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Novel Papillomavirus discovered in an Asian House Gecko (*Hemidactylus frenatus*)

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Papillomaviruses have a high tropism for squamous epithelial cells and cause persistent infection that may lead to disease in the host's skin and mucosal membranes. Papillomaviruses also have an oncogenic potential and are the aetiology or suspected aetiology of neoplasia across a diverse array of taxa. Of the known papillomaviruses, the majority have been isolated from human and other mammalian hosts. Currently, only eleven non-mammalian papillomaviruses from ten different species have been described and they have been found in birds (n = 5), turtles (n = 2), a fish (n = 1), and a snake (n = 1). Using next generation sequencing we have identified the complete genome of a novel papillomavirus in the most widely distributed and highly invasive gecko, the Asian House Gecko (*Hemidactylus frenatus*). This is the first report of the complete genome of a papillomavirus from a lizard. The virus was found using DNA from a maxillary mucosal lesion from an Asian House Gecko sequenced using next-generation platforms, and analysed using appropriate metagenomics software. The novel 7,378 bp genome had a maximum protein identity of 41%, 29%, 43% and 35% occurring across the major early (E1, E2), and late (L1, L2) open reading frames respectively with the most closely related papillomaviruses. Phylogenetic analysis of the concatenated E1, E2 and L1 proteins revealed that the papillomavirus isolated from the Asian House Gecko clustered with, but was basal to, the clade containing other known bird and reptile viruses. The discovery of this novel papillomavirus represents an important milestone in the understanding of papillomavirus evolution and demonstrates the power of next generation sequencing technology in the discovery of novel pathogens.

Tracking traces of morphological evolution in Australian lizards: CT scans wanted

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Skinks are the dominant lizard group in Australia, having evolved numerous morphological adaptations to colonize different habitats. Our recently-funded ARC Linkage project aims to track these adaptations in modern skinks to investigate the association between phenotypic traits and species diversification. We do this using non-invasive X-ray computed

tomography, or CT scanning, to generate high resolution 3D models of museum specimens. However, obtaining high quality CT images can be an expensive process. It involves the use of sophisticated X-ray technology, specialised software, and hours of data post-processing. In order to minimize these costs, especially as we want to compare skinks to other Australian lizards, CT scans are wanted. We are currently creating a directory of scans collected by colleagues across the country which we will link to details on species life-history, ecological and morphological traits, and locality and distribution data. This directory will be open-access with contact details of the scan providers, thus ensuring proper acknowledgement and providing new opportunities for scientific collaborations. It will also help to avoid multiple CT scans of the same specimens, allowing us to instead focus on other target species that might not have been sampled yet.

Comparison of venom gland transcriptomes in island and mainland populations of Australian Tiger Snakes, *Notechis scutatus*

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Venom is a biologically complex cocktail consisting of salts, organic molecules, peptides and proteins and is found in a number of taxonomically distinct species. Considerable research of venom has been directed at snake species due to their medical importance and the human health risks that accompany these animals. Within snakes, a major role of venom is to aid the subjugation and digestion of prey. Therefore, the impact of prey type can have a strong influence on the composition of venom genes, which are expressed in their venom glands. Novel toxin gene recruitment in predatory animal venom and resistance mechanisms by prey items act as reciprocal selection pressures that are a major driver of venom evolution. The Australian Tiger Snake, *Notechis scutatus*, has a unique evolutionary history where its populations have been separated on a number of islands off the coast of southern Australia (6000 to 12000 years ago). Tiger Snake populations include a relatively continuous mainland population whose prey consists of mainly anurans and lizards. Additionally, there are isolated island populations where prey items vary from just lizards to including mammals and birds. We aim to investigate differential expression levels of toxin genes in the venom gland between the continuous mainland population, two small offshore island populations, and a Tasmanian population of Tiger Snake. Comparisons of toxin genes between these populations appeared to show higher expression of specific isoforms in the island population(s). This suggests a role for toxin genes in their adaptation to different prey types.

Sex-linked markers in the Australian Grassland Earless Dragon *Tympanocryptis pinguicolla*

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Australian agamid lizards (Squamata: Agamidae: Amphibolurinae) are well known for having genotypic (GSD), temperature dependent sex determination (TSD) and GSD with temperature override. Heterogamety is important in understanding the natural history of any organism including evolution, levels and patterns of genetic diversity but heteromorphic sex chromosomes have been identified in only nine of ~91 agamid species karyotyped. In cases where heteromorphic sex chromosomes are absent, the isolation of sex-specific sequences can be used to reveal their sex determination mode. In this study, we use DArTseq, a genotyping by sequencing (GBS) approach, to identify differential sequences between sexes of the endangered Grassland Earless Dragon *Tympanocryptis pinguicolla*, a species that has no discernible sex chromosomes but for which incubation studies imply a GSD species. We analysed both SNP and in silico DArTseq markers (presence and absence – PA) in a randomly selected panel of 30 individuals (15 males and 15 females as determined by phenotype). Based on certain filtering criteria, we identified 33 female specific SNP markers and 21 PA markers. When expanded to a total of 171 individuals (89 females and 82 males), only one SNP and 26 PA markers within a range of 11.6 to 15% meiotic recombination were identified as none were 100% sex-linked. Overall, our data suggest that *T. pinguicolla* has a female heterogametic (ZZ/ZW) system but that while our markers are sex linked, they do not always segregate with sex. The discordance observed in our larger dataset could be the result of variable levels of recombination between markers and sex-determining loci or the presence of sex reversed individuals within our larger sample pool, or a combination of the two. We are currently working to convert the identified markers to single locus sex tests for use in breeding or the identification of sex reversed individuals.

Shedding light on the drivers of reptile distribution: Micro-environmental variables predict climatic-related traits of lizards

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The factors underlying species distributions have puzzled ecologists and evolutionary biologists for decades, and the role of abiotic and biotic factors is still debated. Abiotic factors might challenge animals by imposing on them different requirements to accommodate their climatic-related traits (i.e., physiology) in order to maintain homeostasis. Here, through global and systematic meta-analyses, we show how environmental variables predict key climatic-related traits of lizards. We compiled datasets including resting and standard metabolic rate (MR), field metabolic rate (FMR), evaporative water loss (EWL), thermal preference (T_{pref}), critical thermal

minimum (CTmin), and maximum (CTmax) of lizards worldwide. We extracted an array of micro-environmental variables (package NicheMapR in R) for each species in the database from the location the individuals were collected. Then, for each climatic-related trait as response variable, we constructed phylogenetic models with the micro-environmental variables set as predictors. Our results show complex ways by which the abiotic factors influence the climatic-related traits of lizards. Additionally, we found strong phylogenetic signal for Tpref, CT min and CTmax, medium for MR and FMR, and a low phylogenetic signal for EWL. Interestingly, our work provides insights into the ecophysiological and evolutionary mechanisms by which lizards adjust their physiological traits in response to environmental variation, the target abiotic factors affecting their range, and the potential responses those animals could exhibit in novel environments. Our study, therefore, sheds light on the processes driving the distributional ranges of lizards.

The molecular basis of adaptation to environmental change: Linking epigenetics, plasticity and genetic assimilation using geographically isolated populations of Tiger Snakes

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Over the last few decades, the role of adaptive plasticity in facilitating the colonisation of novel environments has become clearer. Concurrently, our understanding of the role epigenetic markers play in up- or down-regulating organismal functions has also vastly progressed. Using a uniquely powerful case of rapid evolution in geographically isolated populations of the Australian Tiger Snake, we aimed at linking plasticity levels for swallowing performance (high in recently introduced island populations; eroded by means of genetic assimilation in long isolated island populations) with epigenetics markers profiles; generating one of the first empirical evidence for the role of epigenetic mechanisms in driving evolution in natural populations. DNA was collected (mouth swabs) from a number of Tiger Snake populations from SA, TAS and WA in 2017 and 2018. Reduced Representation Bisulphite Sequencing was used as a cost-effective alternative to Whole Genome BS. Preliminary results (Principal Component Analysis) showed a strong segregation of epigenetic profiles between recently introduced Carnac Island snakes (highly plastic) and their mainland counterparts (not plastic); while epigenetic profiles from Williams Island (long isolated, no longer plastic) were overlapping with mainland WA, and with Carnac island to a lesser extent. Overall, mean CpP methylation was surprisingly high in Carnac Island snakes (66.70%), and lower in both mainland WA and Williams Island (55.50% and 56.15% respectively). These findings are discussed in light of the recent evolutionary history of Australian Tiger Snakes.

Exploring the social and mating systems of Estuarine Crocodiles *Crocodylus porosus*

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The social behaviour of an individual, including their social ties and interactions, can have major influences on their access to resources, mate choice and survival. Thus, understanding the social behaviour of a species can provide important insights into their general ecology, population dynamics and viability, and can be crucial in the development and implementation of effective conservation and management strategies. While there has been a recent increase in the number of studies examining reptilian social behaviour, highlighting a wide range of social behaviours and systems present, the majority of studies have primarily focused on Squamates, and in particular lizards. Crocodylians though display a wide range of highly conserved vocal and visual communication behaviours, hinting towards the presence of complex social systems. Utilising an integrative approach, combining novel biotelemetry technologies, with genetic relatedness and an examination of their reproductive ecology, this project aims to examine the social and mating systems of Estuarine Crocodiles, *Crocodylus porosus*. The results from this project will provide valuable insights into the social behaviours of crocodiles, providing crucial information for the development of effective conservation and management strategies for crocodylians, not only in Australia but globally as well.

Ontogenetic shifts in the nesting behaviour of female crocodiles

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Body size and age are crucial factors influencing reproductive capacity and success. As females grow, their reproductive investment and success often increase due to improved overall physiological condition and experience gained through successive reproductive events. While much of this work has been conducted on birds and mammals, surprisingly little is known on how body size affects nesting decisions in other long-lived vertebrates. We monitored the movements and nesting behaviour of 57 wild female estuarine crocodiles *Crocodylus porosus* over a 10-year period (and across consecutive nesting seasons) using externally mounted satellite tags, implanted acoustic transmitters and a network of submerged acoustic receivers. Applying Hidden Markov models to the telemetry-derived location data revealed that female nesting behaviours could be split into three distinct states: (i) ranging movements within home ranges and at nesting sites; (ii) migrations to and from nesting sites; (iii); and nesting/nest guarding. We found that during migration events, larger females migrated further and remained away from dry season territories for longer periods than smaller individuals. Furthermore, not only were

migratory movements stimulated by increases in rainfall, larger females migrated to nest sites at lower rainfall thresholds than smaller females. We provide some of the first evidence of body size influencing nesting decisions in an ectothermic vertebrate, with shifts likely resulting from an increased willingness to invest in nest protection among larger and more experienced females.

Importance of different habitat structures as means of connectivity in agriculture landscapes: an analysis of home range and habitat use by *Calotes versicolor*

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Agriculture is the greatest threat to terrestrial reptiles worldwide, affecting 74% of species assessed for the IUCN Red List. Reptiles are particularly sensitive to agriculture and habitat fragmentation, but are routinely understudied. The lack of published literature and data on reptile diversity in the agriculture landscapes of Pakistan requires immediate attention to understand their population statuses and inform land management. This presentation will provide details of my study which aims to discover the use of different habitat elements by reptiles across fragmented landscapes. We investigated if reptiles make use of cropland temporarily when the crops are growing, and if they make greater use of hedgerows or forests after crops are harvested. We determined if there are specific habitat structures that can be preserved within these agricultural areas to aid species conservation. A population of agamid lizard, *Calotes versicolor*, was studied for six months throughout its entire season of activity in the agriculture ecosystem with few remnant patches of dry deciduous scrub forest in District Chakwal, Pakistan. We radio-tracked 32 individuals (♀17, ♂11) across different habitat structures. Individuals were equipped with small radio transmitters and were relocated after short intervals (minimum 3 times a day) until the end of the tracking period. We determined how dragon activity area size (minimum convex polygons), daily movement rate, inter-day displacement distance and perch height varied according to animal sex, size and land use (i.e., farm vs. forest). Analyses are currently underway and results will be presented at the conference.

Remarkable longevity in New Zealand's terrestrial herpetofauna

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Long-term population studies of endemic New Zealand amphibians (Anura: Leiopelmatidae), lizards (geckos: Diplodactylidae; skinks Scincidae) and tuatara (Rhynchocephalia) reveal remarkable longevity in the wild, with estimates exceeding those generally reported for similar-sized species elsewhere. From our own studies, New Zealand frogs take 4–7 years to reach maturity with estimated life-spans up to 38 years in Archey's Frog *Leiopelma archeyi*, 45 years in Hamilton's Frog *L. hamiltoni*, and 18 years in Hochstetter's Frog *L. hochstetteri*. Similarly, studies by many people reveal exceptionally long life-spans in the lizards. Most geckos take 2–8 years to reach maturity, with maturity fastest in diurnally active *Naultinus* species, which are known to reach at least 10 years. Slowest maturity is seen in larger-bodied nocturnal geckos. For example, Duvaucel's Gecko *Hoplodactylus duvaucelii* takes 7 years to mature and reaches at least 50 years and *Woodworthia* 'Otago/Southland large' takes 8 years to mature and reach at least 30 years. Record longevity is reported for the relatively small nocturnal gecko *W. cf. brunnea* with an individual reaching 53 years. Unsurprisingly, data on these geckos are from longest running mark-recapture studies; most lizard species and populations have not been studied long enough to obtain higher values. Among diurnal skinks, smaller *Oligosoma* species mature within 2–4 years, living at least 8 years. The larger-bodied Grand skink *O. grande* and Otago Skink *O. ottagense* mature more slowly (3–6 years) and live at least 21 years, with similar values in the nocturnal Whitaker's Skink *O. whitakeri*. In captivity, longevity of endemic lizards approaches or exceeds 40 years of age. In the tuatara *Sphenodon punctatus* maturity takes 10–15 years, with oldest known individuals reaching 80–90 years. Reasons for this extraordinary longevity amongst the New Zealand herpetofauna are discussed, including examination of life-history traits, and concepts of the slow-fast continuum and the pace-of-life syndrome.

Refuges and recovery: responses of rainforest frogs to chytridiomycosis

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Chytridiomycosis drove a wave of amphibian declines across Australia's eastern seaboard late last century. Low elevation refuges appear to have been crucial for the persistence of several species in the Wet Tropics; however, there have been limited elevational surveys to

establish the scale of recovery. This study sought to fill that gap, completing surveys across the historic elevational range of four declined rainforest endemics: *Litoria dayi*, *L. nannotis*, *L. rheocola* and *L. serrata*. The aims were four-fold: (i) to establish the contemporary elevation distribution of these species; (ii) to assess the prevalence and intensity of chytrid infections among them; (iii) to document environmental drivers of infection risk, and; (iv) to establish whether infection risk influences the contemporary elevational distribution of these frogs. We surveyed five rainforest streams, conducting surveys at 200 m elevational steps from mountain-base to summit (30 sites in total). Two species—*L. serrata* and *L. rheocola*—were found over their full historical elevational range, while *L. nannotis* was not detected above 800 m asl and *L. dayi* was not detected above 400 m asl. Chytrid prevalence was lowest in *L. dayi* (18%), highest in *L. serrata* (47%), and similar in *L. nannotis* (35%) and *L. rheocola* (28%). In all cases, infection risk increased linearly with elevation (being strongly negatively correlated with night-time air temperatures), but was only negatively related to site occupancy for *L. dayi* and *L. nannotis*. Our data suggests that there has been strong recovery from chytridiomycosis in *L. serrata* and *L. rheocola*, partial recovery in *L. nannotis*, but limited recovery in *L. dayi*, which remains restricted to low-elevation disease refuges. We discuss the implications of this work for managing remnant populations, and for pursuing targeted reintroductions at sites where historical extirpations cannot be reversed by natural recolonisation.

Conservation genomics of the Kuranda Tree Frog

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The Kuranda Tree Frog (*Litoria myola*) is a species of both evolutionary and conservation significance. Its relatively recent evolutionary history makes it an ideal system to study adaptation and speciation, while habitat modification and fragmentation pose an imminent threat to its survival. To aid in the effective management and conservation of this species, we assessed population connectivity, effective population size, and genetic diversity using 7132 genome-wide neutral Single Nucleotide Polymorphisms (SNPs) sampled from all known breeding populations. Connectivity between breeding sites was generally higher than expected, with most showing no differentiation. However, cluster analyses consistently identified the farthest east population as distinct from the rest, with limited connectivity in between. This pattern could not be attributed to isolation by distance. The effective population size estimated from our genetic data was ~2000 individuals. Despite this, we detected no evidence for reduced genetic diversity and limited indication of inbreeding. We discuss how these results can guide conservation of this Critically Endangered species.

Regularisation methods for detecting population differentiation: an example with *Lerista*

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Regularisation is a technique which places restrictions on the solution to optimisation problems such that the resulting parameter estimates have certain desirable properties. Regularisation is a well-known method in statistics but is rarely applied to problems in biology. An advantage of regularised methods is that they can be used to analyse data where there are many variables (“large p”), but a small sample size (“small n”). This is often the case in taxonomy where there may be a large number of morphological characters measured on only a few specimens. Here we describe results using a regularised Discriminant Function Analysis (rDFA) and a regularised multiple logistic regression applied to morphological characters from two populations of *Lerista rochfordensis*, a vulnerable small fossorial skink from North Queensland. Based only on 16 specimens, we show that the two populations can be discriminated morphologically using rDFA and that a minimum of 6 characters are necessary to resolve the difference between the two populations using regularised logistic regression (the LASSO).

Bioacoustic monitoring reveals the calling activity of an endangered mountain-top frog (*Phyloria kundagungan*) in response to environmental conditions

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Globally, amphibians have declined at an unprecedented rate in recent decades with more than 30% of amphibian species listed as threatened by the International Union for Conservation of Nature. The Mountain Frog, *Phyloria kundagungan*, is an endangered amphibian species endemic to the upland rainforests of northern New South Wales and southeast Queensland, Australia. This species is considered to be at risk from future climate change however, the population trajectory of *P. kundagungan* is poorly known and surveys have been hampered by their cryptic calling behaviour and subterranean habits. Environmental conditions are strong drivers of amphibian calling behaviour but are often poorly understood aspects of amphibian ecology. With detailed knowledge of the calling phenology of this species, surveys can be appropriately timed thus increasing detection probabilities.

The influence of environmental variables on *P. kundagungan* calling activity was investigated at six sites across the species’ geographic and altitudinal range. Audio recording equipment (Wildlife Acoustics, Songmeter II) was deployed at each site and programmed to record sound every hour for ten minutes between July 2016 and March 2018. Soil temperature along with a range of meteorological conditions were recorded every hour at each site. Kaleidoscope 4.5.4

(Wildlife Acoustics, Inc.), an automatic call recognition programme was used to automatically detect *P. kundagungan* calls in sound files.

Kaleidoscope detected a total of 2,031,848 *P. kundagungan* calls in 8760 hours of sound recordings. The true positive rate for the presence of *P. kundagungan* calls in 5000 randomly selected recordings was >98%. The results of this study indicate that, *P. kundagungan* calling activity is driven primarily by soil temperature and time of day. This study will allow future targeted surveys of this visually cryptic species to be conducted under conditions that induce calling activity and further understand the implications climate change may have on this endangered mountain-top frog.

What predicts the extinction risk of Australian skinks?

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Extinction risk varies greatly between species. A species' extinction risk depends upon its intrinsic biological traits, its response to extrinsic threats and the intraspecific variation within its intrinsic traits. Research into what drives extinction risk in reptiles is scarce compared to other terrestrial vertebrate groups. Furthermore, such research is typically limited by the confounding effects of species' geographic range size. Controlling for these confounding effects, this study aimed to determine the best intrinsic and extrinsic predictors of extinction risk in a highly diverse reptile group, Australian skinks (Scincidae), and to examine whether their extinction vulnerability was associated with the intraspecific variation of their intrinsic traits. To control for the effects of range size, species categorised as Threatened by the IUCN Red List were paired with Non-Threatened species from within the same genus, with species within pairs also required to have overlapping geographic ranges. Data for several intrinsic and extrinsic variables were collected for each included species, with the best extinction risk predictors determined from linear mixed effects models. Contrary to findings of most previous research, all examined variables were weak predictors of extinction risk, with all substantially supported models having low explanatory power. There were also no differences between Threatened and Non-Threatened species in their intraspecific variation, for morphology or clutch size. Ultimately, these results suggest that the included variables, as well as patterns of intraspecific variation, are inadequate nationwide predictors of Australian skink extinction risk. However, with some variables showing strong predictive potential within specific regions of Australia; this study highlights how research with a more concentrated geographic scope is likely to identify more precise predictive patterns.

Reptile twitchers can pose a threat to the reptiles they photograph

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In some instances reptile photographic twitchers either knowingly or unwittingly, and often unlawfully, can significantly disturb or alter habitat or refuges of reptiles they photograph (e.g. burrows, rock slabs, etc.).

I have been involved in recent surveys for the critically endangered Retro Slider (*Lerista allanae*), which was re-discovered in 2009 after it had been presumed extinct for some time. Even though leaf litter racking is the best survey technique to find this skink, I have made a point of not returning regularly to re-rake litter at the four sites it is known to occur. This I believe provides time for the litter structure to re-establish. However, recently reptile twitching became an issue for the Retro Slider when a photograph of the skink was posted on the internet by someone not directly involved in its research. Intentional capture and handling of this threatened skink for any purpose legally requires an appropriate state government permit. It is likely the skink was caught by leaf litter racking, which can be expected to alter the layering structure of leaf litter where it occurs. Although the consequences of such litter disturbance on this skink is unknown, it is still of concern as it is only known from four sites, all of very limited area because of land clearing. Two of these sites are single records.

Trialling of a new method to reduce predation risk for the critically endangered Nangur Spiny skink (*Nangura spinosa*)

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The critically endangered Nangur Spiny Skink (*Nangura spinosa*) was only discovered in 1992, and in spite of significant survey effort is still only known from two locations in southeast Queensland. The population at one of these locations has recently seen a significant and concerning drop in numbers to around 50 individuals. The causes of this decline are unclear, but predation is considered a likely factor. Of particular concern are feral cats and foxes, both known predators of lizards and present where the skink occurs. Baited cage traps were unsuccessful in reducing their numbers and predator-proof perimeter fencing was not an option for a number of reasons.

The skink lives in a single entrance burrow spending much time within 60 cm of the entrance. To exploit this behaviour, caging was designed to reduce predation risk within this 60 cm zone. The caging is currently being trialled around five Nangur Spiny Skink burrow entrances. We believe it is a world first, as we could find no published attempt to protect burrow-using reptiles

using a similar caging design. Cameras have been set up to monitor the impact of the caging on the lizard, potential predators and other wildlife. To date there is no evidence to suggest the caging is impeding the skink's movement or changing its behaviour. No native animals have been trapped inside the caging or its mesh. Although the caging is designed to minimise predation by foxes and feral cats, it is proving effective at protecting the skink from Dingoes and Australian Brush-turkeys, both potential predators common to the area. The caging is unlikely to reduce predation risk from marsupial mice, rodents, Lace Monitors or Cane Toads. Further burrows will be caged if the trial is successful.

Patterns of spinal arthritis in toads across Australia

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Loss of fitness can be a consequence of selection for rapid dispersal ability in invasive species. Increased prevalence of spinal arthritis may occur in cane toad populations at the invasion front as a cost of increased invasiveness, but our knowledge of the ecological drivers of this condition is lacking. We aimed to determine the factors explaining the prevalence of spinal arthritis in populations across the Australian landscape. We studied populations across a gradient of invasion histories. We collected 2415 toads over five years and determined the presence and size of spondylosis for each individual. We examined the effect of host size, leg length and invasion history on the prevalence of spondylosis. Host size was a significant predictor of spondylosis across populations. Contrary to our expectations, the overall prevalence of spondylosis was not positively related to invasion history and did not correlate with toad relative leg length. Rather than invasion age, the latitude at which populations were sampled provided an alternate explanation for the prevalence of spondylosis in cane toad populations and suggested that the incidence of this condition did not increase as a physiological cost of invasion, but is instead related to physical variables, such as climate.

Integrating competition and biogeography into the evolution of monitor lizard body size

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Organismal gigantism and dwarfism have been variously associated with biotic and abiotic drivers of diversification such as island and continental biogeography, changing global climate, and competition. Among extant vertebrates, few genera exhibit the size and ecological

diversity present in *Varanus* (monitor) lizards. Extant monitors are island giants and desert dwarves (0.1–3 m), scattered across the globe from Saharan Africa to mangrove swamps of Australasia. And while extensive work has documented the ecomorphological disparity of goannas, little research has attempted to explain these patterns. We extend existing phylogenetic comparative methods to account for historical biogeography and competition between lineages, in an attempt to explain body size evolution in monitors. We start by building the most comprehensive phylogeny of *Varanus* to date, using a dataset of 400 loci. We then reconstruct the historical biogeography of the genus using species occurrence records. Finally, we model body size of Australian monitors, allowing for competitive interactions with other *Varanus* species, as well as marsupial carnivores. Our results shed light on the process of character displacement in Australian goannas, and highlight the importance of including biogeography and competition when modelling macroevolutionary trends.

Describing the use of the caudal knob by Prickly Knob-tailed Geckos, *Nephrurus asper*

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Structures and behaviours of organisms evolve in response to environments. Unique solutions to ecological problems provide fascinating examples of the power of evolution. Particularly interesting are clearly specialised structures for which the function is unknown. Knob-tailed geckos (*Nephrurus* spp.) have developed a unique tail with an expanded distal tip, the caudal knob. Three of the species of *Nephrurus* (of 9 species in the genus), are the only geckos in the world that lack the ability to autotomise (the ability to willingly drop the tail in response to an attack). Currently, the function of their caudal knob remains unknown. Here I examine the behaviours of the Prickly Knob-tailed Gecko (*Nephrurus asper*), using field behavioural observations facilitated by radio telemetry, and behavioural experiments in the laboratory under a variety of conditions. By observing the behaviour of *N. asper* in relation to the caudal knob in a variety of contexts, I aim to understand and describe its function.

