in a wildlife population, but may have important implications for human public health as well.

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Determinants of large cat attacks on humans in central India and impact of mitigation interventions

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We examined human and ecological attributes of attacks by tigers *Panthera tigris* and leopards *Panthera pardus* on humans in and around the Tadoba-Andhari Tiger Reserve in central India and implemented a series of interventions to prevent or mitigate conflicts between people and large carnivores. During 2005–2011, 132 carnivore attacks on humans occurred, 71 (54%) of which were lethal to humans. Tigers and leopards were responsible for 78% and 22% of these attacks, respectively. Significantly, more victims were attacked while collecting firewood than during other activities. The number of attacks has declined in the ensuing five years, partly as a response to interventions to change the behaviour of people entering the forest.

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Heart rate logging in free-ranging mammals

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Recent technology developments in bio-logging enable researchers to monitor physiological parameters such as body temperature (T_b) and heart rate (HR) in undisturbed settings. In Norway, domestic sheep graze free in the forest and on mountain pastures during the summer. This semi-domestic setting provides an excellent opportunity to validate quality, and use of bio-loggers. Thirty HR loggers (Star Oddi, Iceland) were implanted subcutaneously in twenty lambs in two different flocks, and in 10 ewes in one of the flocks. Of the 30 loggers, 22 could be retrieved and the data downloaded. The HR was measured based on a 3 sec ECG strips with 1, 2 or 10 minute intervals. Lambs and ewes were observed on the summer pasture and behavior was recorded. Mean active HR for lambs was 137 bpm (s.d. 16 bpm), and 103 bpm for ewes (s.d. 15 bpm). Mean passive HR of lambs was 110 bpm (s.d. 14 bpm) and 100 bpm for ewes (sd 13 bpm). During three periods, distributed over the summer, the loggers stored the raw ECG data enabling validation of the heart rate data. The sensing quality of 1700 ECG strips was manually assigned and RR intervals of 600 randomly selected manually measured. The HR logger assessed the quality in >99% of the measurements correctly and the difference between the manual measurements and the loggers HR was not different to 0 (t=1.3, p=0.2). We conclude that these HR loggers are suitable for monitoring HR in free ranging large mammals.

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The role of urban environment in shaping parasite communities of wild red foxes in Edinburgh

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Urbanisation of wild carnivores has become a common and taxonomically diverse phenomenon. This forced proximity between people and carnivores may substantially alter the ecology of urban species and influence ecological relationships of wild populations, especially predator-prey and host-parasite. The demographic, epidemiological and human health consequences of these changes are as yet poorly understood. Here we use the red fox (*Vulpes vulpes*) population of Edinburgh (UK) as a model system to investigate how human generated environmental variation influences parasite prevalence and community structure. We conducted an extensive survey in the Edinburgh area, collecting red fox faecal samples from public green spaces, and measured burden and prevalence of intestinal parasites using flotation analysis. We then used generalised linear mixed models to investigate how patterns of variation in parasite burden and prevalence are influenced by ecological and socio-economic variables. Preliminary results indicate that parasite community structure changes markedly across the city, with higher intensity of urbanisation being associated with higher parasite prevalence and lower diversity as a result of higher host population density and differences in marking behaviour. The increase was not linear and in suburban areas we measured an overall decrease of parasite prevalence, even lower than in rural areas. Understanding these fine scale patterns will help design more effective management plans for urban carnivores.

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Magnetic resonance imaging of the brains of three peramelemorphian marsupials