I found that there are four distinct tail behaviours exhibited by *N. asper*: wiggle, vibrate, raise, and probe. The vibrate was strongly correlated to prey interaction, when prey capture was unsuccessful, every individual vibrates soon after. This may be an aid in prey acquisition to distract the prey, to increase the gecko's success in prey capture.

Probing in *N. asper* is the first reported probe behaviour observed in lizards. Tail probes may be used as a method of sensing mechanical stimuli in the environment. When the geckos were in the presence of prey, the probe frequency increased, potentially being used as a tool to feel the substrate for signals from the prey (i.e., vibrations). When presented with different substrates, the geckos probed significantly less in the finer substrate. This supports my hypothesis that the probe behaviour may be used for sensing mechanical stimuli (i.e., substrate choice).

The ecology and dynamics of Lace Monitor *Varanus varius* populations in north eastern Australia

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The Lace Monitor, *Varanus varius*, is an overlooked lizard. Despite its relative abundance within much of its range and the likely very important ecological role of the species very little has been published on its ecology. We used baited trail cameras to collect data on the activity patterns, abundance, movements, and residency of Lace Monitors at five sites on the northern Atherton Tablelands, north-east Queensland between summer 2016 and summer 2018 inclusive. Goannas were active at all times of the year, albeit much more so during summer compared to July. Preliminary analyses demonstrate that Lace Monitors were active at ambient temperatures greater than 23° C and that the vast amount of activity (85% detections) were had during the two hours either side of midday. The number of monitors present on each 30.6 ha site ranged from zero to 12 individuals. Home ranges of four monitors which were redetected between the February and July 2018 sampling sessions were between 0.06 km² and 0.18 km², and maximum straight-line distance travelled during one 14 day sampling session was 2244 m. We will present data from more sampling sessions and explore these with respect to seasons, diel weather and individual size class. Lace Monitors proved themselves an ideal animal for trail camera-based studies of activity, movements and abundance.

Does insurance against genetic incompatibility drive extreme polyandry in a frog?

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Sequential polyandry may evolve as an insurance mechanism to reduce the risk that females choose mates that are genetically inferior (intrinsic male quality hypothesis) or genetically incompatible (genetic incompatibility hypothesis). The prevalence of such indirect benefits remains controversial, however, because few studies have estimated the contributions of additive and non-additive sources of genetic variation to female fitness. Here we use artificial fertilisation techniques combined with a cross-classified breeding design (North Carolina Type II) to simultaneously test the ‘good genes hypothesis’ and the ‘genetic incompatibility hypothesis’ in the Brown Toadlet (*Pseudophryne bibronii*); a species with extreme sequential polyandry. Our results revealed no significant additive or non-additive genetic effects on fertilisation success. Additionally, our results revealed no significant additive genetic effects, but highly significant non-additive genetic effects (sire by dam interaction effects), on hatching success and larval survival to initial and final metamorphosis. Taken together, these results

indicate that offspring viability is significantly influenced by the combination of parental genotypes, and that negative interactions between parental genetic elements manifest during early development. Overall, our findings provide quantitative genetic evidence that insurance against genetic incompatibility could favour the evolution and maintenance of sequential polyandry in *P. bibronii*. More broadly, we argue that insurance against genetic incompatibility might contribute to the widespread occurrence of polyandry in anuran amphibians.

Elevation seizes the (*Litoria*) *dayi*: current status of amphibian chytrid fungus in remaining populations of the Australian Lacelid Frog

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Knowledge about the distribution of diseases within wildlife populations is critical for focusing conservation and management efforts. The amphibian chytrid fungus *Batrachochytrium dendrobatidis* (Bd) caused dramatic declines in the abundance and distribution of numerous frog species in the Queensland Wet Tropics in the 1990s. Since then, many species have recovered to varying extents but the Australian Lacelid (*Litoria dayi*) has not. Despite the presumed importance of Bd in the restricted distribution and reduced abundance of *L. dayi*, the current infection dynamics of Bd in this species were poorly known. We aimed to investigate the status of Bd in *L. dayi* by quantifying Bd prevalence and infection intensity across elevational gradients at three national parks within the Queensland Wet Tropics. We found that increasing elevation was a positive predictor of both infection prevalence and intensity of Bd in *L. dayi*. Additionally, predicted probability that a given individual would be infected had strong elevational patterns, with probabilities ranging from 36% at lower *L. dayi* elevation limits to 91% at higher elevations where *L. dayi* is currently found. Furthermore, these predicted probabilities reached an asymptote near 100% slightly above the current upper elevation limit of *L. dayi*. These results suggest that Bd continues to hamper recovery of this species and that an elevational infection threshold prevents them from recolonising upland sites. Thus, chytridiomycosis caused by Bd is affecting the species' ecology and subjecting it to vulnerability of extinction. This study provides the first step towards understanding the factors preventing recovery in *L. dayi* and will be useful for management and conservation efforts. However, more research will be required to fully understand the dynamics of this system.

Identification of novel Hepatitis D virus-like agents in invertebrate, fish and amphibians

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Hepatitis delta virus (HDV), as the smallest virus known to infect mammals, has been identified only in human infected with hepatitis B virus (HBV), but currently found in birds and snakes, further extending the host range to invertebrates, fish and amphibians in our study. HDV genome is covalently closed, circular RNA approximately 1.7 kb nucleotides in length. Encoded only one protein (Hepatitis Delta Antigen ; HDAG) from one specific open reading frame within its viroid-like self-complementary RNA, HDV also constitutes an unbranched rod-like folding structure. By exploiting metatranscriptomic approaches, we characterize 4 divergent HDV-like agents, including one from subterranean termite (*Schedorhinotermes intermedius*), one from a mixture of fish (*Macroramphosus scolopax*, *Ophidion* sp., *Eptatretus burgeri*, *Okamejei acutispina*, *Proscyllium habereri*, *Lophius litulon*, *Eleutheronema tetradactylum*, *Zeus faber*, *Antennarius striatus*, *Halieutaea stellata*, *Gonorynchus abbreviatus*) and amphibian ones are from Asiatic Toad (*Bufo gargarizans*) and Chinese Fire Belly Newt (*Cynops orientalis*), respectively. Consistent with HDV features, the agents discovered in our study demonstrate size between 1.5 kb to 1.8 kb, circular genomes and self-complementary, unbranched rod-like structures. Despite the putative 4 HDAGs identified are highly divergent in the resulting amino acid sequences alignment with other human HDAGs, of importance that similar HDV-like signatures including the coiled-coil domains, leucine zippers, isoelectric point values and conserved residues with essential biological functions for post-translational modification are denoted. Notably, we didn't identify known hepatitis B viruses in those corresponding libraries. The results further suggest that the necessity of coexistence of HDV and HBV is debatable. Collectively, these findings not only broaden the diversity of HDV in non-human species, but also shed light on our understanding of the origin and evolutionary history of HDVs.

Conservation status of Australian squamates

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Squamate reptiles represent one of the most diverse lineages of terrestrial vertebrates on earth, with 10,417 described species. Yet, despite this impressive diversity, they are also the vertebrate group for which we know the least about their conservation status. Only 58% of squamates have been assessed against International Union for Conservation of Nature (IUCN) criteria, with ~19% considered Threatened, and 16% listed as Data Deficient. Australia represents a diversity hotspot for squamates, and is home to 10% of the world's lizard and snake diversity. However, until recently, only 15% of Australian squamates had been assessed by the IUCN, the lowest percentage of any region in the world. Here we describe the outcomes of two IUCN assessment workshops conducted in 2017 (February in Perth, June in Melbourne) that assessed the conservation status of virtually all described species (~980 species). Overall, 7% of Australian squamate species were listed as Threatened (i.e., Critically Endangered, Endangered, or Vulnerable), 2% Near Threatened, and 4% Data Deficient. The vast majority of species (87%) were listed as Least Concern. Most Threatened species (67%) were listed solely on attributes of their geographic range (Criterion B), while 22% were listed based on having very small or restricted populations (Criterion D). Most Threatened species were found to occur in northern Australia or south-east Queensland. We discuss the implications of these findings for the conservation and management of Australian lizards and snakes.

Voluntary thermal tolerance in different life-history stages of a retreat-dwelling gecko (*Woodworthia* “Otago/Southland”)

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Assessing the implications of climate change for conservation of ectotherms requires knowledge of the upper limits of behavioural thermal tolerance (i.e. voluntary thermal maximum, VTmax). Ectotherms employ behavioural mechanisms to avoid overheating and heat stress by withdrawing to shelter. Most studies of VTmax among lizards have examined species that openly bask in the sun. We developed a protocol for assessing VTmax in a semi-nocturnal gecko that inhabits rocky retreats by day. Given that this species shows variation in thermal

preference with pregnancy status and sex, we predicted that VTmax would vary with these factors also. Our protocol involved heating geckos individually within a retreat, at a rate simulating the temperature rise that would be experienced in the wild on a hot summer's day. To date, we have compared four groups of geckos (late pregnant females, non-pregnant females, males and juveniles) from a laboratory colony, in late summer/autumn. The voluntary exit of geckos from the retreat site was filmed from an adjacent room. As soon as the geckos left the heated retreat, we recorded skin surface temperature using an infrared camera. Control geckos, which were exposed to overhead lighting without heating, rarely left the retreat. The behaviour exhibited by geckos at the approach to VTmax included exposure of heads at the retreat's periphery, tongue flicking and gaping. Although we have not observed a significant difference in mean VTmax among groups to date, pregnant females appeared to tolerate heating for longer than other groups. This implies that pregnant females were able to regulate their heating rate, perhaps involving different positioning within the retreat and/or increased use of evaporative cooling (e.g., via mouth gaping). In further work, we plan to extend VTmax testing to field-collected animals earlier in pregnancy, and to relate our findings to how climate change might influence future microhabitat use.

Susceptibility of frogs to chytridiomycosis correlates with increased levels of immunomodulatory serotonin in the skin

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Frogs demonstrate varying degrees of susceptibility to the chytrid fungus *Batrachochytrium dendrobatidis* (Bd), a pathogen responsible for the global decline and extinction of amphibians. A recent non-targeted metabolomics study of infected and uninfected Alpine tree frogs (*Litoria verreauxii alpina*) revealed a correlation between skin serotonin (5'-hydroxytryptamine) and the progression of Bd infection (Grogan *et al.*, 2018). We investigated the role of serotonin concentrations in the skin of infected and uninfected frogs in relation to their degree of chytridiomycosis susceptibility. We identified a correlation between skin serotonin concentration and pre-moribund infection intensity in susceptible frog populations via non-targeted metabolomic analysis. Immunohistochemistry showed that serotonin accumulated in skin granular glands of uninfected frogs, but was absent in infected moribund frogs. *In vitro* growth assays showed that serotonin reduced growth of both Bd sporangia and Jurkat lymphocytes. The inhibition of Bd growth did not recover with addition of tryptophan (serotonin precursor) or kynurenine (metabolite of tryptophan). Tryptophan is likely metabolised into

immunosuppressive serotonin in the host. Our results suggest that the immunosuppressive effects of serotonin contribute to the increased susceptibility of frogs to chytridiomycosis.

Elevated salinity reduces chytrid transmission and improves host survival: Implications for translocations

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Emerging infectious diseases are one of the greatest threats to global biodiversity, with chytridiomycosis in amphibians perhaps the most extreme example of this phenomenon. Translocations are increasingly used to fight disease-induced extinctions. However, many fail because disease is still present or subsequently establishes in the translocation environment. Can environmental mismatch between host and pathogen, whereby environmental manipulation generates unfavourable environmental conditions for pathogens but remains favourable for the host, improve survival in populations? We tested the hypothesis that manipulating environmental salinity in outdoor mesocosms under near identical environmental conditions applying in a nearby translocation program for an endangered amphibian, would improve survival and determine the mechanisms involved. 160 infected and 288 uninfected, captive-bred, juvenile frogs were released into 16 outdoor mesocosms in which salinity was controlled (high or low salinity treatment). The experiment ran for 25 weeks from the mid-austral winter to the mid-austral summer of 2013 in a temperate coastal environment, Australia. Increasing salinity from ca. 0.5 ppt to 3.5–4.5 ppt reduced pathogen transmission between infected and uninfected animals, resulting in significantly reduced mortality in elevated salt mesocosms (0.13, high salt versus 0.23, low salt survival at 23 weeks). Increasing water temperature associated with season (from mean 13° C to 25° C) eventually cleared all surviving animals of the pathogen. Thus, we identified a mechanism by which environmental salinity can protect amphibian hosts from chytridiomycosis by reducing disease transmission rates and conclude that manipulating environmental salinity in landscapes where chytrid-affected amphibians are currently translocated could improve the probability of population persistence for such species. More broadly, we provide support for the paradigm that environmental manipulation via environmental mismatch can be used to mitigate the impact of emerging infectious diseases.

Venom gland elongation in Night Adders (Viperinae: *Causus*)

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The venom glands of venomous snakes are typically restricted to the head; however, peculiar exceptions do exist. The elongation of the venom gland system, in some cases leading to glands that extend to more than a third of the body length, seems to have independently evolved at least four times amongst the front-fanged venomous snakes.

Causus (“Night adders”) is a clade of small African vipers that contains six well-recognised species, of which two have elongated venom glands (*C. rhombeatus* and *C. maculatus*). *Causus* are unique amongst vipers in their atypic morpho-ecologic characteristics: all are anuran specialists and active-pursuit predators with high rates of prey consumption, they possess slender head and body morphology with scalation akin to a colubrid and/or elapid, and they are fossorial to semi-fossorial. Recent molecular phylogenetic data analysis nests them well within the Viperinae clade. This suggests that their morpho-ecological condition is derived (i.e., apomorphic) as opposed to a representation of an ancestral or basal viperid condition (i.e., plesiotypic) as previously thought.

The aim of this research was to investigate variation in venom composition and/or functional activity in relation to difference in gland size. We investigated and compared the composition, functional activity, and coagulopathic action of venom from two night adder species: the Long-glanded Rhombic Night Adder *Causus rhombeatus* and the Short-glanded Forest Night Adder *Causus lichtensteinii*.

The proteomic composition and functional activity of both species’ venoms were shown to have minimal variation. This alludes to the possibility of venom gland elongation being associated with a set of morpho-ecological traits as opposed to a shift in composition/functional activity of the venom.

The presence and persistence of frog species in the New England Tablelands of NSW

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Frog populations have declined globally, but the nature and extent of declines in most areas is poorly understood as historical survey data is lacking for most regions. This project aims to understand changes in the distribution of frog species in the New England Tablelands in northern NSW. The region is ideal to this study, as extensive surveys were carried out in the 1960s and 70s, and the frog fauna has since undergone dramatic changes. To understand the nature and scale of these declines, and what factors influence species presence, over 200 sites that were historically surveyed will be revisited four times during the period from December to April, for three years. Presence or absence of each frog species will be recorded as well as habitat and environmental covariates. This will be used to create occupancy models to enable understanding of habitat characteristics which influence each species occupancy (the likelihood of sites being occupied by each species) and its associated detection (probability of detecting the species at a site given it is occupied). Of the 80 sites visited so far, only 11 of the 36 historical species have been detected. The final occupancy models will be used to determine which habitat characteristics are critical for each frog species. Understanding the importance of key habitat characteristics for frog species persistence will have beneficial implications for frog conservation worldwide.

The Loggerhead Turtle ‘Hatchery’—Promoting conservation through public engagement

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In 2019, the World Science Festival Brisbane, hosted by the Queensland Museum, is entering its 4th year. One of its signature events is the Loggerhead Turtle Hatchery which runs over a four day period. Eggs collected from Mon Repos, in late January, are incubated at 29.9°C and timed to hatch during the festival in March. These are collected, freshly laid, over five nights to ensure that hatching lasts throughout the duration of this event. They are initially incubated at the Mon Repos Turtle Research facility for three to four weeks to ensure the developing embryos are sufficiently robust to withstand a road trip to Brisbane. The egg temperature is monitored daily and incubation continues through to the first signs of pipping which, ideally, should correspond with the start of the festival. The final stages of incubation and hatchling emergence take place in transparent incubators in the museum’s public galleries,

with the event live-streamed on the internet. The hatchlings are displayed in large aquaria, once their yolk sacs are fully resorbed. Following the festival, they are cared for at Sea Life (Mooloolaba) and then released, at the earliest possible date, into the Eastern Australian Current. The Hatchery is conducted with appropriate permits from the Department of Environment and Science and with approval from an animal ethics committee.

The focus of this exercise is to display a natural event that occurs out of sight, deep within a nest chamber and to incorporate this with a strong conservation message. We discuss the Turtle Conservation Project and 50 years of research at Mon Repos, the research outcomes and how a decline in Loggerhead Turtles nesting on the Woongarra Coast was detected and then reversed. We also promote Mon Repos as a tourist destination. Hatchling turtles have tremendous appeal and incorporating them as a focal point for this event allows us to deliver these messages to an audience of 8,000 + visitors who attend annually. This information is delivered by museum staff with support from World Science Festival volunteers, some with research experience at Mon Repos and other nesting beaches. In addition to festival visitors, the Hatchery receives significant media coverage and reached a cumulative media audience of more than 2,400,000 in 2017. We believe that the survival of the hatchlings is not compromised by this event and that it is justified by its conservation and ecotourism benefits.

The Hatchery continues to evolve with changes to the layout and conservation messages from year to year. In March 2019, the program will work with schools informing children on the impacts of plastic debris on marine creatures and the extent of this problem with an emphasis on marine turtles. Teachers will be guided by curriculum-linked resources promoting awareness of this issue.

Bad neighbours: the dynamics of amphibian chytrid fungus infection in three frogs species in Sydney

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Wildlife disease is a major cause of global biodiversity loss. Amongst the most devastating is the amphibian chytrid fungus, *Batrachochytrium dendrobatidis* (Bd), contributing to over 100 amphibian extinctions worldwide. In Australia, our understanding of Bd is derived from studies that are highly geographically biased, focusing on major biodiversity hotspots such as tropical north Queensland and the alpine region, therefore, our ability to extrapolate lessons learnt in these unique environments to other regions is unknown. This study aims to gain a greater understanding of the dynamics of Bd in the Sydney Region and analyse the intensity of Bd infection in three frog species; the Blue Mountains Tree Frog (*Litoria citropa*), a relatively poorly-studied species likely to be susceptible to Bd infection, and the Common Eastern Froglet (*Crinia signifera*) and the Stony Creek Frog (*Litoria lesueurii*), two species known to be reservoir species for Bd (a species that persists despite a high Bd infection prevalence and serves as a source of infection for other species) in the alpine region of Australia. By determining if *L. citropa* is effected by Bd, and confirming whether *C. signifera* and *L. lesueurii* maintain high

levels of infection in the Sydney region (suggesting that they are acting as reservoirs for Bd), we can inform conservation management of susceptible frog species that share habitat with these abundant frogs.

Preferred body temperature both rises and falls during pregnancy in a live-bearing gecko in ways that may be adaptive for embryos

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Preferred body temperature (PBT, also known as selected temperature, Tsel) is measured in squamate reptiles as the body temperature selected in a thermal gradient. This variable has attracted much interest from reptile biologists because of its relevance to topics including thermoregulatory strategy, the evolution of viviparity and species-distribution modelling under climate change. Although PBT is often treated as a single variable for a species, previous research shows that it can vary with factors including sex and season. The value also often changes with pregnancy status; however, some studies have shown elevations in PBT with pregnancy, whereas studies on other species have shown declines. Here, we extend our group's previous research on PBT in a viviparous, cool-climate gecko (the New Zealand taxon *Woodworthia* "Otago/Southland"), in which pregnancy can last over a year. We show that (i) in late pregnancy, PBT varies with thermal regime (basking opportunity and night temperature); (ii) PBT drops in the immediate pre-partum period and (iii) PBT has risen again within the week after birth to match the PBT of neonates. Our results, when combined with earlier studies, reveal a profile across the full reproductive cycle in which PBT is elevated until late in pregnancy (presumably enhancing embryonic development), low during the pre-partum weeks (presumably enhancing survival of fully-developed embryos by keeping metabolic rates low when yolk has been consumed) and intermediate when post-partum (spent) or vitellogenic. Whether this pattern occurs in species with less extended gestation requires further testing.

How does Australia's largest lizard species respond to mine site restoration?

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Globally increasing rates of mine site discontinuations are resulting in the need for immediate implementation of effective biodiversity and conservation management strategies. Over 60 000 mines across Australia have been identified as discontinued, yet despite restoration being a legislative requirement, the number of these sites confirmed as restored and officially closed is extremely low. Monitoring vegetation structure and condition is a common method of assessing restoration success, however monitoring animal responses is relatively uncommon. Animals are generally assumed to return to pre-disturbance abundances following the return of vegetation (Field of Dreams hypothesis; 'build it and they will come'). In practice, recovering animal biodiversity and community structure can be some of the most difficult components to achieve and assess following the restoration of degraded sites.

Using VHF/GPS loggers, we tracked the movements and habitat usage of a Perentie (*Varanus giganteus*), Australia's largest lizard species, in November 2018 at a mine site in Mid West Western Australia. Both reference and restoration areas were frequented by the varanid, and usage of restoration appears to be long term and not only opportunistic. Several areas of the landscape appear to serve as refuge/burrow areas, with night refuges occurring within both reference and restoration landscapes. While return of species diversity and abundance to restoration landscapes will likely require significant time and investment, current restoration practices appear to be facilitating the return of large native reptilian species.

Using monitors to monitor restoration: presence may not indicate persistence

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Globally, increasing rates of mine site discontinuations are resulting in the need for immediate implementation of effective biodiversity restoration and conservation management strategies. Monitoring vegetation structure and condition is a common method of assessing restoration success; however, monitoring animal responses to an altered and altering landscape is relatively uncommon. Animals are generally assumed to return to pre-disturbance abundances following the return of vegetation (Field of Dreams hypothesis; ‘build it and they will come’). In practice, recovering animal biodiversity and community structure can be some of the most difficult components to achieve and assess following the restoration of degraded sites. Reptiles are threatened and declining globally, yet, despite their ecological significance, little is known about how reptiles respond to habitat change and restoration. Members of the Varanidae play an ecologically important role as top predators and tend to have large foraging areas and home ranges, yet their responses to habitat alteration have been poorly studied. Behaviour, abundance, habitat use, and ecophysiology of varanid species are likely to be heavily impacted following mining. Understanding such responses of varanid species to habitat degradation and rehabilitation is important to determine indicators for success in mine site restoration.

We assessed habitat utilisation by varanids in sites of varying distance to active mining activities (one reference site, and two restoration sites with adjacent reference vegetation), by GPS mapping and measuring burrows, diggings, and tracks. Proximity to active mining significantly impacts varanid land use, with both reference and restoration sites closest to active mining activities being used infrequently. While restoration areas were used by varanids, such use appears to be opportunistic, with the exception of the site furthest from active mining, which appeared to be facilitating varanid return.

The evolution of cutaneous senses in sea snakes

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The evolution of epidermal scales was a major innovation in the evolution of lepidosaurs, providing a barrier to dehydration and physical stress, while functioning as a sensitive interface for detecting stimuli in the environment. I explore two sensory pathways in snakes that can be mediated by the skin: 1) mechanoreception (touch) and 2) cutaneous photoreception (tail phototaxis). Mechanoreception in snakes involves tiny scale organs ('sensilla') that are concentrated on the surface of the head. I reconstructed the evolutionary history of sensilla in 19 species (Elapidae: Hydrophiinae) to better understand sensory shifts that may have occurred during transitions from land to sea in snakes. Then, I described the sensilla ultrastructure in two species of sea snakes, investigating the question: have sensilla retained a mechanoreceptive function and/or been co-opted for the detection of water motion? Cutaneous photoreception (CP) is the detection of light not involved in image-forming (eye) vision. Olive Sea Snakes (*Aipysurus laevis*) are the only reptiles reported to have cutaneous photoreception and it is expected to aid in concealment from predators: resting snakes respond to local illumination of the skin by retracting their vulnerable tail-paddles under rock or reef overhangs. We conducted behavioural tests in eight species of sea snake, developing a preliminary hypothesis for the evolutionary origin of this trait. We then profiled skin transcriptomes of phototactic snakes to identify candidate genes involved in CP. We also quantified tail damage in museum specimens to see whether the probability of sustaining tail injuries is influenced by tail phototactic ability in snakes. Tactile and cutaneous photoreception are often overlooked sensory modalities in snakes but are fundamental to the sensory ecology of many species. Studying these systems in sea snakes can increase our understanding of how organisms respond to major ecological shifts during evolution.

A genome-wide search for local adaptation in a terrestrial-breeding frog highlights vulnerability to climate change

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Terrestrial-breeding amphibians are likely to be vulnerable to warming and drying climates, as their embryos require consistent moisture for successful development. Adaptation to such environmental changes will depend on sufficient genetic variation existing within or between connected populations. Here we use single nucleotide polymorphism (SNP) data to investigate genome-wide patterns in genetic diversity, gene flow and local adaptation in a

terrestrial-breeding frog (*Pseudophryne guentheri*) subject to a rapidly drying climate and recent habitat fragmentation. The species was sampled across twelve central and range-edge populations (192 samples), and strong genetic structure was apparent, as were high inbreeding coefficients. Populations showed differences in genetic diversity, and one population lost significant genetic diversity in a decade. More than 1500 SNP loci were putatively under directional selection, and 1386 of these loci were correlated with environmental variables such as temperature, rainfall, evaporation and soil moisture. Among these loci, one locus showed homology to a gene involved in the activation of maturation in *Xenopus* oocytes, which could play a role in the successful and rapid development of embryos in marginal climates. This is the first study to apply genomic methods to detect local adaptation in an amphibian species, and shows why management strategies such as assisted gene flow may be necessary to assist isolated populations to adapt to future climates.

Surveying frogs from the bellies of their parasites

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Reliable occurrence data are vital for conservation management of species and their habitats, but the collection of sufficient species records is often made difficult by factors that reduce species detectability. Frogs are a highly threatened taxon globally, requiring urgent conservation attention. However effective management of frog species can be hampered by a lack of comprehensive occurrence records, caused by cryptic behaviour, complex habitats, and true rarity. Recently, iDNA (invertebrate-derived DNA) has emerged as a potentially powerful tool for increased detection of terrestrial vertebrates. Invertebrate parasites have been shown to be effective samplers of some vertebrate diversity, and can be trapped and have the DNA in their meals sequenced to identify and detect their vertebrate hosts. Despite being important candidates for conservation action, and attracting sometimes impressive amounts of blood-feeding parasites, frogs have never been targeted in iDNA surveys. Most vertebrate surveys incorporating iDNA have been general or targeted mammals. We are determining the feasibility of targeted frog iDNA surveys by trapping hematophagous frog parasites in eastern NSW, Australia and analyzing their blood meals. We are using traps baited with the calls of a common frog (*Litoria barringtonensis*) and a threatened frog (*Mixophyes balbus*) to investigate whether frog iDNA can be collected and used to detect some frog species more effectively than traditional audio-visual transect searches.

Electric blue: venom composition and activity of the Long-glanded Blue Coralsnake (*Calliophis bivirgatus*)

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The genus *Calliophis*, sometimes called Asian coral snakes, are the most basal branch of the elapid radiation. *Calliophis bivirgatus* is found from Thailand to Indonesia and is one of the most strikingly colored snakes in the world. Beyond its beauty, *C. bivirgatus* is fascinating because of its diet composed largely of other ophiophagous venomous snakes, extraordinarily elongated venom glands, and toxins in its venom that cause a rigid paralysis, instead of the limp paralysis caused by other elapids such as cobras or death adders. The venom is the first from a vertebrate known to display such activity. Using a combination of transcriptomics, proteomics, and *in vitro* testing of toxic activity, we characterize the venom of this iconic snake species. These data shed light not only on the current ecology of these snakes, but also the origin of the elapid snakes in general and their venomous arsenals.

Coagulating colubrids: Evolutionary, pathophysiological and biodiscovery implications of venom variations between *Dispholidus typus* and *Thelotornis mossambicanus*

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Venoms can deleteriously affect any physiological system reachable by the bloodstream, including directly interfering with the coagulation cascade. Such coagulopathic toxins may be anti- or procoagulant. Snake venoms are unique in their use of procoagulant toxins for predatory purposes. The Boomslang (*Dispholidus typus*) and the twig snakes (*Thelotornis* species) are iconic African snakes belonging to the family Colubridae and produce strikingly similar lethal procoagulant pathologies. Despite these similarities, antivenom is only produced for treating

bites by *D. typus*. The mechanism of action of both venoms have been understudied. In this study, we investigated the venom of *D. typus* and *T. mossambicanus* utilising a range of proteomic and bioactivity approaches, including determining the procoagulant properties of both venoms in relation to the human coagulation pathways. Clotting capabilities of the two venoms were assessed both with and without calcium and phospholipid co-factors in real time plasma clotting assays. We found that *T. mossambicanus* produced a significantly stronger coagulation response compared to that of *D. typus*. Functional enzyme assays showed that *T. mossambicanus* also exhibited a higher metalloprotease and phospholipase activity, but had a much lower serine protease activity relative to *D. typus* venom. The neutralising capability of the available boomslang antivenom was also investigated on both species, with it being 11.3 times more effective upon *D. typus* venom than *T. mossambicanus*. In addition to being a faster clotting venom, *T. mossambicanus* was revealed to have a more complex venom than *D. typus*. This study increases our understanding of not only the biodiscovery potential of these medically important species but also increases our knowledge of the pathological relationship between venom and coagulation cascade.

Rearing environment influences behavioural variation and behavioural syndrome structure in Southern Rainforest Sunskinks

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Behaviour plays a vital role in ecological and evolutionary processes. It is, therefore, important to understand how behavioural variation and potential constraints on optimal behavioural expression, such as behavioural syndromes, arise and are maintained. We tested the role of early experience by investigating how rearing environment influenced behavioural variation and behavioural syndromes in adult laboratory- and wild-reared male Southern Rainforest Sunskinks (*Lampropholis similis*). Individuals from both cohorts were measured for their activity, exploratory, sociability, and boldness behaviours and used these traits to compare repeatability, behavioural variation and behavioural syndrome structure. Repeatability did not differ between cohorts, but skinks reared in the laboratory were bolder and had greater behavioural variation than those reared in the wild. There was also evidence for an activity-sociability syndrome in laboratory-reared skinks but not in wild-reared skinks. Our results highlight the importance of lifetime experiences, particularly early development, in shaping the behavioural profile of a population.

Social tolerance in the Eastern Water Dragon (*Intellagama lesueurii*)

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Animals live in a dynamic social environment shaping their behaviour throughout their entire lives. In the last century, scientists have documented a large number of social interactions resulting from social behaviours including affiliation, aggression and tolerance. Social tolerance affects the access to a variety of resources and may play an important role in the evolution of sociality. Yet, despite its widespread occurrence across the animal kingdom, social tolerance has largely been studied in mammals exhibiting complex social structures. Here, we investigate social tolerance behaviour in an urban population of Eastern Water Dragons (*Intellagama lesueurii*), a long-lived and social reptile species with fission-fusion like social dynamics. We assessed social tolerance using nonaggressive physical proximity and tested for individual repeatability in social tolerance over six years. Then, we studied the effect of different habitats on individuals' social tolerance behaviour. Our results showed that both males and females were repeatable in their social tolerance behaviour across years. Repeatable social behaviour may be advantageous as it might allow individuals to predict the future behaviour of others, therefore reducing uncertainties about their social environment. On the other hand, the degree of social tolerance varied between habitats, which could be explained by multiple environmental features. First, resource availability affects aggressive behaviour in many species, with low resource competition leading to lower aggression levels. Therefore, differences in resource availability between habitats could affect aggression levels and thus social tolerance. Second, population density may play a role in social tolerance, where the benefit from not getting involved in fights becomes greater as the number of competitors increases. Further investigation is needed to disentangle the factors contributing to these habitat differences but our findings emphasize the importance of broadening this study area to other animal taxa.

Reptile survival in an urban jungle

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When it comes to urban wildlife management, there are basic questions that we don't know the complex answers to. How does human involvement affect the survival of urban species? What happens to injured reptiles that have been cared for, rehabilitated and released back into areas where they originally occurred? Can rehabilitated reptiles survive when returned to the wild, especially large pythons that have been in care for 12 months or more? I plan to study these questions as part of a PhD to gain insight into the spatial ecology and survival of relocated and rehabilitated Coastal Carpet Pythons *Morelia spilota mcdowelli* in an urban environment.

How sex can go wrong in the cold: sex reversal of wild alpine skinks *Bassiana duperreyi* (Eastern Three-lined Skink)

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In reptiles, sex can be determined genetically (genotypic sex determination or GSD) or environmentally, depending on their incubation temperature (temperature sex determination or TSD). Typically, the two alternatives of sex determination were thought to be incompatible and were never observed in the same species, however sex reversal of some GSD species under extreme environmental conditions, confirmed in wild populations, has revealed that intermediate states are possible. Sex determination in the endemic Australian skink *Bassiana duperreyi* is influenced by both genetic factors and nest temperature, but experiments using definitive genetic sex tests to ascertain phenotypic sex have been conducted in laboratory conditions. Whether sex reversal occurs in natural nests, and whether sex reversed individuals survive to adulthood wild populations is not known. Furthermore, it is not clear whether the interaction of sex reversal of male XX individuals under low temperatures occurs at a rate sufficient to trigger loss of the Y chromosome and evolutionary transitions between GSD and TSD. To address these questions in wild population of *B. duperreyi*, we used genome subtraction to characterise Y-chromosome markers. We successfully isolated seven Y chromosome markers from *B. duperreyi* which were then validated against a panel of 20 known phenotypic males and 20 known phenotypic females. We then applied these molecular sex markers to detect the sex reversal at two life stages, at different elevations, in the wild populations. We discovered 14% adults and 26% of hatchlings were naturally sex reversed in the alpine population but not in lowland populations. We provide further evidence that sex reversal by cool temperatures in *B. duperreyi* occurs in the wild, influences the sexual genotypes-phenotype combinations in adult populations, and is as such a potential means of rapid evolutionary responses to climate change.

Population cytogenetics of goannas

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The aim of my project is to understand the role of chromosome evolution in speciation of monitor lizards. In particular, we have chosen the spiny-tailed goannas (*Varanus acanthurus* complex) as models because they are a small, easy to breed species with a broad range. They display chromosome polymorphisms across their range and a ZZ/ZW sex chromosome system. This project will investigate molecular as well as environmental factors that influence these mechanisms. Our specific tasks will involve developing and testing sex-linked markers using next generation sequencing as well as uncovering molecular evolution of heteromorphic sex chromosomes across wild populations, and the role of chromosome polymorphisms as a means of a post-mating isolation mechanism leading to speciation within this group.

Anguimorph lizard venoms disrupt the clotting ability of human fibrinogen

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Anguimorph lizard venom is a controversial topic, partly due to the lack of demonstrated functional activity. Despite numerous reports of bite victims having adverse effects beyond the mechanical damage of the bite, little research has been conducted on the toxins responsible or the pathways in which they act. Persistent bleeding is commonly reported after bites from helodermatid and varanid lizards. Previous studies have shown that one mechanism in which the anticoagulants could act is via the non-specific cleaving of fibrinogen chains. However, the ability of the venoms to prevent clot formation has not been demonstrated. Using a Thromboelastograph (TEG), clot strength was measured after incubating human fibrinogen with helodermatid and varanid lizard venoms. Clot strengths were found to be highly variable across the 27 species tested, with the weakest clots produced by incubation with varanid lizard venoms from the *Odatria* and *Euprepriosaurus* clades. Some of the most fibrinogenolytically active venoms belonged to *V. prasinus* and *V. scalaris*, which are arboreal species and therefore prey escape potential is a strong evolutionary selection pressure. The results are also consistent with reports of profuse bleeding from bites from these species as well as from other notably active species, such as the perentie (*V. giganteus*), also common in captivity. Our results provide evidence in favour of the predatory role of anguimorph lizard venom and sheds light on the evolution of reptile venoms.

Correspondence of genomic and phenotypic lines across a contact zone of the Tawny Dragon, *Ctenophorus decresii*

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Natural contact zones between lineages in the early stages of speciation offer a unique opportunity to directly measure the progress of speciation. Furthermore, speciation is facilitated when traits under divergent selection are linked to reproductive isolation, such as coloration. The Tawny Dragon, *Ctenophorus decresii*, is a compelling study system comprising two divergent lineages, with lineage-specific sexual coloration, that meet in a narrow contact zone. We used double digest restriction site associated DNA sequencing (ddRADseq) to identify SNPs and investigate genome-wide patterns of divergence and introgression. The findings confirm genetic admixture but gene flow appears to be asymmetric. In addition, we investigated hybrid phenotype across the contact zone and found a steep cline with genetic hybrids more strongly resembling one parental lineage. Ongoing research in this study system to clarify contact zone

dynamics and genomic regions associated with coloration will contribute to our understanding of the role of coloration in speciation.

Life lessons from *Gehyra*

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This year, 16 new species of *Gehyra* have been described, making *Gehyra* by far the most speciose genus of gekkonid lizard in Australia with 45 species. This large number of species recently described was the end result of years of collecting, measuring and sequencing thousands of specimens from the arid zone and monsoonal tropics. This talk will review previous conceptions of *Gehyra* over the years and how the various collaborations formed to examine different kinds of genetic and morphological evidence to result in the new works. The species concepts applied, and how the new kinds of genetic evidence have improved understanding of the group will also be discussed, including some speculation on the evolution of body size, habitat shifts and biogeographic scenarios. Despite being difficult to identify with so many similar-looking species, *Gehyra* is a fascinating group of lizards and resolving their systematics has been in step with recently developed methods, making them a model system for resolving other cryptic groups of herpetiles.

Seasonal thermal plasticity in White's skink, *Liopholis whitii*

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Thermally variable environments are particularly challenging for ectotherms as physiological functions are thermo-dependent. Thermal plasticity is defined as reversible, within individual changes to thermal traits. Thermal plasticity is predicted to be important for ectotherms in highly variable environments. Our understanding of thermal plasticity comes predominantly from controlled laboratory experiments; but how it occurs in natural populations experiencing thermal variation is not yet well understood. Ectotherms in highly seasonal environments are predicted to have greater thermal plasticity. Our study aimed to investigate the presence of seasonal thermal plasticity in a natural high elevation population of White's skink (*Liopholis whitii*). We monitored the thermal variation across the field site (Lake Jindabyne, NSW) and over the season. We used a mark-recapture method to test the thermal tolerances and performance of male *L. whitii* across their active season. Maximum and average temperatures

were found to vary across the field site, and temperatures gradually increased across the season. Evidence of seasonal plasticity was identified in the critical thermal minimum and thermal tolerance breadth, but not in the critical thermal maximum. Our results are consistent with much of the previous literature; but this is one of the first studies to identify these patterns in a field population. Thermal performance was also found to be plastic, but not in a seasonal pattern. These results indicate that performance may be more plastic than previous literature suggests. Overall our study provides evidence of seasonal thermal plasticity in a field population of high elevation *L. whitii*. Our results highlight the need to pair laboratory and field studies in order to understand thermal plasticity in an ecologically relevant context.

Correlates of climatic niche evolution in lizards

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Climatic niches, which can be defined as the set of climatic conditions associated with the occurrence of a given species, have become a central concept in understanding why species live where they do. However, the dynamic nature of climate on Earth makes such conditions oscillate in time and space, which can directly affect the evolutionary dynamics of climatic niches. Although such variation in the tempo and mode of climatic niche evolution has been widely documented, little is known about the mechanisms underlying such variation. Here we investigated patterns of climatic niche evolution in lizards and whether species traits such as body size and geographical range size can influence these patterns. We used distribution maps, climatic and phylogenetic information, and species trait data for 2800 species to investigate what determines the position of species in the climatic niche space and what are the effects that species traits have on the rates of climatic niche evolution. We found no significant relationship between the mean body size of each species and their positions in the climatic niche space. However, a significant relationship was found between their position in the climatic niche space and the mean range size, indicating that smaller range sizes can be found in areas of the climatic niche space with mild temperatures, humid conditions and less precipitation seasonality. There was no significant relationship between rates of climatic niche evolution and body or range size. Despite expectations of a relationship between body size and climate, these results show that body size evolution appears to be decoupled from the evolution of climatic niches in lizards. One possible explanation for such results is that lizards actively thermoregulate by behaviour and this would act as a buffer in relation to changes in climatic conditions, allowing the species to live in a given type of climate independently of their body size.

Social networking of the Otago skink (*Oligosoma otagense*)

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The social behaviour of New Zealand's native lizards is poorly understood. This study explores the social behaviour of the Otago skink (*Oligosoma otagense*), one of New Zealand's largest-bodied and rarest species of lizards. The Otago skink has previously been observed in pairs and groups, but little else is known about its social behaviour. In this study we asked, do Otago skinks form stable social groups? This study was conducted on a translocated population inhabiting an enclosure at Orokonui Ecosanctuary in Dunedin. The first aim of the study was to compare the stability of social groups over time. Regular photo surveys of solitary and non-solitary animals were made from April to October. Individual skinks were subsequently identified from photographs by the unique pattern-markings present on their bodies. The second aim of the study was to analyse the composition of social groups, and in particular, we asked if social groups were based on family relationships. Genotyping was conducted on tail tissue obtained from 6 subadults and 2 juveniles, and 15 loci were isolated and amplified from these tissue samples. There was an initial expectation of a potentially high level of inbreeding within the captive sourced population, and this would have caused an increased difficulty in determining the composition of social groups. Preliminary results from the genetic analysis, however, show sufficient distinguishing variation among individuals. The findings from this study will provide valuable information and insight on the habitat, movements and social associations of the skinks, with implications for future translocations of existing natural populations.

A trial reintroduction of Blue-tailed Skinks (*Cryptoblepharus egeriae*) into an introduced predator free enclosure on Christmas Island

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The Blue-tailed Skink (*Cryptoblepharus egeriae*) is Extinct in the Wild, existing only as two captive populations on Christmas Island and at Taronga Zoo. Endemic to Christmas Island in the East Indian Ocean, it was considered common in 1979, however by June 2010 blue-tailed skink had disappeared. Fortuitously, extinction was circumvented as 66 individuals were brought into captivity by early 2010. By August 2018 the captive breeding population had increased at least 1629 individuals across the two captive colonies. A central component of the conservation plan is the reintroduction and establishment of self-sustaining populations back onto Christmas Island. Hard releases are unlikely to be successful as the removal of the species thought to have contributed to the decline (invasive snakes and centipedes) is not currently possible. Therefore Parks Australia has constructed a large enclosure (~2600 m²) from which invasive species can be eradicated, excluded or heavily managed. In April 2017 the first attempt to reintroduce Blue-tailed Skinks was undertaken, but was ultimately unsuccessful as by October

2017 the skinks had disappeared. Giant centipedes (*Scolopendra subspinipes*) and inadequate habitat quality/quantity were likely to have been the primary reasons for the unsuccessful establishment. Giant centipedes have since been eradicated from the enclosure and habitat quality increased. In August 2018 a second reintroduction of 170 Blue-tailed Skinks was conducted. Here I provide an overview of both release events, and reflect on the reasons for the much greater success of the second reintroduction attempt.

Evolution of pythons: understanding the remarkable morphological diversity behind the world's largest snakes

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Identifying the evolutionary forces driving phenotypic diversity is fundamental to understanding adaptive radiation. Among these correlates to morphological evolution, researchers often have identified phylogenetic inertia, ecological adaptation and allometry as drivers and/or constraints. We present the results of various research projects looking at different aspects of evolution in pythons, an adaptive radiation of Old World snakes that comprise one of the broadest ecological, phenotypic and size disparities among reptiles. We generated data for 396 exons with an anchored hybrid enrichment approach and, combined with multiple fossil calibrations, reconstructed the phylogenetic and biogeographic history of pythons. We show that they mostly likely originated in Asia and then dispersed into Africa, Melanesia and Australo-Papua in the last 10 million years. We also generated head and body shape data from 1,700 museum specimens spanning all pythons at all ontogenetic stages, and adults of the boas, another group of large snakes with similar diversity as pythons. Using geometric and traditional morphometrics techniques, and also new analytical approaches, we found that micro-habitat is the main driver of head shape diversity and that there is clade-wide convergence between pythons and boas, suggesting the extreme adaptive value of head phenotypes in these snakes. We then examined shape change through ontogeny in all the pythons. We show that, contrary to the traditional view of allometry, shape is extremely labile and evolvable and not a constraint on morphological evolution. We also show that heterochrony, a dissociation between size, shape and age, is also extremely important at initial stages of evolution and that shifts in allometric trajectories make possible exploration of novel morphospace at later stages of evolution. This integrative study shows how complex and varied are the drivers of morphological diversity, and how important it is to consider different aspects of evolution in studies of adaptive radiation.

Temporal variation of the skin bacterial community and *Batrachochytrium dendrobatidis* infection in the frog *Phyllorhina loveridgei*

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Microbial symbiotic communities are ubiquitous in animals and plants as some can play an important role in disease resistance of host, hence the focus of much current research. Globally, amphibian population declines and extinctions have occurred due to chytridiomycosis, a skin disease caused by the pathogen *Batrachochytrium dendrobatidis* (Bd). Currently amphibian skin bacteria are increasingly recognized as important symbiont communities with a relevant role in the defense against pathogens, as some bacteria can inhibit the growth of Bd. This study aims to document the Bd infection status of wild populations of a terrestrial cryptic frog (*Philoria loveridgei*), and to determine whether infection status is correlated with changes in the skin microbial communities. Skin samples of *P. loveridgei* were collected along an altitudinal range within the species distribution in subtropical rainforests in southeast Australia. Sampling was conducted in two years during two breeding seasons with the first classified as a “La Niña” year. We used Taqman real-time PCR to determine Bd infection status and 16S amplicon sequencing techniques to describe the skin community structure. We found Bd-positive frogs only in the second sampling year with low infection intensities, and no correlation between Bd infection status and altitude, frog sex or size. Skin bacterial diversity was significantly higher in *P. loveridgei* frogs sampled in the 1st year than in the 2nd year. In addition, 7.4% of the total OTUs were significantly more abundant in the 1st year compared to the 2nd year. We identified 67 bacterial OTUs with a significant positive correlation between infection intensity and an OTU’s relative abundance. Forty-five percent of these OTUs belonged to the family Enterobacteriaceae. Overall, temporal variation was strongly associated with changes in Bd infection status and bacterial community structure of wild populations of *P. loveridgei*.

Evolutionary history of Neotropical savannas geographically concentrates species, phylogenetic and functional diversity of lizards

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The Cerrado is a global biodiversity hotspot and the most biodiverse tropical savanna in the world. Brazilian conservation policies often neglect non-forest ecosystems, where less than 47% is natural vegetation. Determining where the diversity of Cerrado taxa is concentrated is important for prioritizing conservation efforts at local scales. To bypass the inadequate taxonomy and integrating phylogenetic, functional, and spatial data, we aim to provide a multidimensional panorama of the lizard diversity present in the Cerrado by mapping the spatial patterns and genetic diversity for the lizard communities and identifying areas with unique diversity using endemism measures. For this, we generated species and lineages distribution models and collected natural history data for all Cerrado species. For our phylogenetic analyses, we obtained mtDNA trees including published and newly generated data. We looked for areas with high diversity values and intersected the phylogenetic endemism results with protected areas polygons in Brazil. The diversity maps presented similar patterns and highlighted the central area of Cerrado, a known climatically stable area and recognized as important for species richness in other taxa, characterized by a vast plateau, result of the uplift of the central Brazil Plateau. For endemism, we found four distinct areas with high concentrations of spatially restricted evolutionary diversity, highlighting not just stable areas, but also the more heterogeneous valley regions, emphasizing the importance of including evolutionary relationships when visualizing species distribution patterns. Protected areas correspond to only 10% of the Cerrado area and hold 11.64% of the phylogenetic diversity. Overlapping conservation units with the endemism areas, we noted that much of this diversity is not protected. The creation and manipulation of areas for conservation is essential for the survival of the Cerrado, and given its importance for ecosystem services and high deforestation rates, these changes should be urgently adopted.

Assessing the impact of avian predation on New Zealand's lizard fauna

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Within New Zealand, the impact of avian predation on native lizard fauna is largely unknown, despite birds being regarded as important predators of reptiles globally. At least twenty-one species of native birds and eight species of introduced birds are known to prey on lizard fauna. However, few studies have directly addressed avian predation on native lizards, with the majority of evidence sourced from published anecdotes. Furthermore, no studies have successfully quantified the effects of avian predation on endemic lizard population dynamics.

Within New Zealand, mammal eradication has been used to aid the recovery of endemic populations. However, with Predator Free 2050 approaching and Predator Free New Zealand as a goal, there is little ongoing discussion about the possible meso-predator release of birds and the resultant effects this may have on prey species such as invertebrates and herpetofauna. To date, 87% of our 100+ endemic lizard species are considered 'Threatened' or 'At Risk' under the New Zealand Threat Classification System, and even opportunistic feeding by avian species is likely to have a significant effect on lizard populations. The cumulative effect of episodic predation by a variety of species could result in stepwise extinction of New Zealand's vulnerable lizard populations.

This research will identify and assess avian predation on lizards within New Zealand through the use of 3D-printed lizard replicas. Attacks on replicas will be used as a proxy for avian predation pressure and will allow the identification of high-impact species and quantification of relative impacts on and across lizard populations.

Visual evolution in scincid lizards

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Eye evolution has been one of the most thoroughly researched aspects of anatomical evolution. However, little research has been done into the visual systems of squamate reptiles, surprising given the almost unique opportunities to investigate evolutionary regression and reacquisition of traits. The research put forth here seeks to use innovative genetic capture methods to analyse the genes controlling visual development of the eye in two genera of Australian skinks, *Lerista* and *Ctenotus*, to examine the transcriptome of the eye, link this to eye anatomy, habitat and ecology to substantially expand knowledge in this field of work.

Rethinking social evolution to incorporate social plasticity: moving our lens beyond that of pair bonds to how individuals negotiate their social landscape

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At the core of the study of social evolution lies the knowledge that social interactions are integral to the lives of all animals, because even the most solitary of sexual species must interact with mates to reproduce. From this body of work, we have learned that animals may form pro-social relationships (also known as preferences or affiliations) to reduce costs associated with social or environmental pressures such as predation, resource competition, or sexual harassment, and that these relationships are important because they can improve an individual's survival or reproductive success. Just as environments are highly variable, so too is sociality. As such, all animals, despite their level of gregariousness, should modulate their social behaviour in accordance to the socioecological environments they experience. Despite this, little is known about social plasticity in the wild. Here, I will show, focusing on data collected from Eastern Water Dragons, that extending our definition of sociality to how individuals negotiate their social landscape is enabling us to understand the drivers of social plasticity in the wild.