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We used magnetic resonance imaging to study the anatomy of cortical regions, nuclear groups and major forebrain tracts in the brains of three peramelemorphian marsupials (*Perameles nasuta*, *Isoodon obesulus*, *Macrotis lagotis*). These brains had been stored in formaldehyde solution in a museum collection for more than 80 years, and one of our goals was to demonstrate the feasibilty of extracting detailed comparative neuroanatomical information from the preserved brains of rare, endangered and extinct animals. High resolution anatomical and Diffusion Tensor Imaging was performed using a 9.4-T Bruker BioSpec 94/20 Avance III MRI system (Bruker, Ettlingen, Germany) located at the Biological Resources Imaging Laboratory at the University of New South Wales in Sydney. For image aquisition the system was equipped with gradients of 660 mT m^{-1} maximum strength and 4570 Tm s^{-1} slew rate (BGA-12S HP, *Bruker*, Ettlingen, Germany) and a 50 mm Quadrature Receive/Transmit RF-coil (RAPID Biomedical, Wuerzburg, Germany) for signal generation and reconstruction. We were able to differentiate areal and laminar topography within isocortical areas (primary somatosensory – S1; and visual - V1, V2), as well as subdivisions within olfactory and limbic allocortical regions (cingulate, hippocampal). Resolution of subcortical structures was sufficient to differentiate a and b segments within the visual nucleus of the thalamus. We identified several previously unrecognised longitudinal association fibre systems as well as a rich array of sensory thalamocortical connections. Our findings demonstrate the feasibility of using this sort of imaging of archived brains to analyze the neuranatomy of rare and evolutionarily significant species.

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On the interplay among ambient temperature, basal metabolic rate and body mass

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One of the most pervasive results of studies analyzing ecological variation of metabolic rates in endotherms is that ambient temperature is negatively correlated with mass-independent basal metabolic rate (residual BMR). However, to date, no study has evaluated if the strength of this correlation change with the size of the sampled species. Here we used published data on body mass (m_b), BMR, and annual mean temperature (T_{mean}) for 465 mammal species (and/or subspecies) to analyse this point. Both conventional and phylogenetic analyses indicate that correlation coefficients between residual BMR and T_{mean} increased with body mass, from values close to -0.5 at body sizes <100 g to values close to 0 at body size >1,000 g. Consequently, the current vision about the relevance of ambient temperature shaping the evolution of metabolic rates in endotherms probably is affected by the large number of small species in both nature and physiological data sets. Although this result does not deny the relevance of ambient temperature for most of the extent endothermic species, it claims for a pluralistic approach to explain the evolution of residual BMR. For instance, it could be possible that ambient temperature is the best predictor of residual BMR at the left side of the body size distribution curve, but that factors related with food availability (e.g. habitat productivity) could be the best predictors at the right side of this curve. Further studies aimed to collect more data on metabolic rates are welcome if we wish to achieve a more comprehensive understanding on animal energetics.

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The present status of two endangered insular populations of the leopard cat *Prionailurus bengalensis*: Implications for their conservation

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Two native wild felids are distributed in Japan, *Prionailurus bengalensis iriomotensis,* endemic to Iriomote-jima Island, and *P. b. euptilura*, commonly found on the Korean Peninsula. Although both are similar-sized small felids inhabiting small islands, their ecological characteristics such as feeding habits and habitat selection differ, which can be attributed to the climate and the biotic environmental factors (species composition of fauna on each island and presence of competitors). The population size of both the felids is estimated to be approximately 100–150 individuals; however, their population trends and distribution patterns differ. They are both listed as endangered species/subspecies in the Red List in Japan, and the Iriomote cat is listed as an endangered subspecies in the IUCN Red List, because of their small population sizes and restricted habitats. The two felids face some common threats, which include habitat destruction, road accidents, and negative effects of introduced species; these issues therefore need to be addressed for the conservation of these felids. However, the degree of the effect of each threat differs between the two felids, and each felid also has some unique problems partly because of differing ecological features and partly because of the diverse social background of each island, such as human population, industries, and the history of relationship between humans and wildlife. Here, we compare the status of the two wild felids and discuss various conservation strategies.

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Digitisation of the marsupial collections at the Natural History Museum, London

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Constituting almost 7% of the world’s extant mammals, marsupials predominate in the Australasian region and are also present in the Americas. The 300 or so species of living marsupials show astonishing variation in size, behaviour, ecology and exploit virtually all terrestrial environments. Recent studies on the phylogenetic systematics of marsupials have done much to clarify the relationships of both extant and extinct forms but several controversial problems remain. With the Natural History Museum collection being one of the main reference collections for research on this group, there is a clear need to make this resource available as widely as possible so taxonomy, ecology and conservation researchers can access this unique resource. The marsupial collection of the Natural History Museum contains circa 500 primary type specimens. This richness of specimens is largely due to the accessions of Australian mammals formed by Mr John Gould, and other notable donors of specimens include Lord Derby, Dr G Bennett, Messrs O Salvin, F D Goodman, John Macgillivray and F R Rayner. M R Oldfield Thomas also contributed significantly to marsupial taxonomy and privately financed collecting expeditions to South America that resulted in the acquisition and description of several new marsupial species. In light of this, the Natural History Museum supported an initiative to digitise this collection, photographing and data-basing all of this material so it can be made available on the web through the NHM Data Portal.

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Game-on, game-off: Bridging ecological and neurological pathways to fear

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Both ecologists and neurologists focus a great amount of effort into studying predator-prey interactions, each using this framework to understand unique aspects organism functions of micro- and macro-levels. Here, we suggest a framework that bridges both the reflex-based neurological fear, and the information-based strategic, ecological fear. In addition, we identify within this program two research directions than would greatly benefit from cross-field collaboration, paranoia and naiveté. Individuals with over-sensitive fear receptors, i.e. paranoid individuals, should be evolutionarily at a disadvantage. Overestimating risk greatly increases the missed opportunity costs thus reducing the individual’s fitness. On the opposite, the inability to perceive risk accurately (at the multiple levels of naiveté) has even greater implications. We attribute naiveté as the key factor for biological extinctions we observed in this past century; the best recorded examples are for Australian mammalian fauna. These junctures of eco-evolutionary and neurological dynamics should be fruitful collaborative frameworks, but are rare. The combination expertise can influence wildlife management and conservation and help find the mechanisms resulting in syndromes that afflict large portions of the human populations living in the shadow of wars and other density-dependent stressors.

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Two decades of climate driving the diversity of tropical small mammals

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Projections on global climate disruption are temperature increases, rainfall reductions in dry areas and the opposite on wet areas, and more extreme climate events. How these processes affect biodiversity known for taxonomic diversity (and less on functional diversity) of plants and for animals is emerging. Most studies on mammals focus on temperate habitats, lack long-term demographic data and rely on bibliographical traits. The causes of tropical mammal taxonomic and functional diversity are unknown. We compared taxonomic and functional richness and diversity, abundance and biomass against a neutral model, temperature and rainfall in two contiguous and distinct (upland and arroyo) tropical dry forests. Rainfall (seasonal and atypical) affected small mammals more in the harsher conditions of the upland forests than in the arroyo forest, a richer, more diverse, and stable habitat. These findings stress the threats of global climate disruption on the mammals inhabiting tropical dry forests, the most endangered terrestrial ecosystems on Earth.

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A new species of the spiny rat *Proechimys* (Rodentia: Echimyidae) from the northern Peruvian Yungas

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The spiny-rats of the genus *Proechimys* are the most speciose and widely distributed of the Echimyidae. Within them, *P. simonsi* is one of the largest and perhaps one of the most readily recognizable due primarily to the white coloration ventral fur, fine and soft hairs, hypothenar pad on plantar surface of hindfeet absent, and the deep mesopterygoid fossa. Its distribution comprises lowland rainforest and montane forests (yungas) on the eastern slope of the Andes, with elevation range upward to 2000 m. In a recent assessment to the northern Peruvian yungas, Amazonas department, Bongará province, a spiny-rat of the genus *Proechimys* was captured at 2439 m, an elevation very unusual for the genus. This specimen was compared with *P. simonsi* from the type region in Junín and from other populations, and found that it is morphologically distinct. This specimen is externally similar to *P. simonsi*, but it is comparatively smaller and darker, the fur is longer and softest, the skull is slimmer, the ventral fur and the metatarsals are immaculately white, the fourth upper molar is smaller than the third, and the tail length is approximately 90% of head and body length. Based on these differences, we suggest that this specimen represents a new species of the *simonsi* group. Our statement was complemented with a phylogenetic analysis of the mitochondrial DNA sequences, which showed the Bongará's specimen has a genetic distance of 9 to 13 % compared to other populations. This analysis also corroborates that *P. simonsi* represents a species complex.

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