Endless forms most deadly: the dynamic diversification of snake venoms

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A paradigm of snake venom evolution is variation at all trophic levels spanning from age of the snake to isolated geographical populations. Such changes in venom are driven by evolutionary selection pressures ranging from prey type to the potential for prey escape or retaliation. Venoms may vary from neurotoxic to coagulotoxic within the geographical range of a particular species or may have equally profound changes just in the lifespan of a single snake. These changes may decimate the efficacy of an antivenom raised using the venom of one population or age group. Even in a group of snakes where the overall venom function is largely unchanged, variations in the underlying biochemical mechanics may similarly result in dramatic differences in antivenom efficacy. Snakebites by other groups of extremely potent snakes are without any effective treatment due to differences in venom biochemistry relative to their nearest neighbour for which an antivenom is made. In some cases, potent defensive venoms have evolved, such as in hooding snakes such as cobras, that result in extreme local tissue damage which greatly impedes the ability of antivenom from reaching the tissues due to damage to the vascular bed, leading to permanent disability in the survivors. These are examples of the types of fundamental evolutionary research questions that directly inform upon clinical management strategies.

Assault from all sides: hybridization and introgression threaten the already critically endangered *Myuchelys georgesi*

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Hybridization and introgression between species is remarkably common, even between distantly-related taxa. This suggests that the frequency of hybridization between species has been greatly constrained, not by evolutionary divergence in isolation, but by lack of opportunity. This constraint is being relaxed by human-mediated dispersal. Here we document a case where such dispersal of a widespread species of freshwater turtle (*Emydura macquarii*, Murray Turtle) into the highly restricted range of a critically endangered endemic turtle (*Myuchelys georgesi*, Bellinger Sawshell) has provided opportunity for the two to hybridize. This has raised concerns about the potential impact of hybridization on the endemic species, and its continued persistence in the face of challenges brought about by habitat alteration, increased competition, disease, and genetic pollution. This study serves to highlight the risks associated with human-mediated dispersal, which can bring into contact species that would otherwise have never or rarely met, and so provide opportunity for hybridization and introgression between even distantly-related species with uncertain consequences for already threatened species.

Grandmothers and deadly snakes: an unusual project in “citizen science”

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The growing involvement of amateur enthusiasts in wildlife-research projects has changed the way that researchers gather data. Driven by limited resources for field studies, a passion among the general community for hands-on involvement with nature, and the growth of social media, many projects now rely upon the general public to collect datasets that otherwise would have been prohibitively expensive or logistically impossible (McKinley et al. 2017). Nonetheless, most of those “citizen science” projects involve small, harmless forms of wildlife; and many projects rely on children and working-age adults as the volunteer helpers. We describe a different situation: a project on venomous seasnakes, *Hydrophis major*, in the French Pacific island of New Caledonia, conducted by a team of grandmothers.

Evaluating cognition and thermal physiology as components of the pace-of-life syndrome

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The pace-of-life syndrome (POLS) suggests that behavioral traits are correlated and integrate within a fast-slow physiological continuum. At the fast extreme, individuals having higher metabolic rates are more active, exploratory, and bold with the opposite suite of traits characterizing those at the slow physiological extreme. A recent framework suggests that behavioral types may also differ consistently in their cognitive style. Accordingly, we propose that cognition could be further incorporated into the POLS framework comprised of behavioral and thermal physiological traits. Under this premise, fast behavioral types having high thermal traits are predicted to acquire a novel task faster but at the cost of accuracy while slow behavioral types with low thermal traits would be more attentive, responding to cues at a slower rate leading to higher accuracy and flexibility. This was tested by measuring physiological and behavioral traits in Delicate Skinks (*Lampropholis delicata*) and testing their learning ability. Correlations were detected between cognition and behavior but not thermal physiology. Contrary to our predictions, individual positioning along these axes opposed our predicted directions along the fast-slow continuum. Fast lizards preferring lower body temperatures expressed higher activity, exploration, sociality, and boldness levels, and learned the discrimination learning task at a slower rate but made the most errors. Additionally, modelling results indicated that neither thermal physiology, behavior nor their interaction influenced cognitive performance. Although the small number of animals completing the final stages of the learning assays limits the strength of these findings. Thus, we propose that future research involving a greater sample size and number of trials be conducted so as to enhance our understanding into how the integration of cognitive style, behavior, and physiology may influence individual fitness within natural populations.

Dragons of the trees, the rocks, and the ground: the evolution of cranial shape in a continental-scale evolutionary radiation of lizards (Lepidosauria: Agamidae)

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Morphological disparity can be generated during adaptive radiations in response to factors such as new resources, freedom from competition, and an absence of predators and

pathogens. The oldest ancestor of the extant Australian radiation of agamid lizards (Amphibolurinae) arrived in Australia from Southeast Asia approximately 30 million years ago. Since then, Australian agamids have become a species-rich and ecologically diverse clade. Today, they are comprised of around 108 species distributed among every Australian habitat, and are particularly successful in arid environments. We have relatively sound knowledge of their taxonomic diversity and phylogenetic relationships, but their morphological diversity remains largely unexplored. Despite being such a taxonomically and ecologically diverse clade, their adaptive character has not been explicitly tested. Here, we use three-dimensional geometric morphometrics to characterise skull shape in Australian agamids and their Asian agamid relatives (Draconinae), and investigate the association between skull shape and ecological life habit. We find that in addition to phylogenetic affinity and evolutionary allometry, ecological factors play a major role in skull shape evolution of this clade, confirming their adaptive character. Through our evaluation of the cranial morphospace we find common themes of ecomorphology, where tree-dwelling species have long skulls and snouts, terrestrial species have short, blunt skulls, and saxicolous species have dorsoventrally flat skulls. These characteristics likely result from trade-offs to optimise functional capabilities, which often play a role in the evolution of skull shape.

Chytridiomycosis causes catastrophic organism-wide metabolic dysregulation including profound failure of cellular energy pathways

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Chytridiomycosis is among several recently emerged fungal diseases of wildlife that have caused decline or extinction of naïve populations. Despite recent advances in understanding pathogenesis, host response to infection remains poorly understood. Here we modelled a total of 162 metabolites across skin and liver tissues of 61 frogs from four populations (three long-exposed and one naïve to the fungus) of the Australian Alpine Tree Frog (*Litoria verreauxii alpina*) throughout a longitudinal exposure experiment involving both infected and negative control individuals. We found that chytridiomycosis dramatically altered the organism-wide metabolism of clinically diseased frogs. Chytridiomycosis caused catastrophic failure of normal homeostatic mechanisms (interruption of biosynthetic and degradation metabolic pathways), and pronounced dysregulation of cellular energy metabolism. Key intermediates of the tricarboxylic acid cycle were markedly depleted, including in particular α -ketoglutarate and glutamate that together constitute a key nutrient pathway for immune processes. This study was the first to

apply a non-targeted metabolomics approach to a fungal wildlife disease and specifically to dissect the host-pathogen interface of Bd-infected frogs. The patterns of metabolite accumulation we have identified reveal whole-body metabolic dysfunction induced by a fungal skin infection, and these findings have broad relevance for other fungal diseases.

Specific MHC class I supertype associated with parasite infection and colour morph in wild Tawny Dragons

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The major histocompatibility complex (MHC) is a large gene family that plays a central role in the immune system of all jawed vertebrates. Non-avian reptiles are underrepresented within the MHC literature and little is understood regarding the mechanisms maintaining MHC diversity in this vertebrate group. Here, we examined the relative roles of parasite-mediated selection and sexual selection in maintaining MHC class I diversity of a color polymorphic lizard. We discovered evidence for parasite-mediated selection acting via rare-allele advantage or fluctuating selection as ectoparasite load was significantly lower in the presence of a specific MHC supertype (functional clustering of alleles): supertype four. Based on comparisons between ectoparasite prevalence and load, and assessment of the impact of ectoparasite load on host fitness, we suggest that supertype four confers quantitative resistance to ticks or an intracellular tickborne parasite. We found no evidence for MHC-associated mating in terms of pair genetic distance, number of alleles, or specific superotypes. An association was uncovered between supertype four and male throat color morph. However, it is unlikely that male throat coloration acts as a signal of MHC genotype to conspecifics because we found no evidence to suggest that male throat coloration predicts male mating status. Overall, our results suggest that parasite-mediated selection plays a role in maintaining MHC diversity in this population via rare-allele advantage and/or fluctuating selection. Further work is required to determine whether sexual selection also plays a role in maintaining MHC diversity in agamid lizards.

Skink community structure across an elevational gradient in the Australian Alps

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The rapid changes in altitude, and associated habitat, of mountain ecosystems make them ideal natural experiments for testing the effect of environmental heterogeneity and species

assemblage. Our understanding of the sensitivity of Australian reptiles to elevational clines is limited, as no previous study has investigated community structure above 1100 m. Moreover, pressure from ectoparasites is not well understood in Australian high elevation reptile communities. To address this, our study examined lizard distribution across three elevation zones (alpine, subalpine and montane) spanning from 900–1840 m above sea level. We aimed to address (1) how species diversity and abundance change with distinct vegetation based elevational zones, (2) what aspects of the habitat are most important to each species and how does habitat usage change with species abundance and elevation?, (3) is parasite load greatest where species live in high density or with high species richness?, and (4) is variation in parasite load across species due to habitat use or elevation? Active searches were conducted in the Mount Kosciusko National Park, NSW, Australia, from October 2017 to January 2018, to identify community structure across elevational zones, along with skink habitat preferences and the ectoparasite load on captured skinks. Skink diversity and abundance were found to negatively correlate with increased elevational zone. The alpine zone had significantly lower diversity and abundance of skinks. Parasite prevalence was also significantly diminished in the alpine zone, suggesting that high elevation conditions pose significant restrictions on ectoparasites. Parasites only infected a subset of the skink community, with increased parasite load as the active season progressed. This is likely to be a driving mechanism shaping community structure within host populations. As such, high elevation reptile species may be experiencing a trade off with harsh conditions but reduced predation by ectoparasites. This study provides evidence of the complex interplay between elevation and species diversity, as well as the differences in ectoparasite pressure along elevational gradients.

Innovative husbandry techniques for the successful captive reproduction of two notable Australian elapid snake species from the genus *Hoplocephalus*

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The Australian elapid snake genus *Hoplocephalus* contains three recognised species, the Pale-headed Snake (*H. bitorquatus*), the Broad-headed Snake (*H. bungaroides*) and the Stephen's Banded Snake (*H. stephensii*). All three species have reasonably limited distributions being confined to specific habitats in eastern Australia. These regions are identified as all being at risk from commercial development from industry or urbanization, thus putting each species at risk of becoming endangered or extinct. Despite captive populations of all three species being represented in many zoological and private herpetological collections, they have proved difficult to reproduce in captivity. In this paper we reveal the husbandry techniques employed to consistently reproduce two *Hoplocephalus* species, namely *H. bitorquatus* and *H. stephensii*. We found that climatic manipulations in temperature, humidity, air pressure and daylight hours were important factors in initiating reproductive behaviour, while atypical prey items and feeding techniques were required for the successful rearing of the juveniles. The information

ascertained from this work has important implications for captive reproduction programs of endangered snake species worldwide.

Habitat restoration and reconciliation for reptile species conservation: a global review

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Habitat restoration and reconciliation (hereafter, “enhancement”) are promising strategies for reptile conservation because the Reptilia are extremely sensitive to habitat loss. To assess this hypothesis against the published and grey literature, we developed a standardised framework for assessment of ‘conservation success’ for reptiles resulting from habitat enhancement, based on an assessment of translocation success by Miller *et al.* (2014). Seventy-five studies yielded information on 567 responses of 251 reptile species from all major groups of the Reptilia to habitat enhancement. Evidence for or against the shortest-term success criterion, Stage 1 (use of enhanced habitat), was documented in the majority (86%) of cases. In contrast, 8% of responses measured Stage 2 criteria (reproduction in enhanced habitat), 43% of responses measured Stage 3 criteria (demographic benefit demonstrated in enhanced habitat), and 1% examined long-term population trends or population models sufficient to evaluate Stage 4 criteria (self-sustaining or source population established in enhanced habitat). Stages 1 and 2 were fulfilled in 85% and 84% of evaluable cases, respectively. However, fewer cases were successful at Stage 3 (30%), and Stage 4 (43%). Use of enhanced habitat is commonly measured, and indicates high uptake of enhanced habitat by reptiles. However, evidence for longer term success is low, and short-term measures alone appear to be inadequate for predicting ultimate success.

Using isolation with migration models and the Spotted Snow Skink, *Niveoscincus ocellatus*, to estimate divergence time of sex determination systems

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Sex determination directs gonadal differentiation in sexually reproducing organisms. Sex determination systems are exceptionally diverse and have undergone multiple and independent evolutionary transitions, particularly among reptiles. Both the mechanism of sex determination and the degree of sex chromosome evolution influence potential trajectories for population isolation, speciation and extinction. How significant this influence is remains an important question. Investigating the timescales over which sex determining systems and sex chromosomes evolve is central to resolving this question. The viviparous Spotted Snow Skink,

Niveoscincus ocellatus, has a wide climatic and altitudinal distribution in Tasmania. Mitochondrial haplotypes suggest three major lineages in this species diverged within the last two million years. Within one of these lineages, two populations at climatic extremes exhibit divergent systems of sex determination, and thus represent an incipient sex determination transition. A highland population has genetic sex determination and a lowland population has temperature sensitive sex determination. Both conserved and population-specific sex-linked loci have been described in *N. ocellatus*. Here we used isolation with migration models based on neutral single nucleotide polymorphisms to estimate the timeframe of divergence in sex determination systems, and whether this occurred in the presence or absence of gene flow. Our analysis suggests this divergence occurred less than 1 million years ago in the absence of gene flow. Our results are consistent with the high degree of conservation in sex-linked loci between populations, and the small amount of genetic changes that appear associated with the transition in sex determination systems. The lack of gene flow accompanying this divergence suggests a strong reproductive barrier between these lineages, despite their probable sympatry during glacial periods.

Automated recording systems and sound recognition software in the conservation management of the critically endangered Kroombit Tinkerfrog

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The Kroombit Tinkerfrog, *Taudactylus pleione*, is a critically endangered species restricted to 12 montane rainforest patches totalling 596ha in Kroombit Tops National Park in central Queensland, Australia. Most of these rainforest patches are difficult to access as they occur in steep, narrow gullies, mostly below the eastern escarpment. Despite many years of targeted research, eggs and tadpoles have not been observed and females and juveniles very rarely. As Kroombit Tinkerfrogs are small (maximum length ~30 mm), cryptically patterned and inhabit rock piles and leaf litter, detectability is dependent upon the male advertisement call. Males tend to call more or less continuously for extended periods. The call is relatively loud and simple in structure. Combined, these factors suggested the use of automated recording systems and call recognition software may efficiently and significantly enhance knowledge of the seasonal and daily patterns of calling and thus refine survey and monitoring methods and target conditions under which breeding likely occurs. Automated recordings systems (Song Meters and more recently BARs) were used to capture ~800 K one minute field recordings (e.g., 1 min every 30 min throughout the day) from up to nine sites over seven seasons. The sound recognition software SoundID was used to batch analyse these recordings. Accuracy of the analyses was assessed through random and targeted validation. The results have confirmed the local extinction of the species from three sites and provided detailed calling phenology from extant sites. Whilst more detailed analyses are pending, it is clear that in the case of Kroombit Tinkerfrog the combination of automated recording systems and sound recognition software has

greatly enhanced knowledge of calling phenology, detectability and assessment of site occupancy, and will be a significant tool in the conservation management of this species.

Heritability of thermal phenotypes in a temperate Australian lizard

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Reptiles are thought to be among the most at risk taxa from changes to global climate. With such concern has come a concerted effort to understand the manners in which organisms will respond to climatic change. For many species, range shifts are not possible, and subsequently understanding the potential for in-situ responses via evolution and plasticity becomes paramount. Underpinning the genetic basis of evolutionary responses to change is trait heritability. We determined the narrow-sense heritability (h^2) of five thermal phenotypes within a population of 233 Jacky Dragons (*Amphibolurus muricatus*) of known pedigree. We also investigate how morphometric traits along with experimental thermal environments contribute to variation in thermal phenotypes.

The agamid genus *Lophosaurus* Fitzinger, 1843: preliminary comparative morphological data among the three species *L. spinipes*, *L. boydii* and *L. dilophus* from wet preserved museum specimens

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The recently resurrected agamid genus *Lophosaurus* (Denzer & Manthey 2016) consists of three Austro-papuan species: *L. spinipes* (North East New South Wales-South East Queensland); *L. boydii* (North East Queensland) and *L. dilophus* (Papuan New Guinea). All are restricted to closed forest habitats. This provides the opportunity to examine allometric differences among the three congeners along a latitudinal gradient.

Here we present our preliminary morphological data to date. Several measurements were made on each of the available specimens: SVL; total length; hind limb length; head length, width, depth and inter-ocular distance.

The southern *L. spinipes* is the smallest species with a mean SVL of 125 mm. The northern Papua-New Guinean *L. dilophus* is the largest with a mean SVL of 205 mm.

Using tail length, hind limb length and head length as a percentage of SVL following Greer (1990), the relationships among these variables within species did not change significantly with increasing SVL. However, significant allometric differences were found among species for each

of these variables. In each case the two Australian species were more similar to each other than either was to the PNG *L. dilophus*. This was most pronounced with SVL vs. tail length.

Asymmetric signal discrimination leads to asymmetric genetic introgression between two parapatric rhacophorid treefrogs

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Anurans communicate mainly on acoustic signals; correct discrimination between similar signals could help maintain genetic integrity between closely related species. *Buergeria japonica* and *B. otai* are sibling species in Taiwan, with a parapatric distributional pattern and extremely narrow contact zones. Both of them use a common type of long call (type 1a/1b), whereas *B. otai* presents another unique type which never appears from *B. japonica* (type 2). Due to this asymmetry in signal utilization, we aimed to test whether the ability of signal discrimination influences genetic introgression across their species boundary. We constructed playback experiments to male frogs in the contact zones during breeding season in 2016 and 2017. The males of both species showed the strongest response to their own kind, which implies that they could distinguish conspecific signals from heterospecific ones. However, the responses of *B. otai* toward conspecific signals are different between two contact zones: one population response more toward the common long call (type 1b), while the other response more to the unique long call (type 2). Some individuals of *B. otai* could not distinguish between type 1a and 1b. In the genetic test, we applied RAD-seq to evaluate the direction and magnitude of introgression between the sibling species. The results show that there is continuous gene flow from *B. japonica* toward *B. otai*, but not in the reverse direction. Combination of behavioral and genetic experiments suggests that the signal discrimination ability may influence the magnitude and direction of asymmetric gene flow between closely related species.

Interspecific competition among related turtle species: the case of the Bell's Turtle (*Myuchelys bellii*) and Macquarie Turtle (*Emydura macquarii*)

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Among turtles, interspecific competition is rarely investigated between species that naturally share geographic ranges; more commonly, it is viewed through the lens of a novel invader entering a system and outcompeting native species. Two species of chelid turtles that naturally co-occur in the New England Tablelands of New South Wales may be competitors: the

Bell's turtle (*Myuchelys bellii*) and the Macquarie turtle (*Emydura macquarii*). In their zone of sympatry the Bell's Turtle is the less common species, suggesting a competitive edge for the Macquarie Turtle. This is concerning, as the Bell's Turtle is a threatened species restricted to upland streams in the New England Tablelands, while the Macquarie Turtle is a widespread habitat generalist. Areas of co-occurrence are increasing as introduced populations of Macquarie turtles are invading habitats occupied by Bell's Turtle alone. Mesocosm trials will be conducted to investigate the potential impact of competition between these two species. Hatchlings of both species will be placed in single- and mixed-species treatments, and their growth and body condition monitored over 18 months. The hatchlings will be fed a varied diet of natural foods (algae, aquatic invertebrates) to allow them to establish any natural resource partitioning behaviour and minimise any scramble-based competition. Cameras will record the behaviours of the hatchlings, with particular attention to instances of intra- and inter-species aggression or resource monopolisation. By comparing growth rates and changes in body condition among single- and mixed-species treatments, we can determine the magnitude of the potential impact of interspecific competition on Bell's Turtle conservation. This study will offer insight into a rarely-studied aspect of competition ecology, and provide data to inform conservation measures for the Bell's Turtle. This study is part of a larger Bell's Turtle research and conservation project conducted by the University of New England and Northern Tablelands Local Land Service.

Föhn effects and habitat structure modulate assemblages of lizards in the eastern Andes

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When tropical easterlies meet the rising terrain in the eastern Andes, different climatic conditions, known as the Föhn effect, appear in the divide, the windward and particularly the leeward sides. We expected this climatic heterogeneity to be reflected in the fine scale distribution of assemblages of ectotherms. Lizards were surveyed at different elevations (3600–4300 m), slopes and aspects in the leeward (western) side of Cordillera de Sama, southern Bolivia during December 2012–January 2013 and November 2013–January 2014. Habitat was characterized by quantitative standard methodologies. Lizard preferred temperatures were measured in thermal gradients in laboratory. Activity budgets, restriction hours, and thermal quality were estimated according to the physiology of each species with time series of operative temperatures recorded in physical models connected to dataloggers in each sampling site. We found four species of *Liolaemus* (Iguania: Liolaemidae), from the most to the less thermophilous: *L. ornatus*, *L. puna*, *Liolaemus* sp. and *L. orientalis*. Each species' abundance seems conditioned to different extents by its thermal physiology and habitat preferences. The integration of thermal ecophysiology and habitat properties in the study of ectotherm communities can provide useful insights to predict which species may have higher risk confronting climate warming. Considering our spatially complex scenario of microclimates and habitats, if global temperatures

keep rising, species limited by cold microclimates such as *L. orientalis*, or by a particular habitat such as *Liolaemus* sp., might be at higher risk of decline. The observed mismatch between the thermal aspect of fundamental and realized niches is an indicator of the importance of other processes that condition the distribution of each species such as biotic interactions or other abiotic factors not taken into account in our study.

Body size predicts between-individual differences in exploration behaviour in the Southern Corroboree Frog

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Proximate mechanisms underpinning between-individual variation in repeatedly expressed behaviours (animal personality) remain poorly understood. Recent theoretical models have focused on the concept of adaptive state-dependent behaviour, proposing that repeatable differences in behaviour emerge due to individual differences in repeatable state variables such as metabolic rate, age, sex or body size. Few studies have attempted to investigate the effect of state on personality empirically, and evidence for links between individual variation in state and personality remains equivocal. We used a captive colony of Southern Corroboree Frogs, *Pseudophryne corroboree*, to (1) test for innate, temporally repeatable behavioural differences (animal personality) along the activity, exploration/avoidance and boldness/shyness behavioural axes, (2) test for behavioural syndromes (between-individual correlations between behavioural traits) and (3) determine whether behavioural traits are correlated with body size at the between-individual level. Individuals exhibited repeatable variation along all three behavioural axes, but between-individual correlations did not deviate from zero, providing no evidence for behavioural syndromes. Body size explained 40% of the between-individual variance in exploration behaviour, with larger frogs exhibiting greater mobility and travelling further in a novel environment. These associations indicate that there is potential for innate body size variation in *P. corroboree* to act as an important state variable underpinning repeatable between-individual behavioural differences. Future research may test this idea experimentally. Continued investigation of state-dependent individual behaviour in *P. corroboree* and other animals is likely to provide important insights into the proximate causes of animal personality.

Maternal nesting behaviour in city dragons: a species with temperature-dependent sex determination

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Urban environments present some of the greatest challenges to species. This is particularly true for species that exhibit thermally sensitive traits, such as temperature-dependent sex determination (TSD). This is because urban environments not only present species with entirely novel ecosystems, but they also experience exacerbated temperature increases. These temperatures may result not only in offspring mortality, but also in also skewed population sex ratios. In order to persist in cities, urban dwellers with TSD will need to actively manage the temperature of the nesting environment. Here, we investigate the nesting ecology of a long-lived, urban dwelling reptile, the Eastern Water Dragon (*Intellagama lesueurii*), to understand how TSD species may respond to urban environments. Based on data collected from 72 nests over two nesting seasons, we show that city dragons not only dug significantly deeper nests than previously observed across their natural riparian habitat, but also nested in novel substrates. Furthermore, we observed a behaviour not previously described in this species, where mothers travel outside of their core home range in order to nest. This excursion behaviour is linked to the selection of specific microhabitats and potentially represents a greater maternal investment.

Molecular adaptation and resistance to the α -neurotoxin of cobra in snakes

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Some animals overcome prey, or protect themselves, using toxins. For their part, the species threatened by toxins may evolve resistance to those toxins. This can result in what has been characterized as an evolutionary arms race. One example of a toxin to which resistance is known to evolve the α -neurotoxins in elapid venom that bind to the α -subunit of the nicotinic acetylcholine receptor (nAChR) at the neuromuscular junction. Alteration of an ancestral aromatic residue (position 189) to a glycosylated asparagine (N) is linked to autoresistance in elapids. Although similar modifications have been found in mammals, very little is known from Squamata. Here, we investigate these issues by looking for potential resistance-related molecular adaptations to α -neurotoxin in multiple snake species. DNA was extracted from tissue samples of 34 snake species. The α -subunit of the nAChR ligand-binding domain was sequenced, and then aligned with orthologous region of reference sequences. We find that 17 different snake species have the asparagine at position 189. Specifically, the adaptation was

found in 9/9 Elapidae, 4/5 Viperinae, 2/2 Natricidae, 1/2 Dipsadidae and in 1/6 Colubrinae examined. We also find evidence of secondary loss of the adaptation within clades where it is otherwise present. These findings expand our knowledge of the phylogenetic distribution of the cobra-type adaptation in snakes. They show that it has evolved multiple times independently across snake phylogeny. Future work could include studies of the putative functional role of this adaptation.

Chytrid in a created habitat

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Captive breed-and-release and habitat mitigation programs are two conservation strategies that are increasing in use and effectiveness, but the success of these programs is frequently hampered by the continued presence of threatening processes. In the case of amphibian reintroductions, a key threatening process that is difficult to eliminate is the deadly fungal pathogen, *Batrachochytrium dendrobatidis* (Bd). This pathogen is the proximate cause of decline for the threatened Green and Golden Bell Frog, *Litoria aurea*, and has contributed to the failure of previous breed and release programs of this amphibian. To investigate whether it is possible to establish a captive-bred population of *L. aurea* that could persist in the presence of Bd, we conducted a breed and release program into a created habitat that included increased salinity to inhibit fungal growth rates, exclusion of potential reservoir hosts, and source animals bred from parents “experienced” with the strain of Bd present in the release environment. The population persisted in the created habitat beyond four years (the time scale of monitoring) but suffered higher infection levels compared to nearby extant populations of *L. aurea*. These infections significantly reduced apparent survival. We found that infection dynamics were linked to temperature, host-density in the previous season, and size and age of host, and that these factors differed from extant populations and likely contributed to the high levels of Bd infection at the created site.

From an unknown to the most known: reference genome, phylogeography, and adaptation of the Ornate Burrowing Frogs (*Platyplectrum* genus)

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The burrowing frogs of the *Platyplectrum* genus have not received significant taxonomic attention for quite some time, despite an excessive number of changes to the genus name. However, *Platyplectrum ornatum* has long been suspected to have one of the smallest genome sizes in the vertebrates. The wide distribution of the two currently described species across vast environmental gradients also suggests undescribed diversity within the genus. I will present data on the new reference genome now generated for *Platyplectrum ornatum*, and the broad phylogeographic patterns within the genus as identified using DArTseq data. Finally, I will discuss how a reference genome enables investigations into molecular adaptation across ecosystems and environmental gradients.

Identifying sex-chromosomes in the Australian Marbled Gecko

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Sexually reproducing organisms require both males and females for species survival. However, different species have evolved a variety of mechanisms to establish the sex of their offspring – e.g. genetically, via sex-specific genes or sex chromosomes, such as human XX females/XY males; or environmentally, such as incubation temperature. Geckos represent a model system for studying evolution of sex-determining mechanisms as both genetic- and temperature- driven systems occur. The Australian Marbled Gecko (*Christinus marmoratus*) determines sex genetically, but unlike mammals (and more like birds) the female has different sex chromosomes (ZZ males/ZW females). Chromosomal studies of *Christinus* and the Japanese Gecko (*Gekko hokouensis*) indicate that though both species have a ZZ/ZW system, they are not homologous, and sex chromosomes have evolved independently in each species. The independent evolution of sex chromosomes in geckos prompted us to investigate the homology of the *Christinus* ZW. We compared RADseq data from both male and female *C. marmoratus*, from the eastern part of their range, to detect differences between the genetic complements of

each sex, allowing identification of sex-specific molecular markers (sequences found only on the female W). Subsequently, we sequenced and assembled a modest genome for *C. marmoratus* and were able to match the female-specific sequences to larger genomic scaffolds. Identification of genes present on these scaffolds revealed homology of *Christinus* sex chromosomes with different chicken chromosomes to those of *G. hokouensis* whose sex chromosomes are homologous with the avian ZW. We confirmed these bioinformatic results using PCR. Further, these sex-specific PCR markers can be used to investigate conservation of this sex-determination system in other *Christinus* species.

Mechanisms of diversification in West African rainforest amphibians and reptiles

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Identifying the processes that have promoted the accumulation of tropical rainforest biodiversity has been an important goal for evolutionary biologists and ecologists who seek to understand global patterns of diversification. The tropical rainforests of West and Central Africa contain spectacular species richness and endemism, yet the factors responsible for generating this diversity are understudied. This collaborative project aims to investigate the diversification of 20+ species of frogs, lizards, snakes, and crocodiles that are endemic to the Guineo-Congolian forests. Our project uses genomic methods to discover and describe species (systematics), model population dynamics through time (historical demography), and investigate how these diverse communities developed (evolutionary biology). We find that forest-obligate species in this region are typically composed of genetically distinct populations or cryptic species with geographic distributions that mirror the locations of major forest blocks. By leveraging genome-wide SNPs and inferences from phylogenetics, demography, and ecological models, our project takes an integrative approach to test among major hypotheses regarding the population genetic consequences of climatological fluctuations, forest fragmentation, and river barriers. In addition, we are developing new tools and techniques for accelerating the pace of biodiversity discovery, including new methods to delimit species with genomic data and new phylogenetic approaches to test whether populations share the same divergence time. Understanding diversification processes is important for describing the composition of biodiversity, interpreting how ecosystems and biomes develop over time, and guiding decisions on how to preserve threatened biotas.

Enteric bacteria in Sleepy Lizards vary in richness, prevalence and co-occurrence patterns

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Disease infection is one of the major costs of group living. Understanding infection dynamics over time and space could help us understand population dynamics and ultimately, help prevent disease outbreaks. Animals are often exposed to multiple pathogens at the same time, but little is known about co-infections within hosts. The aims of this research are to describe the host-pathogen relationship of the sleepy lizard and investigate co-infections between bacterial strains. We hypothesised that bacterial infections vary over time and that some bacterial strains co-occur more frequently than expected, while other strains would co-occur less frequently than expected within host individuals. Males and females often invest different amounts of energy in immunity, and pathogens' survival ability varies in its environment. We predicted that bacterial infection would differ between sexes and microhabitats. We considered positive associations (observed > randomized) in occurrence between two strains as facilitation, and negative association (observed < randomized) as avoidance/inhibition. The project builds on a well-established study system of Sleepy Lizards, *Tiliqua rugosa*, and their enteric bacteria. First, we compared the richness (number of bacterial strains per lizard) and prevalence (number of infected lizard) between six sampling points, and found that richness and prevalence significantly increased over time, and with ambient temperature. Our two sites differed significantly in richness and prevalence but there was no difference between sexes. Second, we used a network approach to calculate the bacterial co-occurrence and whether co-occurrence happened more or less than expected. Most strain combinations did not differ from random, and hence did not co-occur more frequently, or less frequently, than expected. However, some strains showed a positive association (facilitation), while fewer showed a negative association (inhibition). Our findings could improve treatment of infected animals and knowledge of multi-infection disease network.

Life on the edge—Green and Golden Bell Frogs at Meroo Lakes

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Baseline monitoring was conducted between November 2016 and March 2017 for the Green and Golden Bell Frog (*Litoria aurea*) (GGBF) at Meroo Lakes in southern NSW. Monitoring consisted of nocturnal aural/visual surveys along 30 transects, with four replicate surveys of each transect. Sites were typically sedgeland and tea-tree thickets on the margins of one of three large lakes, but included a quarry, two small swamps and five freshwater dams. The location, sex and maturity of any GGBF detected were recorded along with a range of habitat variables including vegetation type and water chemistry parameters. A total of 183 GGBF were located, including 118 adults and 65 sub-adults, and 24 of the 30 monitoring sites were occupied. During dry conditions adults were generally located within dense saw sedge (*Gahnia* spp.) away from the lake margins, but juveniles located in sedge and salt marsh around lake edges. After rainfall adult frogs concentrated within the areas of sedge. The lakes were saline prior to flooding rains (> 30 ppt), with frogs observed sitting within these waters, and the centres remaining saline after flooding rains (> 20 ppt). However, the margins became fresh (< 2 ppt) and was where calling males concentrated. Fish were present in the lakes, but minimal within the areas of flooded sedge. Only one of 43 frogs sampled during November tested positive for the amphibian chytrid fungus. The population at Meroo appears to be robust and widespread and with few obvious threats. The presence of saline conditions may be the key to mitigating the impacts of the chytrid fungus in this population and large coastal lakes may be key to the long-term survival of this species.

Modelling three-dimensional interstitial spaces to protect endemic skinks (Scincidae) from invasive mice (*Mus musculus*)

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Three-dimensional spaces have profound impacts on many aspects of ecology, including refugia from predation, yet can be difficult to quantify and characterise. We present a novel method for characterising complex 3D spaces in piles of rocks, and its application in the protection of translocated skinks (Scincidae) from predatory mice (*Mus musculus*). At-risk and declining New Zealand skink species are increasingly being moved from development sites ('mitigation translocations'). Creating rock piles as compensation for destroyed lizard habitat is common, however pile composition is based on best guesses of wildlife managers rather than scientific experiment. Using the computer games program Unity and its in-built physics engine PhysX, we modelled virtual rock piles and measured gaps within them. This virtual approach

allowed us to measure gaps inside piles without disturbing their structure, and to repeat the simulation with rocks of varying shapes and sizes. CT scans of real rock piles confirmed our predictions. Understanding how rock pile composition affects gap sizes allowed us to design rock piles to provide skinks shelter from mice, which require larger gaps. The predicted best compositions are being tested in the field for their efficacy at protecting translocated skinks from mice. Many reptile and amphibian species make use of complex 3D spaces and this approach could be a useful tool to understanding their ecology.

Does urbanisation influence parasitic nematode burdens in Tiger Snakes (*Notechis scutatus*)?

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Tiger Snakes (*Notechis scutatus*) in wetlands of South-Western Australia are commonly parasitised by the nematode *Ophidascaris pyrrhus*. Previous research indicates that urban Tiger Snakes of Perth WA suffer higher parasite burdens compared to snakes on the offshore island Carnac Island. A host's parasite burden can increase if the host is in a highly suitable ecosystem for the parasite to complete its lifecycle, or if its environment induces a range of external stressors that may compromise the host's immune system. If this is true, we predict that as urbanisation (a potentially stressful environment) increases around wetlands (a suitable ecosystem for parasites) in South-Western Australia, Tiger Snakes would demonstrate higher nematode burdens. To assess this we counted nematodes in the stomachs of 92 Tiger Snake museum specimens distributed across the urban and non-urban interface. Collection dates begin in 1917 allowing us to assess the spatial and temporal influence of urbanisation on parasite burdens. Data analysis is current and results are pending.

How sexual and natural selection shape sexual size dimorphism: evidence from multiple biological scales

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Sexual size dimorphism (SSD) is pervasive across taxa and reflects differences in the effects of sexual and natural selection on body size between the sexes. Sexual selection is often cited as the primary driver of SSD, though, more recently, the role that natural selection can play has also been highlighted. However, disentangling the complex eco-evolutionary interactions between these two mechanisms remains a major challenge for biologists. Here, we used a comparative approach across multiple biological scales to explore how the interplay between sexual and natural selection shapes the evolution of SSD in Australian agamid lizards. Australian agamid lizards show substantial variation in SSD, ecological traits and species density making them an ideal study system in which to look at the interaction between sexual and natural selection in the evolution of SSD. At the species level, population density influenced the direction of SSD (female to male biased SSD), whilst ecological generalism influenced the extent of this male-biased SSD. At the population level, density positively correlated with SSD in native habitats, but negatively correlated with SSD in city habitats. Last, agonistic behaviour acted as the primary driver of SSD at the within-population level. Our results indicate how sexual and natural selection can interact at different biological scales, and shows the importance of considering both selective mechanisms when investigating patterns of SSD.

Identifying patterns in long-term acoustic recordings

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Automatic audio recording devices have advanced to the point where continuous, high-resolution monitoring of the environment is possible. However, the technology to process this immense volume of data is only just catching up. Long-form audio recordings can be summarised using acoustic indices, whereby audio data over a certain window (e.g., one minute) is summarised to one numerical value. Indices can then be plotted in a ‘false-colour spectrogram’, enabling the visualisation of ecological patterns. Machine learning techniques, such as artificial neural networks, can then be applied to automatically find patterns in these complex datasets. I will give a brief overview of these techniques, then discuss how they can be used to identify calling frogs.

Molecular detection of *Ranavirus* sp. in wild Eastern Water Dragons

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Ranaviral infections have been reported in captive lizards held overseas, and recently juvenile Eastern Water Dragons were shown to be susceptible to Bohle iridovirus (*Ranavirus* sp.) under experimental conditions. Here we report a molecular survey of wild Eastern Water Dragons to determine if Australian lizards are infected with *Ranavirus* sp. Oral-cloacal swabs and morphometric data was collected from 54 wild Eastern Water Dragons at several different locations in the Paluma Range National Park (PRNP), Queensland. DNA was extracted from these samples and a validated polymerase chain reaction (PCR) was used to detect ranavirus in these samples. Of the 54 samples, five samples reacted in the PCR. These samples were from sub-adult and adult males sampled at four different locations along two freshwater creeks in the PRNP. The outcome of this study demonstrates that *Ranavirus* sp. is present in wild Eastern Water Dragons living in north Queensland. This is the first time molecular evidence of *Ranavirus* sp. reported in Australian lizards.

Experiences with disease and preventative strategies: A survey of Australian reptile owners

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Reptile ownership is globally increasing in popularity with an estimated 250,000 Australian households keeping a snake, lizard or turtle as a pet. Keeping reptiles in captivity requires appropriate husbandry practices, knowledge of reptilian diseases, and strategies to prevent introduction and/or spread of diseases. A cross-sectional study of Australian reptile owners was conducted in November-December 2017 using SurveyMonkey®. A total of 179 participants completed the survey which included multiple choice and open-ended questions. Participants were asked about their socio-demographic characteristics, license status, reptile collection profile, husbandry, health and quarantine management practices, disease knowledge and relevant preventive strategies and use of veterinary services. Quantitative data was analysed descriptively and qualitative responses were analysed thematically and grouped into themes. Overall most participants had a license for the animals they held but highlighted a number of issues with the licensing systems in Australia. Participants employed appropriate husbandry practices and health preventative strategies but failed to adequately quarantine newly acquired animals. Two thirds of participants had had a health issue within their collection. The most common health issues encountered by participants were mites, respiratory diseases and unexplained death. Participants' knowledge of reptilian diseases was limited to common husbandry diseases such as metabolic bone disorder. Many participants did not access veterinary services because of cost and/or lack of relevant veterinary expertise availability. This study highlights the need for a review of the licensing system, the need for veterinary capacity building for the care of captive

kept reptiles and the provision of better education of existing and prospective reptile owners about the importance of quarantining animals, cleaning and disinfection protocols, and increased knowledge about the clinical signs, transmission and prevention of reptilian diseases.

Assessing pheromone divergence among eastern Australian velvet geckos

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Genetic studies show that Australia's true reptile diversity is currently underestimated and that many recognised species are comprised of multiple genetically distinct but morphologically similar lineages. Many of these lineages probably represent biological (i.e., reproductively isolated) "cryptic species", but resolving species boundaries in such groups is often difficult. In other groups, such as frogs, we use their mating trait (e.g., mating calls) to distinguish and describe morphologically similar species; however, the mating traits of reptiles are generally poorly known, particularly among "cryptic" groups. Velvet geckos (*Oedura* spp.) are one such group and include both morphologically distinct and cryptic species. Phylogenetic analyses of eastern Australian *Oedura* indicate the presence of a number of deeply divergent but morphologically similar candidate species. Pheromones are likely the mating trait in these geckos and it is possible that species possess divergent pheromones, and that these pheromones could be used for resolving cryptic species. We tested whether pheromones differ between *Oedura* lineages. We found that pheromone blends differ significantly among both morphologically distinct (described) and cryptic (undescribed) lineages. These results suggest that pheromone data can help resolve the true diversity and taxonomy of *Oedura* geckos, and Australian reptile diversity more broadly.

Conservation genomics in an endangered Australian skink *Tiliqua adelaidensis*

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The Australian Pygmy Bluetongue Skink (*Tiliqua adelaidensis*), is an endangered species endemic to South Australia. *Tiliqua adelaidensis* exists in highly fragmented habitat and has no capacity for long distance dispersal. Long term conservation of this species will rely on assessments of population health, the species' own ability to rapidly adapt to changing conditions, and continued research into translocation efforts. The objective of this project is to identify areas of the genome that may allow adaptation to new environmental challenges. RNA-seq and transcript analysis is being used to measure and compare gene expression between samples collected at the beginning and end of the dry season. Kidneys and livers from eight individuals have been (and are being) sequenced to ensure the capture of genes associated with

surviving dry periods, and so that results can potentially be used as reference sequences for concurrent studies. Whole long-read Iso-Seq transcripts will also be sequenced to compare transcripts and ensure the accuracy of *de novo* assembly methods in the absence of a closely related genome for transcript assembly. This study will measure the epigenetic plasticity at the individual level, and a Pygmy Bluetongue's ability to adapt, in the short term, to changing environmental conditions.

Utilizing FrogID to refine our knowledge of the distribution of *Uperoleia* (Anura: Myobatrachidae) in NSW

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Uperoleia is an Australian genus of ground frogs in the family Myobatrachidae. They occur in a wide variety of habitats across northern and eastern Australia. The past decade has seen a greater taxonomic understanding of *Uperoleia*, with four species described since 2008, and most other species re-described to some extent. In NSW, 5 species are known, one of which, *Uperoleia mahonyi*, was only described in 2016 and is considered endangered. This has brought some focus to a current lack of knowledge of the finer detail of distribution of *Uperoleia* across NSW, information which can inform their conservation. Historic records of *Uperoleia* pose difficulties due to morphological similarity of the genus. Even the specific identity of historical records based on museum vouchers are difficult or impossible to confirm. FrogID is Australia's first large scale citizen science project focusing on the collection of a database of recordings of calling frogs, using a smartphone. Since its launch in November 2017, over 500 submissions from NSW have been identified as containing one or more *Uperoleia* species. Submissions of *Uperoleia* received by FrogID have been identified to species level using expert opinion and comparison to published call descriptions. We compared the records of *Uperoleia* species identified using FrogID to the records in the Atlas of Living Australia database, and to records of genetically identified *Uperoleia*. We identify areas where FrogID and other data resources display similar trends, and highlight gaps and areas of disagreements in the datasets, priorities for future research. For one such area, we use on-ground surveys to confirm *Uperoleia* identification, resulting in a highly significant confirmation of range for one *Uperoleia* species. We outline the benefits of using FrogID to gather a large database of call recordings in understanding frog distributions across NSW.

How does thermal physiology mediate the latitudinal cline in a colour pattern polymorphism of the Delicate Skink?

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What influences animal colouration? Colour may represent adaptations for signalling, thermoregulation or crypsis in complex functional trade-offs. When intraspecific colour variation is present as discrete colour polymorphisms, this suggests that evolution may favour multiple strategies to cope with variation in environmental selection pressures. Spatial variation in the distribution of discrete colour morphs may indicate population-specific adaptation under local selection. When this spatial variation is present as a cline or gradient, however, these strategies are likely to overlap along with colour morphs across populations. The maintenance of genetic variation through a latitudinal cline in colour morph frequencies may be explained by broader clinal patterns, such as climate-related temperature. This is consistent with the thermal melanism hypothesis, which predicts faster heat uptake in dark-coloured material than for light-coloured material. Differences in the thermal physiology of colour morphs that vary in frequency across latitudes may therefore explain the persistence of such polymorphisms. *Lampropholis delicata*, the Delicate Skink, is common across latitudes spanning Queensland to Tasmania, and demonstrates a polymorphic, pale mid-lateral stripe. This polymorphism is both population- and sex-biased: the stripe occurs in higher frequencies in northern populations than southern populations and is much more common in females than males. By investigating variation in heating and cooling rate, and sprint performance at different temperatures, we may be able to determine if adaptation to latitudinal differences in temperature is important in explaining the distribution of colour morphs in this species.

An experimental approach to corroboree frog translocations

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Conservation translocations from *ex-situ* breeding programs are being increasingly utilised for the management of threatened amphibians. However, effective reintroduction protocols are yet to be developed for many species, influencing the success of population establishment. The Southern and Northern Corroboree Frogs (*Pseudophryne corroboree* and *P. pengilleyi* respectively) are critically endangered species that have rapidly declined in recent decades due to the introduction of amphibian chytrid fungus (*Batrachochytrium dendrobatidis*). Both are now established in multiple ex-situ facilities, with husbandry, breeding and genetic management protocols implemented to secure the species long-term.

Our research will investigate the development of effective reintroduction techniques that will increase the chance of population establishment post-release, including measuring the influence of phenotype, life stage at release and the seasonal timing of release.

A superior start to life? The effect of carotenoids on the growth and development of Southern Corroboree Frogs

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Dietary carotenoids are expected to improve vertebrate growth and development, though evidence for beneficial effects remains limited. One reason for this might be that few studies have directly compared the effects of carotenoids from different classes (carotenes versus xanthophylls) at more than one dose. We tested the effect of two doses of dietary β -carotene and lutein (representing two different carotenoid classes) on the growth and development of larval Southern Corroboree Frogs (*Pseudophryne corroboree*). Individuals were supplemented with either β -carotene or lutein at one of two doses or given a diet without carotenoids (control), and larval survival, larval growth, time to metamorphosis, and metamorphic body size were measured. Larvae receiving a high dose of β -carotene metamorphosed significantly faster than all other dietary treatments, despite no significant differences in growth rate. This result indicates that β -carotene supplementation in *P. corroboree* has positive effects on development independent of growth effects. Our study provides new evidence for differential effects of carotenoid class and dose on vertebrate development. From a conservation perspective, our findings are expected to assist with the recovery of *P. corroboree* by expediting the generation of frogs required for the maintenance of captive insurance colonies, or the provision of frogs for release. More broadly, our study highlights the potential for dietary manipulation to assist with the ex situ management of threatened amphibian species worldwide.

Microbiomes of the Krefft's River Turtle (*Emydura macquarii krefftii*)

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Microbiomes have important ecological interactions with their host species. Studying host microbiomes is, therefore, important for understanding host ecology and may play a vital role in management and conservation effects (e.g., disease mitigation in amphibians). Nevertheless, some wildlife taxa remain poorly studied, including turtles. Therefore, we conducted a pilot study to examine the microbiomes of Krefft's River Turtles (*Emydura*

macquarii krefftii). We sampled six wild turtles and compared bacterial microbiomes from their buccal cavities, the tops of their heads, portions of the shells with algae, and portions of the shells without algae. We identified a total of 771 operational taxonomic units (OTUs) representing 205 genera and 144 families. The OTUs present on each area of the turtles were generally similar, with 441 OTUs (151 genera; 115 families) found in all four areas. However, the buccal cavity had significantly lower taxonomic richness than the other areas, and 180 OTUs (22 genera; 13 families) were detected in all sampling regions except the buccal cavity. Similarly, taxonomic evenness was high and similar among the head (0.78), algae (0.78), and shell samples (0.75), but significantly lower for the buccal cavity (0.61). Nevertheless, the relative abundance of OTUs differed greatly among body regions, and using PERMANOVAs, we found significant differences between each body site. These results show that the turtles' exterior microbiomes were similar in terms of the taxa present, but the relative abundance of those taxa differed greatly. Further, the buccal microbiome consisted of a subset of the taxa that were present externally. This study is one of the first to examine the microbiomes of freshwater turtles, and it provides important baseline data on which other studies can build.

Bacterial richness is associated with patterns of declines and recovery following a disease outbreak

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Host microbiomes play important roles in infection dynamics, and there is growing evidence that they can protect hosts from emerging infectious diseases and facilitate population recoveries. To further our understanding of the interactions between host microbiomes and the amphibian fungal disease chytridiomycosis, we examined the skin microbiomes and infection loads of four frog species in the Australian Wet Tropics, each of which has a different history with chytridiomycosis (extirpation without recolonization, extirpation with recolonization, decline with recovery, and no decline). We predicted that the abundance of inhibitory bacteria would match the patterns of declines and recoveries, with the tolerant species that never declined (*Litoria wilcoxii*) having high levels of inhibitory bacteria and the sensitive species that has not recovered (*Litoria dayi*) having low levels; however, the observed pattern was largely the opposite of our predictions, with *L. dayi* having the highest relative abundance of inhibitory bacteria. We also found positive associations between inhibitory bacteria abundance and infection intensity. Additionally, for both infection status and intensity, we failed to find significant associations with either individual bacteria or beta-diversity. We did, however, find significant associations with bacterial richness. At the broadest level, the richness pattern across species largely matched the patterns of declines and recoveries, with *L. dayi* having the lowest richness. *Litoria dayi* also had a significant negative association between richness and infection intensity. In contrast, most other species had no association between total richness and infection intensity and had a positive association between inhibitory richness and infection intensity.

Additionally, there was a general pattern of higher richness among infected frogs. Disentangling these patterns is difficult, but the data suggest both that richness is playing an important role in infection dynamics, with high richness potentially providing a protective effect, and that chytridiomycosis infections create an environment in which inhibitory bacteria thrive.

Investigating the genetic basis of colour polymorphism in the Tawny Dragon Lizard

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Colour polymorphism, where multiple colour forms coexist within a population, is common in nature; however, our understanding of the underlying genetic mechanisms and genomic architecture of colour morphs is limited. We investigated the genetic basis of polymorphism in the Tawny Dragon Lizard, *Ctenophorus decresii*. Males of this species exhibit four discrete, genetically determined throat colour morphs; orange, yellow, orange-yellow (central orange patch surrounded by yellow) and grey, which also differ in behavioural strategies. We performed low coverage whole genome sequencing of five individuals of each colour morph and mapped the sequences to the recently assembled *C. decresii* genome. In contrast to recent findings in other systems where polymorphism is associated with large inversions containing many genes (referred to as ‘supergenes’), we did not identify any structural variants or genomic regions of high divergence between the four colour morphs of *C. decresii*. We did however, identify 71 single nucleotide polymorphisms (SNPs) which were fixed homozygous between at least two morphs, and a further 99,815 SNPs which were fixed in one morph and heterozygous or fixed for the alternate allele in another morph. Approximately one third of these were intragenic or in potential regulatory regions, which we will further investigate through targeted enrichment sequencing. Our results indicate that the *C. decresii* polymorphism is underpinned by a few genes or multiple genes scattered throughout the genome, rather than a genomic island of divergence.

Do production costs maintain the honesty of colour signals in agamid lizards?

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Yellow-red colour signals in reptiles are produced by pteridines and/or carotenoid pigments within skin cells. Carotenoids are obtained exclusively through diet, while pteridines are synthesised within the body from purine molecules. For this reason, carotenoid-based colours are often thought to be honest indicators of individual quality, and pteridines considered a ‘cheap substitute’. Red carotenoid-based colours are particularly likely to be honest signals of quality because they are produced by the metabolically costly bio-conversion of yellow dietary carotenoids to red carotenoids (ketocarotenoids). We tested whether agamid lizards use carotenoid or pteridine pigments for colour signals, and whether this is related to environmental carotenoid availability. We examined pigment concentrations in adult males of a selection of seventeen agamid species from Victoria, South Australia and Western Australia during the breeding season, and found that redder hues are produced by a relatively higher concentration of the ‘cheap’ pteridine pigment drosopterin, rather than by higher concentrations of ‘expensive’ ketocarotenoids. The concentration of yellow dietary carotenoids tends to correlate with environmental productivity, particularly in the *Diporiphora* clade. Based on these preliminary data, we suggest that the honesty of colour signals in agamid lizards is likely to be maintained by mechanisms other than production costs.

PAUL WEBBER TALK: Phylogeography and conservation genetics of herpetofauna in Gippsland, Victoria

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The far south-east of Victoria is particularly important in terms of unique environments, with two biotas meeting (eastern and southern), with high reptile and amphibian diversity for Victoria and also a high number of conservation listed species. We conducted extensive surveys in spring 2016 and 2017 focussing on the Croajingolong National Park, from east of the Mallacoota west to the Gippsland Lakes. We aimed to document reptile and amphibian species present in the region and assess the presence of conservation listed taxa. We then undertook phylogeographic investigations on selected taxa. The threatened frog species *Uperoleia martini* and *Litoria aurea* were of particular interest and the lizard species *Egernia saxatilis* and *Pygopus*

lepidopodus. Each of these species had received little attention in this regions, with questions about phylogeographic diversity and distributions. We sequenced mtDNA and nuclear genes (in the case of *Egernia saxatilis*), finding significant phylogeographic structure. Our findings have implications for the conservation management of threatened frogs species in Gippsland and provide new information for common and wide-spread lizards.

Using large-scale citizen science data to examine acoustic responses of frogs to anthropogenic disturbance

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One of the major drivers of global biodiversity declines is urbanisation. To halt biodiversity declines, and facilitate ecosystem functioning, a comprehensive understanding of how species respond to environmental change is required. Urban environments have increased noise and light pollution, potentially affecting acoustically communicating species, including frogs. Urban areas may force frogs to modulate or alter their calls to communicate with potential mates, as they must compete with anthropogenic noise. My research examines the effect of urbanisation on the advertisement calls of the widely distributed Red Tree Frog (*Litoria rubella*) using a large citizen science dataset from the Australian Museum's FrogID project. This is the first large-scale analysis of the effects of urbanisation on a species across its entire range—a feat never before possible due to the remoteness and vast size of many species' ranges. My research will help inform future conservation decisions for Australian frogs. Furthermore, as frogs are sensitive to environmental perturbations and can act as an indicator for other species, this research may aid in understanding potential impacts of urbanisation on other taxa in urban ecosystems.

New Zealand's alpine geckos: ecology, ecophysiology and conservation

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New Zealand's alpine zones include an extensive suite of cold-climate ecosystems covering c. 11% of the land mass. They support rich communities of indigenous biota including a diverse lizard fauna, with at least 13 gecko and 17 skink species recorded (all viviparous),

though many are not yet formally described. Populations are generally poorly surveyed and understood. Distributions of most taxa appear highly localised, and like many other reptile taxa in New Zealand, are probably relicts of former, more widespread distributions. As part of a wider alpine research programme, we are working to understand the ecology, ecophysiology, threats to and management options for two alpine gecko species, the Cascades Gecko, *Mokopirirakau* “Cascades”, and the Orange-spotted Gecko, *Mokopirirakau* “Roys Peak” in the southern South Island of New Zealand at altitudes of 1000 to 1600 m a.s.l. Initial research suggests that geckos are locally abundant at some locations, but absent from large tracts of their former ranges. The warmest summer temperatures available to geckos (measured either by copper models simulating basking or under the top rock of daytime retreat sites) can exceed 30° C on fine days; however, temperatures in these locations are often below 15° C, and crevices that are more sheltered sometimes drop to near freezing. Snow covers the site for prolonged periods during winter. Data from palpating pregnant females suggest that females are likely to produce two offspring biennially at most. As such, the existence of remnant alpine populations is precarious, particularly when mast seeding of tussock grasses, *Chionochloa* spp. and beech (Nothofagaceae) in adjacent forest drives irruptions of introduced predators (mice and stoats), though these links are still poorly understood for the alpine zone.

Genomes in Oz herps: progress and prospects

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This talk, and the following symposium, is intended to explore the case for building genomic resources across Australian squamates. Globally, our knowledge of the structure of reptile and amphibian genomes is poor relative to that for birds and mammals. Australia is famous for exceptionally high lizard diversity, and substantial radiations of frogs, snakes and lizards, including some Gondwanan groups. These radiations exemplify fascinating evolutionary phenomena, including repeated origins of viviparity, limb reduction, sex determination/chromosome systems, parthenogenesis, cryptic species, and adaptations to extreme aridity and (in snakes) marine lifestyles. Several labs have used comparative transcriptomics (or exon capture sequencing) to address questions such as those above. However, with the notable exception of the central bearded dragon (*Pogona vitticeps*), high quality genome assemblies are lacking for Australian herps.

Well characterized genome assemblies can significantly enhance our understanding of transitions in evolution, e.g., through analyses of gene expression, gene family diversification and molecular evolution. This power of combining genomics with comparative analyses of traits and ecology has been amply demonstrated in recent analyses of speciation and adaptive radiation in several “model” systems internationally. Coordinated development of genomic resources can also promote new collaborations across labs studying different elements of the same radiations.

The question is where to put the effort and how to make the case for the necessary investment in sequencing and bioinformatics to enable this. To prompt discussion, I suggest that criteria could

include systems with: (i) high scientific value and impact; (ii) multiple research labs in Australia and internationally that can exploit new genomic resources; (iii) tractability for field or lab experimental studies. As one of many possible examples, I will use the spectacular Sunskinks (*Lampropholis*) to illustrate these points.

Behavioural differences throughout the range expansion of an invasive skink, *Lampropholis delicata*

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Behaviour can play a fundamental role in the success or failure of invasive species. Invasion is a multi-stage process, with each stage exerting unique selection pressures that are expected to favour certain behavioural types. Capitalizing on the well-documented invasion history of the Delicate Skink, we tested how behaviour has evolved with range expansion by comparing the behaviour of lizards from the native source population, with those from both well established and invasion front populations in the species' introduced range in New Zealand. Differences in behaviours between populations will be discussed in the context of establishment history and invasion success. Our results provide new insights into possible behavioural drivers of invasion as well as novel insights into how behaviour is affected at a population level by shifting selection pressures.

Systematics of oophagous sea snakes (Hydrophiinae) in Western Australia

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Shallow-water habitats in Western Australia support the world's highest recorded diversity and endemism of sea snakes (Hydrophiinae). However, sea snake declines in this region over decadal timescales have highlighted an urgent need for improved estimates of species diversity and distributions. This study integrated molecular and morphological analyses with an aim to revise species boundaries in two groups of oophagous sea snakes: the *Emydocephalus* and the *Aipysurus mosaicus* complexes. DNA tissue sampling was expanded from previous studies to span geographic ranges of both groups. Phylogenetic analyses of

mitochondrial sequences recovered deep divergences within existing species: *E. annulatus* from Australia was recovered as paraphyletic with respect to *E. ijimae* from Japan, and *A. mosaicus* comprises three clades with levels of divergence usually found among *Aipysurus* species. Thousands of independent nuclear RADseq markers were then generated for representatives of the major mitochondrial clades in each species complex. Analyses of these data yielded congruent support for the mitochondrial clades in the *Emydocephalus* complex but not the *Aipysurus mosaicus* complex. Finally, examination of morphological variation provided further independent support that the west coast lineages of both species complexes are distinct. Together these results provided strong support that the west coast lineage of *Emydocephalus* represents a distinct new species, which we describe herein as *Emydocephalus orarius* sp. nov. Due to mitonuclear discordance we conservatively maintain *Aipysurus mosaicus* as a single species, including the west coast population. The new species brings the number of short range endemic sea snakes in Western Australia to seven. Given the recent localised but severe declines of sea snakes in the Timor Sea, improved knowledge of sea snake biodiversity in Western Australia is vital for good conservation management planning.

Using RADseq to identify sex specific loci in two social skink species

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The current state of knowledge concerning sex chromosome evolution is based on a handful of 'exceptional' taxa with heteromorphic sex chromosomes. However, cataloging sex chromosome systems of additional species lacking easily identifiable, heteromorphic sex chromosomes is indispensable if we wish to fully understand the evolutionary patterns and processes affecting the genesis, degeneration, and turnover of vertebrate sex chromosomes. Squamate reptiles are a potential model clade for studying sex chromosome evolution as they exhibit a suite of sex determining modes, yet most species lack heteromorphic sex chromosomes. For example, in the speciose lizard family Scincidae, only 12 of ~1600 species have identified sex chromosome systems, and all are XX/XY (sex in three additional species is environmentally determined). This study uses a recently developed method to identify sex specific genetic markers from restriction site-associated DNA sequence (RADseq) data, which enables the identification of sex chromosome systems in species lacking heteromorphic sex chromosomes. We used RADseq and subsequent PCR validation to identify the sex chromosome system in two species of Australian skinks, the Sleepy Lizard/Shingleback/Bobtail (*Tiliqua rugosa*) and Gidgee Skink (*Egernia stokesii*). Previous work has suggested the former has male heterogamety (via patterns of heterozygosity in microsatellites) and we here confirm an XY sex chromosome

system in this species. We also successfully identified an XY system in *E. stokesii*, the first such data for this species. Easily obtainable, sex-specific, genetic markers will facilitate future studies related to natural history, reproduction, and sociality. More broadly, sex-specific genetic markers are an important tool for studying species, such as these skinks, that lack easily discernible sexually dimorphic phenotypes at all or some life stages.

Sea turtle nest predators and predation rates along the Western Cape

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We monitored a 47 km stretch of beach along the Western Cape, south of Aurukun, Cape York, during 104 surveys from June–October 2018. This beach proves to be an important nesting beach for sea turtles, primarily, Olive Ridley and Flatback Turtles. We monitored a total of 360 nests, 117 Flatback, and 243 Olive Ridley nests. We classified predation types into three categories: complete predation (entire nest was consumed/damaged/destroyed), partial predation (some eggs were consumed), or failed predation (digging occurred at the nest but no eggs were depredated). Predation of turtle nests were highest in Olive Ridley Turtles (41.5% of nests) compared to Flatback (22.2%). Major predators included dingos, goannas, and pigs. Due to high predation levels on Olive Ridley nests, we implemented a management regime of placing plastic meshing over the egg chamber to reduce the levels of predation. We installed meshing over 45.2% of Olive Ridley nests, resulting in 27.0% of failed predation events in dingos and 25.5% in goannas. Meshing did not significantly reduce the predation rates or increase the survival of hatchlings on Olive Ridley nests, although it did successfully prevent some predators from reaching the egg chamber.

The unexpected genetic mating system of the Red-backed Toadlet (*Pseudophryne coriacea*): A species with prolonged terrestrial breeding and cryptic reproductive behaviour

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Molecular technologies have revolutionized our classification of animal mating systems, yet we still know very little about the genetic mating systems of many vertebrate groups. It is widely believed that anuran amphibians have the highest reproductive diversity of all vertebrates, yet genetic mating systems have been studied in <1% of all described species. Here, we use

single nucleotide polymorphisms to quantify the genetic mating system of the terrestrial breeding Red-backed Toadlet, *Pseudophryne coriacea*. In this species, breeding is prolonged (approximately 5 months), and males construct subterranean nests in which females deposit eggs. We predicted that females would display extreme sequential polyandry because this mating system has been reported in a closely related species (*P. bibronii*). Parentage analysis revealed that mating success was heavily skewed towards a subset of males (30.6% of potential sires) and that nearly all females (92.6%) mated with one male. In a high percentage of occupied nests (37.1%), the resident male was not the genetic sire, and very few nests (4.3%) contained clutches with multiple paternity. Unexpectedly, these results show that sequential polyandry is rare. They also show that there is a high frequency of nest takeover and extreme competition between males for nest sites, but that males rarely sneak matings. Genetic analysis also revealed introgressive hybridization between *P. coriacea* and the Red-crowned Toadlet (*Pseudophryne australis*). Our study demonstrates a high level of mating system complexity, and it shows that closely related anurans can vary dramatically in their genetic mating system.

Data deficient and deadly: how a lack of fundamental knowledge impairs clinical treatment of coagulotoxic viper envenomations

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The consequences of snakebite from species within the “True Vipers” (Viperinae) range from the slight to the severe to the downright unknown. Some of these vipers, such as Russell’s vipers (*Daboia* species), are known to cause catastrophic levels of death and injury, and subsequently they have fairly well-characterised venom and a range of specific antivenoms. The consequences of snakebite from genera such as *Pseudocerastes*, however, are data deficient; little is known about their venom, and there is a very limited selection of antivenoms available to treat bites from these snakes. At the extreme, the venoms of such vipers as *Atheris*—common within the international pet trade—remain virtually undescribed, and no specific antivenoms exist. To complicate matters, variation in venom composition is a common occurrence within vipers, but the level of antivenom cross-reactivity for these medically important snakes remains under-investigated. So, just how variable is their venom, and what impact does this have on antivenom efficacy within a genus? And, in genera for which antivenoms are absent, is any neutralisation afforded by using antivenoms which have been developed to treat bites from a closely-related genus, or should we be concerned? In an attempt to shed light on these questions, this talk presents an overview of coagulotoxic venom activity of snakes from the Viperinae clade, and the efficacy and cross-reactivity of antivenoms for these toxins, using these three genera as model systems.

The Sleepy Lizard—Is the bobtail flu, as severe as the man flu

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The Sleepy Lizard (*Tiliqua rugosa*) is an iconic and widely distributed Australian skink that is ecologically well-researched. It has one of the longest and most complete datasets of any reptile in the southern hemisphere (36 years). Very recently, a nidovirus from the same family as the SARS virus in humans (Coronaviridae) was characterised within this species, and has been linked to a serious upper respiratory tract infection (URTI). This URTI can cause significant respiratory problems in these animals, with over 200 individuals being admitted to Kanyana Wildlife Centre hospital between 2014 to 2015 alone. Treated animals have a very high survival rate (84%), however it is thought that in untreated wild individuals, there is a significantly higher mortality rate. Very little is known about this nidovirus, including its distribution and host specificity. Most infected *Tiliqua rugosa* are reported in Western Australia, however a small number of sick animals have been reported in South Australia. Due to the large number of affected individuals in WA; its assumed high mortality rate; and the species-wide distribution across the southern and eastern states of Australia, it is crucial to assess this virus distribution. My PhD project aims to create an antibody test for this virus, then map the distribution of the virus between SA and WA using the newly created antibody test. The project also aims to explore host transcriptomes from infected and non-infected individuals to determine genes expressed when contracting this virus.

Contrast-Enhanced Micro-CT: an alternative to destructive dissections for analysing reptile muscles

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One of the primary drivers behind the changes in skull morphology in reptiles is the development of the jaw muscles which is likely a result of the functional demands associated with the different feeding techniques associated with different prey types. The Dugite or Spotted Brown Snake (*Pseudonaja affinis*) demonstrates a distinct size-related shift in diet which is reflected by distinct morphological changes in skull during growth. Preliminary work on the jaw muscles in this species involved developing methods and protocols for the staining and micro-CT scanning of the soft tissues of specimens and ultimately processing the soft tissue micro-CT data. Initial analysis suggests that the skull changes in *P. affinis* are tightly linked with the development of the jaw muscles. The continued work in this area will examine whether there are

distinct ontogenetic changes in the jaw musculature of *P. affinis* that relate to previously identified ontogenetic changes in skull morphology and shifts in diet. This will be achieved by using soft-tissue micro-CT data already collected of an ontogenetic series of *P. affinis* specimens. Jaw muscles would be digitally segmented using processing/visualisation software and then densities/volumes of each individual muscle will be calculated. The size of these muscles will then be analysed relative to each other and the size of the braincase across the series of specimens. This work will provide insight into the functional morphology and ecology of an Australian elapid.

Ontogenetic shifts in the diet and skull morphology of the Dugite (*Pseudonaja affinis*)

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Since snakes are limbless, gape-limited predators, the skull is the principal structure of prey acquisition, manipulation, and ingestion, and its structure is therefore likely to be an indicator of diet and prey preferences. The Dugite or Spotted Brown Snake (*Pseudonaja affinis*) demonstrates a distinct ontogenetic size-related shift in its diet that might be expected to result in distinct morphological changes in the skull. This study examined whether there are distinct ontogenetic changes in the skull morphology of *P. affinis* that could be related to ontogenetic shifts in diet. We examined an ontogenetic series of *P. affinis* specimens using micro-CT and geometric morphometrics to analyse 3D skull morphology. Multivariate regressions of shape variables revealed significant ontogenetic changes in the shape of the cranium and the measurements of the trophic bones. Relative to body size, trophic bone measurements scaled with significant negative allometry (except ectopterygoid height, which was not significantly different from isometry). Relative to head size however, the majority of the trophic bone measurements scaled with significant positive allometry (except quadrate diameter, which was not significantly different from isometry). The ontogenetic changes found in the skull of *P. affinis* reflect similar changes seen in other macrostomatan snakes, which are associated with increased gape size and mobility of trophic bones in adults compared with juveniles. These changes allow for ingestion, ease of manipulation and processing of larger prey as the snakes grow. Ontogenetic shifts in prey types are therefore reflected in altered morphology of the feeding structures within the heads of these snakes.

From childhood to dragonhood: the evolution of ontogeny in monitor lizards and their kin

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Morphological diversity is a manifestation of changes in ontogeny. Thus, understanding how ontogeny evolves is expected to greatly enrich our understanding of phenotypic evolution. Ontogeny has been traditionally considered to be an evolutionary constraint, but recent studies have shown that the relationship between changes in size and shape (i.e., allometry) is evolutionarily labile. In this work, we used an evolutionary framework to compare ontogenetic development in a clade comprising monitor lizards (Squamata: Varanidae: *Varanus*) and two closely related taxa: the earless monitor lizard (Squamata: Lanthanotidae: *Lanthanotus*) and the Chinese crocodile lizard (Squamata: Shinisauridae: *Shinisaurus*). This clade is ecologically diverse and shows great variation in body size, ranging from 16 g and 228 mm to 80 kg and 3 m. Our total sampling included 1,600 specimens belonging to 80 species out of 85 recognised in the clade. Of these, 1,536 specimens belonging to 57 species were included in analyses of the ontogenetic allometric trajectory. Our results show that most species tend to get more robust as they grow. However, this is not always the case and several features of ontogenetic allometric trajectories are variable both between and within clades. The amount of ontogenetic shape change is not fully explained by phylogeny, is evolutionarily dissociated between the body and limbs, and in limbs it seems to be correlated with adult body size and habitat use. Furthermore, some species pairs that differ in adult shape exhibit ontogenetic allometric trajectories with a similar intercept and direction, providing evidence for change in the rate and/or timing of development (i.e., heterochrony). Thus, our results indicate that ontogenetic development can be labile at relatively shallow evolutionary scales, modular, and related with the ecology of organisms.

Speciation in the mountains and dispersal by rivers: Molecular phylogeny of *Eulamprus* water skinks and the biogeography of Eastern Australia (Short title: All you need to know about *Eulamprus* in 4.5 minutes)

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Scott Keogh and colleagues have been working on the systematics of the *Eulamprus* water skinks for over 2 decades, and we finally published the results this year. I will summarise, in a disproportionate amount of time, this epic research venture in 4.5 minutes (which may be as long as the baby strapped to my front will remain happy). Using Sanger and Next Generation Sequencing we resolved the taxonomy of the group and explored the influence of landscape evolution of eastern Australia on phylogeographic patterns.

Speciation in the mountains and dispersal by rivers: Molecular phylogeny of *Eulamprus* water skinks and the biogeography of Eastern Australia—Part 2

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We used our robust phylogeny for water skinks to explore the influence of landscape evolution of eastern Australia on phylogeographic patterns. Our extensive mtDNA sampling revealed substantial phylogeographic structure in all species, with the exception of the geographically highly restricted *E. leuraensis*. The major divergences between lineages strongly

support previously identified biogeographic barriers in eastern Australia based on studies of other taxa. These breaks appear to correlate with regions where the Great Escarpment is absent or obscure, suggesting topographic lowlands and the accompanying dry woodlands are a major barrier to dispersal for water skinks. While some river corridors, such as the Hunter Valley, were likely historically dry enough to inhibit the movement of *Eulamprus* populations, our data indicate that others, such as the Murray and Darling Rivers, are able to facilitate extensive gene flow through the vast arid and semi-arid lowlands of New South Wales and South Australia.

Outbreak of emerging fungal disease in free-living Eastern Water Dragons

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Emerging fungal diseases pose a significant threat to biodiversity and have driven declines and extinctions across a range of taxa. In the last few decades there have been increasing reports of fatal dermatomycoses in reptiles associated with fungi belonging to the genera *Nannizziopsis*, *Paranannizziopsis* and *Ophidiomyces*, formerly known as the *Chrysosporium* anamorph of *Nannizziopsis vriesii* (CANV) complex. These fungal pathogens have been identified as the causative agents of severe skin lesions and systemic disease in a wide range of reptile species and are now recognised as significant emerging threats to reptiles, worldwide. Members of the genus *Nannizziopsis* have been reported across a diverse range of reptiles and infections are often fatal, with limited treatment success. Until recently, reports have been restricted to captive animals. Here, we report on the detection of an outbreak of severe dermal lesions associated with *Nannizziopsis* in free-living Eastern Water Dragons (*Intellagama lesueurii*) in Southeast Queensland, Australia. With the first case detected in 2014, our research has now confirmed a further five cases in Eastern Water Dragons from multiple, widely separated locations across greater Brisbane, three with severe disease warranting euthanasia. In each case so far confirmed, PCR and genetic sequencing data has revealed 98.5% similarity to *Nannizziopsis barbata*, a fungal pathogen that has been associated up to now with severe, fatal disease in captive Coastal Bearded Dragons, *Pogona barbata*, from Australia. During a recent survey of a well-studied population of Eastern Water Dragons in Brisbane city, we found that over 20% of Eastern Water Dragons examined presented with similar lesions, varying from mild and localised to severe and extensive.

Sticky fingers: Microhabitat choice, adhesive performance and toe-pad morphology in velvet geckos (Genus: *Oedura*)

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In animals, effective locomotion is critical for prey capture, predator avoidance and mate acquisition. Variation in locomotor abilities influenced by the environment, is likely to influence fitness. Thus, animals should select microhabitats in which they perform best. Ecological variation of adhesive systems of geckos among species and populations in response to habitat structure is poorly known. We measured substrate choice and adhesive performance of three different species of velvet geckos (genus *Oedura*), with different preferred microhabitats (one arboreal, one saxicolous, and one generalist), in the laboratory, and examined the morphology of the adhesive apparatus (toe pad area, setae length and density) of the three species to investigate potential variation in morphology in relation to substrate preference and performance. All three species had better adhesive performance on rough substrates, and behaviourally preferred rough substrates compared to smooth substrates. Clinging ability did not differ among the three species when absolute force was adjusted for toepad area. In terms of the adhesive apparatus, the generalist species had the largest toepads with the longest setae and lowest setal density, whereas, the saxicolous species had the smallest toe pads, shortest setae, and highest setal density. Morphological and behavioural differences among species observed in our investigations support the ecomorphological paradigm that behaviour and performance will work together to influence the evolution of morphology.

Supporting global snake bite management with geospatial analyses

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Snake bite envenomation has long been recognized as a serious health issue but has recently been elevated to the status of a 'category A neglected tropical disease' by the World Health Organization (WHO). The severity of the problem is caused by a complex chain of issues. This chain starts with limited recent research on improvement of antivenoms, but is exacerbated by lacking quality controls, low profitability for pharmaceutical companies, difficulties in distribution of antivenoms to rural snake bite hotspots, and affordability problems for the vast majority of the estimated >2 million annual victims of envenomation, most of whom are farmers in the developing world. One of the major knowledge gaps affecting antivenom production is the limited information on the distributions of medically relevant venomous snake species and on geographic variation in intraspecific venom compositions. This study aims to fill these knowledge gaps by (i) creating high quality, high resolution species distribution models for all snake species listed as medically relevant by the WHO and thereby improve on the current expert derived range estimates, (ii) assess the potential for climate change to shift hotspots in

venomous snake bite risk areas. These steps will lay the foundation for further crucial research, which will (iii) use distribution models in combination with global sampling of venom compositions to establish cut of points between ‘venom lineages’ within species and (iv) combine the above to establish venom ‘regions’ that could be covered by individual polyvalent antivenoms. These steps will inform snake bite management, venom selection for antivenom production, and suitability of antivenoms for specific regions. However, it will take global collaborative initiatives between researchers, governments, charities and NGOs to address the remaining links in the issue chain.

Tracking change in call race boundaries and overlap zones across the range of the Spotted Marsh Frog, *Limnodynastes tasmaniensis* (Anura: Myobatrachidae) using FrogID

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Frog species with multiple call races, contiguous geographic regions where they produce distinctly different advertisement calls, provide an opportunity to consider the evolutionary history a species and advance our understanding of hybridisation and speciation. The Spotted Marsh Frog (*Limnodynastes tasmaniensis*) is a common species distributed throughout most of the eastern half of Australia. It has two main call races which can be easily distinguished by number of notes per call- northern (2-5 notes) and southern (single note). At points of contact between the call races there are overlap zones with hybridisation of the calls. The stability of these zones over time, and call variation in the species as a whole has not previously been examined, largely due to logistical constraints. FrogID is a citizen science initiative aimed at capturing validated biodiversity data on frogs on a national scale with users recording frog calls with a smartphone app. Since launching in November 2017, over 2000 call recordings of *L. tasmaniensis* have been submitted from across Australia. We analysed these recordings to obtain the most detailed and geographically comprehensive understanding of the call of *L. tasmaniensis* to date. This allowed us to allocate calls to call races using multivariate analyses, and to map current call race boundaries and overlap zones. Comparison with call race historical data then allowed us to gain an understanding of the temporal stability of call race overlap zones. This project represents the first use of large-scale citizen science data in mapping call race boundaries.

Large-scale patterns of community structure among African squamate reptiles

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Large-scale patterns of community composition remain poorly understood, despite the increasing importance of predicting communities' responses to rapidly changing climate. The evaluation of changes of community structure metrics along environmental gradients is a promising approach, which facilitates general predictions about community structure. In this context, the stress dominance hypothesis (SDH) makes predictions about the relative importance of competition and habitat filtering under different levels of environmental stress. In particular, the SDH states that the relative influence of habitat filtering is greater under stressful conditions, while competition becomes more important in benign environments. Most previous studies addressing the SDH have not encompassed extensive environmental gradients, and mostly focused on local communities, ignoring the impact of regional processes on local community assembly. Here, we used African squamate reptiles as a model system in a multidimensional, phylogenetically informed approach. By incorporating functional diversity, phylogenetic diversity, species richness, and their respective changes across extensive environmental gradients, we show that the functional community structure of African squamates largely confirms the predictions of the SDH. We found significant functional structuring at both local and regional spatial scales, emphasizing the importance of regional and historical processes on local community assembly. In contrast, the phylogenetic diversity patterns of African squamates did not follow this pattern, likely due to the contrasting biogeographic histories of African lizards and snakes.

Advances and inertia in the field of alien amphibian incursions: Asian toads in Madagascar

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Eradication of exotic vertebrates usually involves only mammals; other invasive vertebrates, including amphibians, receive little attention despite growing evidence for impacts. Recently, anuran invasions in Australia, North America, and Hawaii have provided evidence of

ecological impacts that have elicited management responses. In 2014, the Asian or Black-spined Toad (*Duttaphrynus melanostictus*), native to southern Asia, was recorded in Madagascar. Biological similarities to the cane toad raised concerns for Madagascar's globally significant biota, which lacks toads and their toxins. Effective response required coordination between the international community, industry, and national government; however, despite efforts, that has failed. A feasibility study identified the need to test potential eradication tools whilst gathering resources to employ tools at a trial scale. We measured toad densities across habitat types in the infested zone. We also tested the efficiency of toad removal using (1) manual removal employing community labour, (2) pitfall trapping with drift fencing, (3) tadpole traps utilizing bufotoxin lures, and (4) citric-acid sprays. We found that manual collection of toads can remove large numbers of individuals, but considerable effort is required to see catch rates decline. Drift fencing with high-density pitfall trapping is effective but can only be applied to a limited extent (primarily around breeding ponds), and maintenance is a problem in agricultural environments. Tadpole trapping was ineffective, suggesting either that bufotoxin does not serve as a lure in this species or that tadpole stages sensitive to luring were absent during trials. Concentrated (25%) citric-acid spray consistently resulted in 100% mortality for small toads (SVL <35 mm) and high mortality rates (30–100%) in adult toads, even in complex habitats. Our results suggest viable eradication tools may exist for this species, but strategies and leadership to progress eradication or management in Madagascar are extremely weak. Eradicating future incursions can build on these technical advances, but response protocols and coordination are still lacking.

Tool and method development for the eradication of the Plague Skink, *Lampropholis delicata* and Alpine Newt *Ichthyosaura alpestris* in New Zealand

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Invasive reptiles and amphibians have a growing profile in New Zealand. This has resulted in sustained and multi-agency efforts to control their spread or prevent their establishment post-boarder. The Delicate, Garden or Plague Skink, *Lampropholis delicata*, a native to Australia, has become an invasive species across most of the Hawaiian Archipelago, Lord Howe Island and New Zealand's North Island. There is limited understanding of their ecological impacts, but serious concerns remain due particularly to the high levels of local abundance they are known to achieve. A multi-agency response to a plague skink incursion on Great Barrier Island in 2013 that has led to a process of development and testing of interception and detection methods accompanying a joint 'eradication by research' programme to eradicate the skink from the Island. The programme has pioneered the testing of a number of novel tools and strategies including insect sticky traps, thermal fumigation and chickens. The process has highlighted a lack of fundamental knowledge about potential tools, detection and interception methods necessary for successful eradication. Additionally, the project has emphasized a lack of appropriate mechanisms within resource management and biosecurity agencies to ensure

appropriate timely responses to such incursions. Over the same timeframe we have also responded to the detection of a breeding population of Alpine Newts (*Ichthyosaurus alpestris*) in the North Island. The eradication programme is now in its sixth year and has tested a number of strategic, detection, interception and containment tools including modified pitfall traps, habitat modification, detector dogs and the use of skeletochronology and eDNA.

Parallel evolution of enlarged, adhesive toe-pads in two lineages of rock-dwelling lizards (Gekkonidae; *Heteronotia*)

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Adhesive toe-pads featuring hair-like microstructures (setae) are well-known traits in geckos and anoles. They have evolved multiple times in geckos and are typically associated with climbing in arboreal or saxicoline microhabitats. Although the functional morphology of adhesive toe-pads is well studied, their evolution is poorly understood because of the scarcity of intermediate forms between pad-less terrestrial and pad-bearing climbing forms. To shed light into the evolution of adhesive pads we assessed the toepad scale morphology of *Heteronotia binoei*. The *H. binoei* species complex comprises several morphologically cryptic but genetically divergent lineages of terrestrial geckos generally lacking pronounced toe-pads. There are two phylogenetically distinct lineages from north-eastern Queensland, associated with saxicoline habitats, which appear to have independently developed enlarged terminal subdigital scales. Analysis of subdigital scale size, and scale microstructures via scanning electron microscopy (SEM), reveal that the saxicoline lineages have both larger toe-pads and longer, more fully developed adhesive setae with triangular tips (spatulae) in comparison to their terrestrial sister lineages. Furthermore, setae are found not only on the enlarged terminal subdigital scales but also on the inflection scale (where the toe touches the substrate). Considering that the respective saxicoline lineages have diverged from their terrestrial sister lineages fairly recently, this might represent an early stage in the evolution of fully developed adhesive pads.

Conservation planning for the Kimberley sidesteps uncertain taxonomy

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Drawing on phylogeographic data for geckoes and skinks of the Australian Monsoonal Tropics (AMT) we identified priority areas for conservation in the Kimberley region. Our novel phylogenetically informed approach to conservation planning, targets diversity both above and below species level, bypassing named taxa to use genetic data directly in conservation assessment.

Despite many recent species descriptions, the lizards of the AMT contain substantial diversity as yet unrecognised by current taxonomy, revealing novel diversity hotspots and biogeographic patterns. We sampled mitochondrial diversity within eleven genera of skinks and geckoes based on over 5000 individuals from across the AMT and identified over 320 independently evolving lineages.

We divided the area into 5 km² planning units, with information on the lineages likely to occur in each planning unit. We identified sets of areas which would best capture the phylogenetic diversity of the region under a range of scenarios. In particular, we identified 6 key areas of unprotected evolutionary diversity where there may be greatest benefit from additional conservation measures.

In this study we demonstrate how phylogenetic diversity can be applied to a complex, real-world conservation planning problem, and offer a method which can bring taxa with incomplete taxonomy into data-driven conservation assessments.

FrogID: citizen scientists provide validated biodiversity data on Australia's frogs

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There is an urgent need for comprehensive global biodiversity data, particularly for highly threatened taxa such as frogs. Some of the most dramatic frog population declines, globally, have occurred in Australia, but logistical difficulties of surveying frogs (i.e., the large size and remoteness of Australia) have limited our knowledge of biodiversity. Citizen science projects have recently facilitated the collection of broad-scale biodiversity data, but the application of citizen science data collection to frogs has lagged behind other taxa. Citizen science projects targeting frogs have been successful in collecting occurrence data, but typically rely on species identification via user-submitted photographs. Photographs of frogs can be difficult to identify to species and may also inadvertently encourage handling of frogs. We developed FrogID—an expert validated biodiversity database of frog occurrences in Australia, reliant on acoustic validation. FrogID uses smartphone technology, allowing participants to submit recordings of calling frogs, providing (1) a biodiversity database with geo-referenced, presence-only, frog species records, and (2) a digital collection of frog calls. In a short time, FrogID has allowed us to collect data on rare and threatened frog species, document the disappearance of native frog species from parts of their range and detect invasive species, including native species that have established populations outside their native range. In this paper, we (1) introduce FrogID, including technical details, (2) highlight preliminary findings, drawing comparisons with the Atlas of Living Australia – the national biodiversity aggregated database, and (3) identify potential future uses of the data.

Misty Mountains and Moss Frogs: a decade of collaborative research and conservation work by the Australian Museum in northern Vietnam

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Southeast Asian amphibians are both poorly-known and highly threatened. Many new amphibian species have been described only recently and large areas of the region remain undersurveyed. Rapid deforestation is a major threat, with many recently discovered species already on the edge of extinction. It is therefore urgent to more accurately document the diversity and distributions of amphibians in the region, in order to inform and prioritise conservation management planning. To this end, since 2007 we have been focusing on collaborative expeditions in search of amphibians in the region, and in assessing the global

conservation status of the amphibians of the area. One of our geographic focal areas is northern Vietnam, an area of particularly high species diversity and undergoing deforestation. To date, we have conducted eight collaborative amphibian surveys that have resulted in the discovery of five new species, most of which are already threatened, or likely to be threatened, with extinction. Our work is necessarily highly collaborative, with strong partnerships throughout Vietnam and internationally, and we hope to continue advancing our understanding and ability to conserve this highly diverse and threatened group of animals in northern Vietnam and beyond.

Unravelling geographical patterns of introgression in wall lizards using landscape genetics

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Increasing evidence suggests that phenotypic variation in both plants and animals can be the result of genetic exchange between species and subspecies. The rate and direction of genetic exchange will be strongly influenced by patterns of selection and thus mediated by the biotic and abiotic environment. One result of this is a distinctive pattern of genetic exchange across the landscape, making secondary contact zones excellent settings to investigate ongoing selection processes in the wild. Here I examine how aspects of the environment mediate gene flow upon secondary contact in the Common Wall Lizard, *Podarcis muralis*. This species exhibits considerable phenotypic and genetic divergence across its species range with distinct evolutionary lineages having back into secondary contact in northern Italy. We have previously shown strong asymmetric introgression of genes between lineages in these zones of secondary contact driven by sexual selection. However, this introgression appears to be limited at high altitudes. I will present preliminary analysis of the climatic factors that mediate gene flow within these regions. This includes a large data set including phenotypic data from over 170 populations spanning the altitudinal and geographic range of the hybrid zone. These data suggest that climatic variables have an effect on introgression of the phenotypic traits across the landscape. I will discuss these results within the context of the selective mechanisms that may link climate to limited gene flow.

Evolution of snake visual systems in the transition from land to sea

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Our research examines evolutionary innovation in reptile sensory systems, with a particular emphasis on the recent transition from land to sea in front-fanged snakes (Elapidae). This talk will address elapid visual evolution, which is of interest because snakes have an

ancestrally reduced repertoire of visual pigments but have nevertheless successfully colonised a complex photic environment (the sea). We used opsin sequencing and physiological tests of spectral tuning in visual pigments to recover adaptive shifts in colour vision throughout sea snake phylogeny. Sea snakes provide a contrasting system to other secondary marine vertebrates (birds, mammals), which typically have degenerated visual systems compared to their terrestrial ancestors.

***Batrachochytrium dendrobatidis* presence within species: a review on ecological scales and influential variables**

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Since the identification of the infectious agent *Batrachochytrium dendrobatidis* (Bd) 30 years ago, numerous studies have helped to build solid documentation on the impact of amphibian chytridiomycosis, the worst disease ever recorded to affect biodiversity. Bd presence in frogs has been investigated over a broad range of ecological scales. Studies have extended from differences in infection load within individuals, disease prevalence among habitats at the population level, as well as presence of Bd across the landscape level. These studies have examined both environmental and intrinsic species-specific factors to explain the variable occurrence of Bd within species. The scale of interest has a profound influence on our understanding of which processes underpin the disease dynamics and on the scope of our conclusions and predictions. To evaluate the breadth of studies performed to date we quantitatively reviewed the Bd literature, and classified studies with regard to the spatial scale explored, methodological design and overall findings. We systematized which variables were most strongly associated with heterogeneity of disease occurrence. Among the 80 peer-reviewed papers published between 2004 and 2018 that fitted our criteria, air temperature and rainfall or humidity were commonly investigated environmental parameters. Variables such as life stage, distance to urban areas or zooplankton composition were seldom investigated, but were shown to influence Bd prevalence among different populations of the same species. Chytridiomycosis remains a dire threat to amphibians worldwide, and an intricacy of factors influences its occurrence and consequently its effects. Our review emphasises that understanding the complexity of Bd impact requires an integration of studies tackling Bd-host interaction at multiple scales and perspectives.

A₂O: An acoustic observatory for Australia

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Recent advances in electronic storage and recording technologies are transforming environmental science by allowing us to record vocal species 24 hours a day and 7 days a week, providing data of unparalleled spatial and temporal resolution for ecosystem monitoring and research. The ability to monitor sound is particularly relevant to understanding Australia's fragile and mega-diverse environment. The A₂O (Australian Acoustic Observatory) will be the world's largest terrestrial acoustic sensor network comprising 400 listening stations deployed across Australia, sampling 6 ecoregions in tropical, subtropical, and temperate regions. The recorders will be deployed in groups of four, with two in 'dry' habitat and two in 'wetter' habitat at each site, close to wetlands, rivers or other water bodies. Data will be freely available to all online, enabling a wide variety of projects understanding ecosystems, long-term environmental change, data visualization and acoustic science.

Evolution of intra and intersexual signalling in two species of frogs in the *Litoria lesueuri* species group

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This project will investigate the evolution of intra and intersexual signalling strategies within the *Litoria lesueuri* species group, commonly known as the stony creek frogs. Specifically, two species are being examined; *L. wilcoxii*, distributed along eastern Australia from NSW to north Queensland and *L. jungguy*, which is found in north Queensland. Where their distributions overlap, hybridisation has been reported (Donnellan & Mahony 2004). These species lack a vocal sac, yet are known to call beside streams that produce a high amount of environmental noise. Environmental noise can create a masking effect, potentially reducing the efficacy of acoustic communication. Because of the importance of frog calls for reproduction, namely mate recognition and localisation, negative impacts on calling can result in wasted time, gametes and energy, and increase the risk of predation (Gerhardt & Huber 2002; Wells & Schwartz 2007), reducing the fitness of individuals and populations. However, it is currently unclear how the environment in which these species call has constrained the evolution of their calls. Furthermore, recent observations of *L. wilcoxii* have revealed a previously unknown form of visual signalling for this species, including the use of limb movements and body posturing. Like acoustic signals, visual signals can be constrained by a variety of environmental factors, including high ambient noise levels and acoustically complex environments. Therefore, the function of this newly identified communication strategy as well as the potential environmental constraints will be explored. Preliminary findings regarding the currently unexamined calling properties of *L. wilcoxii* and *L. jungguy*, in allopatry and within the hybrid contact zone, as well as the use of visual cues in *L. wilcoxii*, will be presented.

Fragmentation and disturbance drive occurrence and persistence of grassland herpetofauna: implications for management and conservation

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For effective decision making, land managers must understand the interacting effects of landscape, habitat and management processes on wildlife populations. We collected a large cover-object dataset (291 sites, 9 years, 4000+ surveys) in fragmented grassland landscapes in western Victoria. The data were used to assess population trends, and the impacts of landscape, habitat and disturbance processes (fire and grazing) on a range of herpetofauna. Hierarchical dynamic occupancy models were used to estimate the effects of grassland availability, burning and grazing on rates of occupancy, extinction and colonisation. Species exhibited contrasting responses to fragmentation and disturbance, meaning that uniform approaches to management may not serve the needs of all species. Several grassland-specialist species including *Delma impar*, *Pseudemoia pagenstecheri* and *Suta flagellum* were found to rely on disturbance and/or the availability of large areas of native grassland in surrounding landscapes for ongoing persistence in grassland fragments. Our extensive dataset and modelling approach provides insight into the effects of grassland management actions and allows land managers to predict the effects of management regimes.

Conserved thermal physiology in three closely related lizards across an elevation gradient: implications for interspecies interactions under climate change

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The impacts of climate change are expected to be significant for ectotherms inhabiting mountainous regions due to lower upper thermal limits exhibited in highland species compared to lowland species. Despite the capacity for climate change induced distributional shifts in these communities, rarely do studies consider differences in thermal tolerances over a meaningful

biogeographical scale for interspecific interactions. We examined local scale differences in thermal tolerance in populations of three species from the scincid lizard genus *Liopholis* distributed across an elevation gradient in Kosciuszko National Park with the aim of elucidating the species adaptive potential to climate warming. We recorded elevational distribution in the species, and compared habitat, thermal tolerance (critical thermal minimum (CT_{min}); critical thermal maximum (CT_{max}); and thermal sensitivity of locomotor performance). The species include an alpine specialist, *L. guthega*; subalpine to montane *L. montana*; and widespread *L. whitii*. The three species exhibited an elevational replacement distribution and occupied habitat with similar rock and soil cover, suggesting a capacity for basking and shelter resource competition. We found variability in cold tolerance between populations and species, with cold tolerance increasing with elevation. We found limited variability in upper thermal limits. Predicting the winners and losers of climate change is a complex challenge, in part due to spatial variability in climate relevant physiological traits which may leave species or populations vulnerable to rises in temperature. Our results suggest that heat tolerance is conserved within and amongst *Liopholis* species across an elevation gradient of 940 m. Thus it is likely that the three species will be similarly affected by rises in temperature, with no single species at a competitive advantage in terms of thermal physiology.

Pinning the identity to the skink: the curious case of *Hombronina fasciolare*

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The scincid lizard *Hombronina fasciolare* was described by Charles Girard in 1858, based on material purportedly collected by the United States Exploring Expedition in 1840 from the Bay of Islands in New Zealand. It has previously been suggested that the type specimen is not from New Zealand, but instead represents a *Lipinia* species. George Zug agreed that the purported type was a *Lipinia* species, but suggested that the specimen was not the type of *Hombronina fasciolare*, but was instead the missing holotype of *Lipinia vulcania*, a species from the Philippines also collected by the Exploring Expedition. My examination of the type during a visit to the USNM in 2017 finds that the specimen, though in poor condition, does agree well with the description of *Hombronina fasciolare*, and should be considered the type of that species. It is neither a New Zealand skink (all of which are members of the tribe Eugongylini), nor a *Lipinia* species (Sphenomorphini), but is instead a *Scincella*, most likely the native American species *Scincella lateralis*, a species not known from the ports visited by the Exploring Expedition. It is presumed that the type was erroneously mixed with the Expedition's collections in the 17 years between the Expedition's return in 1841 and the lodgement of its collections in 1858 into what would become the United States National Museum of Natural History, during which time the collections were variously shuffled between exhibition spaces and warehouses in New York, Philadelphia and Washington. *Hombronina fasciolare* is the second lizard species with such a history.

The evolutionary and developmental basis of extreme body shape divergence in microcephalic sea snakes

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Snakes exhibit a diverse array of body sizes and shapes despite their characteristically simplified morphology. Among living snakes, the most extreme shape changes along the pre-cloacal body axis are seen in fully aquatic sea snakes (Hydrophiinae) in the genera *Microcephalophis* and *Hydrophis*. These ‘microcephalic’ sea snakes have tiny heads and dramatically reduced forebody girths that can be less than a third of their hindbody girths. Using morphometric and phylogenetic comparative methods, we uncover the evolutionary patterns leading to this extreme body shape in sea snakes and show that this morphology has evolved multiple times in species that specialise on hunting eels in burrows. Then we test evolutionary patterns of vertebral number and postnatal ontogenetic growth to infer the developmental patterns underlying this extreme body shape. We find that microcephalic species develop their characteristic body shapes via changes in both the embryo and postnatal stages: postnatal ontogenetic changes cause the hindbodies of microcephalic species to reach greater sizes relative to their heads/forebodies in adulthood, indicating heterochronic change during sea snake evolution; and increased numbers of vertebrae, especially in their forebodies (anterior to the heart), contributing to the elongation of the forebody and may compensate for its reduced overall growth. Our findings highlight sea snakes as an excellent system for studying rapid morphological evolution, the regulation of segment number and identity in the snake pre-cloacal axial skeleton, and the roles of these developmental traits in snake body shape diversification.

Environmental sex determination in a snake: dry nests produce more sons

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A 17-year field and laboratory study in the wet-dry tropics shows a novel mode of sex determination in the colubrid snake *Stegonotus cucullatus*. Although the species exhibits heteromorphic (ZW) sex chromosomes, eggs incubated on dry substrates hatch disproportionately into sons rather than daughters (especially if the eggs are small). The effect is highly significant even if analysis is restricted to clutches with 100% hatching success, so the sex-ratio bias cannot be attributed to differential mortality of embryos. Dry incubation substrates reduce offspring size, especially in daughters rather than sons. Mark-recapture data show that the sex-ratio shift enhances offspring survival, providing a plausible fitness advantage to drive

the shift from genotypic to environmental sex determination (ESD). This is the first report of ESD in any snake, and the first example of moisture-driven ESD in any vertebrate.

Beyond dragons: Assessing the herpetofaunal wealth of Komodo National Park

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Among Indonesia's greatest natural treasures and most visited parks is Komodo National Park (KNP), which is also a UNESCO World Heritage Site and a Man and Biosphere Reserve. It harbours a biogeographically distinct grouping of animals, but no surveys on its herpetofauna have taken place for the nearly half a century. Recent anecdotal and opportunistic observations suggest the occurrence of several additional and also new-to-science species. “Conservation focused” tourism is becoming a bigger drawcard in the region, but park rangers do not have a sufficient knowledge on the herpetofauna to communicate to tourists on issues as basic as species identification and baseline ecology. To address this immediate knowledge shortfall, we lead a set of intensive sampling surveys for herpetofauna at KNP in collaboration with the national park authority. The effort resulted in publishing a concise pictorial guide, a set of large format educational posters to display at the park, and a capacity-building program for the park rangers.

Seeing the forest for the crocs: the influence of vegetation on crocodilian ecology

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The influence of vegetation on carnivores is a topic rarely discussed, especially with regard to large and formidable predators such as crocodilians. Nevertheless, many aspects of their life histories are influenced and have been shaped by vegetation interactions. Importantly, from a conservation perspective, our understanding of just how vegetation impacts life histories of these predators remains quite limited, particularly in regard to indirect interactions. Through a global review of literature, we identified five primary aspects of crocodilian ecology—habitat selection, nesting ecology, communication, physiology, and feeding ecology—that are shaped by vegetation interactions at different spatial scales. These interactions include direct and indirect impacts, with both positive and negative outcomes from a crocodilian perspective. We synthesise the contemporary understanding of these plant-crocodilian interactions to identify understanding and knowledge gaps and then conceptualise how global environmental change may threaten these critical dependencies.

Quantifying the correlates of risk in Australian amphibians

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Amphibians are experiencing declines globally, and are more threatened than any other vertebrate group. In Australia, four species have gone extinct since the 1980s and many others are facing a similar future. To understand the extinction process many studies have employed the International Union for Conservation of Nature (IUCN) threat status and predictive tools to identify traits which render species vulnerable to declines. Identifying such traits can help guide proactive conservation planning. By compiling a database including life history traits, climate variables and morphology, and the implementation of phylogenetic comparative methods, this study provides the most comprehensive analysis of Australian amphibian extinction risk to date. I tested two main questions: (i) Is extinction risk phylogenetically clustered in Australian frogs?; (ii) What are the best key correlates of extinction? As well as that, I aimed to provide useful information for proactive conservation efforts, by identifying species that are not currently threatened but are likely to be under high risk in the near future. Firstly, it is shown that extinction risk is phylogenetically clustered in Australian frogs and secondly, the correlates of risk for the Hylidae and Myobatrachidae family were identified. Habitat type best predicted extinction risk in hylids, with threatened species found in wet habitats. Myobatrachids had multiple correlates, including large relative ovum size, long legs, high elevation and cooler environments. Whilst many of these traits have links to the presence of the pathogen chytrid, they may also be influenced by changing climates. In contrast to previous studies, geographic range size was not identified as a correlated of risk. My results highlight the importance of using a wide range of extrinsic and intrinsic traits in a phylogenetic framework and can be used to help guide more ecologically relevant and comprehensive conservation outcomes.

Ten years of Tawny Dragons: what have we learnt about colour polymorphism and speciation?

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The small, agamid Tawny Dragon Lizard, *Ctenophorus decresii*, is one of a handful of lizard model systems with male throat colour polymorphism. We have spent about 10 years deciphering the mechanism, function, evolution, inheritance and genetic basis of colour polymorphism in this system—and consequences for speciation. In this talk, I will give an overview of what we now know, and some key unknowns. Tawny Dragons are not ‘rock-paper-scissors’ lizards. Throat colour morphs are defined by the presence or absence of orange and yellow, resulting in 4 categories. The discrete morphs, and colour expression within morphs, are highly heritable, but inheritance is more complex than a single locus and a simple mendelian

mechanism. There are differences in behaviour and physiology between morphs, but they do not correspond to classic alternative reproductive strategies. The relative frequency of colour morphs in populations across the species range is strongly determined by environmental gradients, but frequency dependent selection presumably maintains the polymorphism in all populations. The populations that are not polymorphic should be considered separate species. One of these, *Ctenophorus mirrityana*, has been formally described. The others belong to the ‘southern lineage’ which meets the ‘northern lineage’ at a contact zone, where the lineages hybridise, but introgression is limited. We now have a good quality draft genome for *C. decresii* and have identified genomic regions associated with the colour polymorphism, but we still have a long way to go before we can confidently pinpoint genes controlling colour polymorphism and selection on those genes. Nevertheless, we understand more about Tawny Dragons than most other colour polymorphic lizards, providing opportunity to answer a range of exciting ecological and evolutionary questions.

Forest dragons in New Guinea: refugees or first settlers?

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Australia and New Guinea have many shared faunal elements, yet the environments of these two regions is highly contrasting. Australia is flat, relatively dry and geologically stable, while New Guinea is mountainous, wet and geologically highly dynamic. One hypothesis for the origin of lineages in New Guinea is that they are ‘refugees’ from the increasingly dry and arid Australia to the south. Forest dragons consist of two genera of amphibolourine agamids restricted to the rainforests of Australia and New Guinea. Based on molecular data from over 80 specimens we screened diversity and estimated phylogenetic relationships and biogeographic history of these genera. One genus unambiguously reconstructs to the Australia craton, with more recent colonisation of New Guinea inferred. In contrast, another genus is entirely endemic to New Guinea and biogeographic reconstructions, suggest a longer history of diversification on the proto-Papuan Archipelago.

Activities of two key toxin groups in Australian elapid venoms show strong correlation to phylogeny but not to diet

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We measured the activity of two enzyme groups – phospholipase A2 (PLA2), and L-amino acid oxidase (LAAO) – in the venom of 39 species of Australian elapids (40% of terrestrial species diversity). PLA2 activity ranged from 0 to 481 nmoles of chromophore/min/mg of venom, and LAAO activity ranged from 0 to 351 nmoles of H₂O₂/min/mg of venom. Phylogenetic comparative methods, implemented in BayesTrait showed that venom activity was strongly correlated to phylogeny but not to diet. Some species/individuals lacked activity in one protein family suggesting that snake venoms are redundant systems and that lack of activity of one protein family may not incur a significant fitness cost. Testing for accelerated evolution of these enzyme groups using phylogenetic comparative methods showed strong evidence for faster initial rates of change for LAAO (delta parameter mean 0.2) but no such pattern of evolution in PLA2 (delta parameter mean 0.9), suggesting that PLA2 may confer a higher ongoing fitness benefit. *Notechis scutatus* showed remarkable intra-specific variation in LAAO activity within populations that was not correlated to geographical distribution. LAAO activity was absent in both *Vermicella* and the *Pseudonaja/Oxyuranus* clade supporting the proposed relationships among these disparate taxa. We found two examples of venom activity differences in sister-species with similar diets that cannot be convincingly explained by positive selection, suggesting that genetic drift (founder effect), may in some instances play an important role in shaping venom composition.

Papua New Guinea—a diversity hotspot for *Nactus*

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New Guinea is an island known for its rich diversity of species and habitats, and large areas of continuous forest. Despite its importance, patterns of endemism and biodiversity within New Guinea remain poorly understood. Here we quantify the diversity and the endemism of a leaf litter gecko, *Nactus* in Papua New Guinea (PNG). *Nactus* is an insular genus with the majority of species occurring in islands on the Pacific and Indian Ocean, in addition to three

species in northern Australia. We assembled a mitochondrial alignment from over 200 individuals and all *Nactus* species occurring in PNG and Australia. We used bGMYC, a bayesian approach to identify the lineages (candidate species) from a maximum likelihood mtDNA tree estimated from this data. We complemented this with SNP data, to confirm and visualize the genetic distance between lineages. While PNG has six described species of *Nactus* we find evidence of at least nineteen divergent lineages that we consider candidate taxa. Mapping the distribution of lineages and phylogenetic diversity reveals a striking cluster of distantly related and apparently short-range endemics on the Papuan Peninsula region and nearby island in Milne Bay Province of far east New Guinea. The high endemism and turnover of this relatively small region in New Guinea suggests that it is of high biogeographic and conservation significance.

Tiger Snake (*Notechis scutatus*) adaptation and evolution

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Tiger Snake (*Notechis scutatus*) populations across Australia exhibit variation in many physical traits, including colour patterns, body size, venom composition, head-size plasticity etc. By understanding the molecular mechanisms underlying this variation we can investigate how Tiger Snakes adapt and evolve to novel environments, such as that which will occur under climate change. We have generated a draft Tiger Snake genome that we can now use to examine in more detail the genes and regulatory mechanisms underlying these variable traits. For example, we have identified 57 pigmentation genes, 624 growth genes, and 813 lipid metabolism genes in our draft tiger snake genome that are known from other organisms. In addition, we have identified venom toxin genes being expressed at different levels in the venom gland of island versus mainland populations that may be in response to variation in prey items. We are also currently gathering data about other population-specific variation in life history traits exhibited by the Tiger Snake, such as in mate choice and reproductive anatomy, skull shape differences in relation to prey type, vertebrae size and shape differences in relation to gigantism/dwarfism etc. With much still to be done in the Tiger Snake to 1) characterise trait variation and 2) investigate their molecular basis, I am looking for eager students interested in these topics and/or with skills in the wet lab, bioinformatics, fieldwork or morphometrics.

Reassembling the ‘megafaunal’ skink *Tiliqua frangens* from the late Pleistocene of eastern Australia

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The sub-family Egerniinae contains the world’s largest living skinks with species in the genera *Corucia*, *Bellatorias* and *Tiliqua* reaching snout-vent lengths greater than 300 mm and over a kilogram in weight. These species are surpassed by fossil material representing an extinct egerniine from Pleistocene deposits in Wellington Caves in NSW. New material has confirmed that two named fossil species from Wellington, *Aethesia frangens* and *Tiliqua laticephala*, actually represent a single taxon, *Tiliqua frangens*. This species is now known from multiple cranial elements (including an ontogenetic series of mandibles), vertebrae, osteoderms, and a tibia. *Tiliqua frangens* is likely to have weighed in the vicinity of 3 kg and reached ~45 cm in snout-vent length while being covered in thick, spiked, armour plating. When included in a tip-dated phylogenetic analysis of morphological and molecular data, it is most plausibly placed as sister species to the extant shingleback. *Tiliqua frangens* is the world’s first megafauna skink: a giant horned shingleback which superficially resembles a miniature ankylosaurian dinosaur in shape. The extreme ontogenetic changes in *T. frangens* are unmatched in any other skink and expand our ideas on the limits of morphological diversity in the Scincidae.

Why do so many New Zealand reptiles love seabirds?

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Reptiles can reach extraordinary densities on islands, particularly those around northern New Zealand that have avoided invasion by predatory mammals. Over the past 30 years many islands have been cleared of these introduced species. Here I describe the insights into reptile assemblage structure and function provided by 1) understanding the history of island formation; 2) responses to progressive removals of an array of introduced mammals from all of the islands in the Mercury archipelago; and 3) comparisons between islands inhabited by seabirds and those where seabirds have been lost. On uninvaded islands, seabirds act as ecosystem engineers that modify soil structure through burrowing and nutrient addition, increase the abundance of litter dwelling invertebrates and directly and indirectly affect vegetation composition. These conditions are exploited by tuatara (*Sphenodon punctatus*) and several species of large nocturnal ground-dwelling skinks. However, modification of the forest by seabirds also promotes the growth of native species of small trees that are hosts to a parasitic scale insect, which produce copious quantities of honeydew. These sugar sources are exploited by at least two species of geckos. Indirect effects of seabirds can even be tracked to the terrestrial and marine coastal

margins. Here two coastal specialist species of skinks feed near storm-tossed seaweed and carrion. One of these species, *Oligosoma suteri*, is also able to secrete salt, which enables it to feed exclusively on invertebrates of marine origin. Our understanding of the direct and indirect effects of burrowing seabirds have greatly increased over 30 years of study, but most work has concentrated on small islands (<100 ha). There is now potential to examine reptile assemblages on much larger islands, including some with old growth forest. Whether similarly complex interactions will appear on these larger islands remains unknown.

The agamid genus *Lophosaurus* Fitzinger, 1843: Preliminary comparative data on the diet of the two northern-most species *L. boydii* (Nth Qld) and *L. dilophus* (PNG) from limited museum specimens

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The genus *Lophosaurus* (as proposed by Denzer & Manthey 2016) is comprised of three distinct allopatric species: *Lophosaurus dilophus* from Papua New Guinea and surrounding islands; *L. boydii* from north Queensland; and *L. spinipes* from central coastal New South Wales through to southern coastal Queensland. The three species are quite distinct, and range in habitat from temperate rainforest in the south to tropical rainforest for the two northern species. There is also an obvious inverse relationship between latitude and size from south to north.

Investigations into the morphometrics, diet and reproductive characteristics of the three species using wet preserved specimens from two Australian museums (Australian Museum; Sydney & Queensland Museum, Brisbane) have commenced. The limited number of viable specimens available have been examined and dietary data for *L. boydii* and *L. dilophus* has been collected. The paucity of usable specimens is a limiting factor at this juncture, with many having either been previously eviscerated resulting in the material being unavailable for analysis, or there has been insufficient collection data.

Preliminary results show an interesting emerging trend—the apparent size of prey. In both of the northern species, despite being rather robust species, the predominant food items appear to be ants (Hymenoptera) and small beetles (Coleoptera), especially weevils (Curculionidae).

Morphological convergence in bouldering frogs

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Shared selective pressures can drive evolutionary optimization towards the same solution multiple times, leading to convergence. Therefore, it is common to observe convergent morphotypes in species from different lineages that share a similar ecotype. Australia is home to 18 species of microhylid frogs of the genus *Cophixalus*, which are restricted to the tropical north-east. While most of these frogs are minute species that live in the leaf-litter of rainforest habitat on cool and wet mountaintops, five recently described species live in a starkly different habitat—giant boulder-fields. These are huge piles of granite boulders, often hundreds of metres high, that typically have very little vegetation. The boulder species are all much bigger than the rainforest species, averaging three times their body length and 15 times their mass. Interestingly, phylogenetic data shows that boulder species are far from each other's closest relatives, showing a clear example of parallel evolution in a particular habitat. Here we used a 3D geometric morphometric approach with x-ray micro CT scan data of the skull and several bones of boulder-field and rainforest species. We tested whether boulder-field and rainforest species differed in shape as well as size, their unique morphological adaptations, and the degree of morphological convergence in each bone and overall body shape. We found that morphological convergence was striking between these three independent boulder-field clades. As well as being three times larger than the rainforest species, they displayed unique shape adaptations relevant to their environment. We discuss their morphological convergence in the context of selective pressures imposed by the functional and physiological requirements of boulder fields. We hypothesize that their much bigger size might help reduce water loss through the skin, and work as an anti-predatory mechanism. Similarly, their unique morphology would enable them to successfully navigate through the complicated boulder piles.

Effects of life-history stage on upper thermal tolerance in McCann's skink (*Oligosoma maccanni*)

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Identifying the upper thermal limits of animals is important for predicting how species will cope with climate change. Sub-lethal thermal limits such as voluntary thermal maximum (VTmax - the temperature at which an animal seeks shelter), and critical thermal maximum (CTmax - the temperature at which a righting response is lost), are especially useful as they reflect how behaviour and ecophysiology are affected at high temperatures. However, most studies that measure these limits do not include all life-history stages, often omitting

reproductive females and juveniles. We measured VTmax and CTmax in McCann's Skink (*Oligosoma maccanni*), a small (~ 5 g), diurnal and viviparous New Zealand skink. We compared four life-history stages: pregnant females, postpartum females, males and juveniles. We also assessed the neonates delivered by pregnant females to determine whether exposure to thermal limits in utero had affected their viability. To our knowledge, these are the first measurements of VTmax and CTmax in a pregnant viviparous squamate and the first such measurements in a New Zealand reptile. We found that both VTmax and CTmax differed significantly between some life-history stages. Mean VTmax was between 33–34° C and mean CTmax between 40–42° C. Notably, CTmax was lower in pregnant females than in postpartum females, indicating that pregnancy reduces thermal tolerance. There were also no discernible effects on the sprint speed or mass of neonates that underwent thermal tolerance testing in utero. Our results have implications for understanding the effects of climate change on viviparous lizards, as the upper thermal limits of species may be overestimated if all life-history stages are not considered.

Adaptive resistance to chytridiomycosis is life-stage dependent in an imperiled anuran

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Declines of amphibians caused by the emergent disease chytridiomycosis have been severe, but populations of some susceptible species have persisted or even recovered. Recent research suggests that resistance to the causal agent of the disease, *Batrachochytrium dendrobatidis* (Bd), could result from the selection for alleles of the adaptive immune system. During metamorphosis, however, amphibian immune systems may not be fully functional, indicating that an effective adaptive immune response to Bd may be life-stage dependent. We evaluated the susceptibility of the relict leopard frog (*Rana onca* = *Lithobates onca*) sourced from two areas that currently differ in exposure to Bd. Frogs sourced from an exposed population show greater resistance to the pathogen than frogs sourced from an area where Bd has not been detected. To assess whether this population-level resistance manifests across life-stages, we conducted challenge experiments assessing susceptibility of *R. onca* undergoing metamorphosis or as older juveniles. We found that older juvenile frogs were susceptible to chytridiomycosis, but the degree of susceptibility varied depending on source area. Juveniles sourced from the population exposed to Bd experienced significantly greater survivorship and cleared infections in higher proportions than those sourced from an area without Bd. We observed low survivorship of frogs exposed to Bd as late stage tadpoles and again at metamorphosis, regardless of source area. We speculate that the development of resistance characteristics that do not manifest at each life-stage is a result of seasonal temperatures that modulate the effects of Bd. When frogs are undergoing metamorphosis, summer temperatures may prevent lethal Bd infections, while older frogs are subjected to the selective pressures of Bd

in cooler months when animals are immunocompetent. Host life-history, selective pressures from Bd, and environmental temperatures appear to be shaping *R. onca* adaptation to Bd.

Species delimitation of genus *Sphenomorphus* in elevated mountains in Taiwan

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With high level of isolation, species living in elevated mountains often represent restricted gene flow between populations and form highly differentiated geographic structure. The effects of genetic drift and adaptation in different mountains further promote speciation. This concept, known as “sky islands”, has attracted the attention from taxonomists and evolutionary biologists. *Sphenomorphus taiwanensis*, a small-sized skink, is widely distributed in high mountains of Taiwan and shows potential genetic differentiation among populations. By using SNPs data from ddRADseq, we investigate the phylogeny, genetic structure, and gene flow among populations which helped to reconstruct the evolutionary scenario of the lizards on these “mountain islands”. We discovered a unique lineage with great genetic distance from other lineages, with the morphological differentiation also matches with the genetic evidence. This finding suggested the under-estimation of species diversity within this species group. In order to figure out the mechanism of this high genetic diversity, we will use F_{st}-based method to figure out candidate loci which are correlated to disruptive selection, and further investigate if the genetic distance between populations is correlated with environment factors (IBE-isolation by environment) or geographic distance (IBD-isolation by distance).

Assessing the suitability of captive-reared lizards in a translocation program for the Pygmy Bluetongue Lizard (*Tiliqua adelaidensis*)

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The Pygmy Bluetongue Lizard (*Tiliqua adelaidensis*) is a medium sized skink that was thought to be extinct until the early 90’s. Since its rediscovery a significant amount of research has been conducted to improve long-term conservation of the species. These lizards exclusively occupy spider burrows in the native grasslands of South Australia. A major threat to the species is habitat fragmentation and a change in habitat suitability under future climate change predictions. If habitat in their current range becomes unsuitable they do not have the capacity to disperse into new suitable habitat. The Gardner lab has conducted research to develop a ‘risk assessment’ of translocation as a management tool for this species. A successful breeding program has been developed for this species at Monarto Zoo in South Australia which has the potential to produce lizards that can be translocated into suitable habitat. Captive-reared lizards

have the potential to be utilised in future translocation programs, however due to differences in diet, habitat and exposure to potential predators, time in captivity may affect the outcome of a translocation. In this talk I will focus on one way in which captivity may influence translocation success, which is the potential for time in captivity to influence a lizards microbiome. Gut microbes have not only been shown to affect the health and behaviour of their host but can also differ between wild and captive populations of a species. To date, the potential influence of an individual's microbiome has not been considered in a translocation program of this kind. In this study we are monitoring wild and newly translocated captive lizards monthly, collecting faecal samples from each lizard, in order to assess their microbiomes and how these change over the course of a lizard activity season (Sep-Mar).

How old is my frog?—Aging amphibians using skeletochronology

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Chytridiomycosis is an emerging disease of amphibians which has been implicated in declines and extinctions worldwide, caused by the fungus *Batrachochytrium dendrobatidis* (Bd). The true effect of Bd on amphibian populations may go unnoticed as some populations persist after pathogen arrival. Ongoing disease driven mortality within persisting populations will change their demography, so investigating age structure complexity can reveal the unseen effect of Bd infection. Skeletochronology is a technique that utilises annual growth patterns of long bones to gain an estimation of the age of an animal. Skeletochronology is applicable in ectothermic animals which undergo discrete annual activity cycles. Preparation of histological specimens requires optimisation of cutting and staining methodologies. Factors that may lead to over or under-estimation of age, such as metamorphosis or injury, must be considered to ensure accurate age estimation. This project aims to optimise the preparation of histological specimens for age analysis, and use these techniques to determine the age structure of Bd infected populations. Understanding demographic effects of disease can inform conservation management to reduce the risk of population extirpation.

The role of sloughing on the pathophysiology of chytridiomycosis

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The lethal skin disease Chytridiomycosis is caused by the fungal pathogen *Batrachochytrium dendrobatidis* (Bd), and has been linked to worldwide amphibian population declines. Bd disrupts the skin's physical structure, and ionic and osmotic function. Infected amphibians increase the rate of skin shedding (sloughing) in an attempt to remove the fungus before the onset of chytridiomycosis. However, the cumulative impact of increased sloughing frequency and the disruption of skin function by Bd may interact to reduce the overall physiological health of the animal. This talk will provide important background information for my following poster on what sloughing is, and what is known about the pathology of chytridiomycosis. The aim of this study is to understand the mechanisms of cutaneous skin disruption from Bd infection, and how sloughing may further disrupt skin function in susceptible amphibians.

Unravelling the pathogenesis of chytridiomycosis

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Amphibians are at the forefront of the current global biodiversity crisis, with declines and extinctions due in part to the emergence of a novel fungal skin disease, chytridiomycosis. The cause of death has been linked to the disruption of the skin function and low electrolyte levels in the body. Amphibians increase skin shedding rate (sloughing) to slow pathogen growth. However, sloughing also causes physiological changes in the skin function, specifically cutaneous ion transport. Thus, sloughing may act as a double edge sword, where in the process of removing the pathogen, it may exasperate the effects of cutaneous sodium loss. We hypothesised that infected Green Tree Frogs, *Litoria caerulea* would show a reduction or inhibition of epithelial ion transporters, which are responsible for regulating normal skin function and internal electrolyte balance. We also predicted that during sloughing infected frogs would demonstrate an increase in cutaneous sodium loss, and greater electrolyte imbalance indicating a potential susceptible period which ultimately leads to hyponatremia. We show that non-sloughing frogs with chytridiomycosis have impaired cutaneous sodium uptake, in part because they have fewer sodium transporters in their skin. Interestingly, sloughing was associated with a transient increase in sodium transporter activity and abundance, suggesting that the newly exposed skin layer is initially fully functional until the recolonization of the skin by the fungus again impedes cutaneous function. However, the temporary restoration of skin function during

sloughing does not restore ionic homeostasis, and the underlying loss of ion uptake capacity is ultimately detrimental for amphibians with chytridiomycosis.

To call or be silent: reproductive strategies of Cane Toads

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Anuran mating systems can be categorised into chorusing and scramble competition, which occurs is related to the length of the breeding period (prolonged or explosive). Cane Toads, (*Rhinella marina*), clearly have prolonged breeding, but the literature is unclear about their mating system. To examine how male cane toads' mating behaviour responds to environmental circumstances, we recorded toad activities (calling, searching, holding, emitting release calls, and amplexus) in response to playbacks of single calls and choruses, at five different breeding ponds. In response to playbacks, male toads became active and increased searching activity for mates, by swimming around and attempting to hold various objects, but calling was not initiated by playback. We also found that the behaviours we observed depended on whether playbacks consisted of choruses or single calls. Active searching increased more response to a chorus than a single call, and more males and females engaged in amplexus when choruses were played. Because male vocalisations are used mainly to attract gravid females, it is suggested that silent males hearing calls may initiate searching, as males were expecting to intercept arriving females, particularly when they detect a chorus. Therefore, increased searching rate in response to the sound of other males calling may allow silent males to increase their probability of engaging in amplexus.

Does behaviour differ between colour morphs of the Delicate Skink?

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Colour polymorphism refers to one population having multiple distinct colour morphs. This is seen in the Delicate Skink (*Lampropholis delicata*) in regards to the presence or absence of a white mid-lateral stripe. The striped morph is most frequent in northern Australia, while the plain morph is most frequent in southern Australia. The reasons for the distribution and maintenance of the Delicate Skink's colour polymorphism are currently unknown, but in many taxa behaviours such as exploration and boldness have been shown to differ between morphs. The aim of this study was to determine if behaviour, specifically boldness and exploration, differed between striped and plain morphs. Exploration and boldness were each tested twice for

striped ($n = 40$) and plain ($n = 40$) male lizards, collected from Brisbane. Exploration was tested by placing lizards in a test arena separated by a barrier. The time taken to cross the barrier was recorded as a measure of exploratory behaviour. Boldness was measured by placing lizards in an arena with a refuge and basking site. The time taken to re-emerge from a shelter, and total time sheltering and basking, were recorded after a stimulated predatory attack. It was found that levels of exploration, but not boldness, differed between morphs ($p = 0.024$) with striped lizards being more exploratory. Exploration possibly differed due to the heat-reflecting ability of the white stripe, as white skin colouration absorbs less radiant heat than darker colouration. Therefore, the white stripe may reduce the heat absorbed, allowing a lizard to be more active and explorative with lower risk of over-heating, in warmer climates.

Relative potency of multiple snake-venoms on cat, dog, and human blood plasma

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Snakebite is a regular occurrence for Australian domestic pets and can be fatal. The eastern brown snake (*Pseudonaja textilis*) is an abundant snake in suburban areas on the east coast of Australia and is responsible for an estimated 76% of reported snakebite cases to domestic pets nationally each year, with the primary pathology being disruption of hemostasis. Surprisingly, while 31% of dogs survive brown snake bites without antivenom, cats survive more than twice as many bites (66%), but why this is the case is unknown. Consequently, we tested the relative coagulopathic effects of *P. textilis* venom on cat, dog, and human plasma for comparison. Furthermore, to elucidate the potential immunocapacity of cat or dog plasma to various coagulotoxin types, we tested the effects of multiple snake venoms representing/containing different types of coagulotoxins on cat and dog plasma compared to effects observed on human plasma. We found that cat plasma was no more resistant than dogs to coagulotoxins of most procoagulant snake venoms. Cat plasma displayed some resistance to only one snake venom: the West African Saw-scaled Viper (*Echis ocellatus*). Dog plasma consistently clotted quicker than cats, including in baseline tests, which may explain the greater vulnerability of dogs to coagulotoxins and may therefore skew clinical pathologies. This research helps us better understand the clinical pathologies displayed in envenomed cats and dogs and therefore has important implications in reducing cat and dog deaths from snakebite.

Using pheromones to understand and resolve cryptic lizard diversity

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With over 800 lizard species currently recognised, Australia hosts 12% of global lizard diversity—more than any other country in the world. But even this figure underestimates Australia's true lizard diversity. Genetic studies indicate that many of what we regard as single species are actually complexes of several morphologically similar species, referred to as 'cryptic species'. Cryptic species appear visually identical yet are often reproductively isolated in areas of overlap. How they maintain reproductive isolation is unclear because the mating signals of lizards are largely unknown; hence, our understanding of mate choice and speciation in lizards is poorly understood. Considering that these cryptic lizard species are, by definition, visually similar, we hypothesise that pheromones serve as a mating signal in many cryptic lizard taxa. To test this, we first used gas chromatography to characterise putative pheromones from 22 genetically divergent lineages of the Bynoe's Gecko (*Heteronotia binoei*) species complex across northern Australia. Multivariate analyses of pheromone blends and morphology indicate that pheromones are lineage-specific and that pheromones have diverged relatively more than morphology. We next performed behavioural assays to assess the influence of putative pheromones on female choice, confirming that female *Heteronotia* discriminate among the scents of sympatric males, and typically sniff conspecific scents longer. These results suggest that pheromone data may unlock the tremendous 'cryptic' diversity currently being uncovered in many lizard groups.