Australasian Evolution Society and Phylomania Combined Conference 2017

Abstracts and Attendees
Maths & Physics Building,
University of Tasmania, Hobart
December 4-8

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Abstracts

Sarah Aamidor, University of Sydney: Sex

“Stranger things”: Gynandromorphs and androgenesis in honey bees *Apis mellifera*

Sarah E. Aamidor, Boris Yagound, Isobel Ronai, Benjamin P. Oldroyd (Behaviour and Genetics of Social Insects Laboratory, University of Sydney, NSW, 2006)

Haplodiploid sex determination occurs in all members of the order Hymenoptera (bees, ants and wasps). Under this system, females arise from fertilised (diploid) eggs while males arise from unfertilised (haploid) eggs. The cytogenetic mechanisms underlying haplodiploidy enable peculiar phenomena such as thelytoky (female cloning), androgenesis (male cloning) and gynandromorphs (sex mosaics). We serendipitously sampled 9 gynandromorph honey bee (*Apis mellifera*) workers from a colony in Richmond NSW and subjected them to microsatellite analysis to determine the parentage of tissues such as wing, eye, tongue, sting, ovary and testis. We morphologically assessed the likely sex of each tissue prior to DNA extraction. For example, males have short tongues and workers long tongues. We found that different tissues had different combinations of at least two parental origins. One individual had at least three fathers. Remarkably, one worker, was phenotypically female throughout, but had no maternal alleles. This bee apparently arose from the fusion of two sperm nuclei (i.e., androgenesis). We also found that some gynandromorphs contained queen-like ovaries which suggest there had been a breakdown in the pathways of caste determination. Overall, our results show that when gynandromorphy occurs, unusual biological phenomena can also arise. These phenomena act as an exaptation for the evolution of some of the more bizarre social systems seen in some ants, such as species where queens and males are produced asexually, and workers sexually.

Daej Arab, University of Sydney: Posters

Phylogenetics of cockroaches and termites based on genomic data from the obligate endosymbiont *Blattabacterium cuenoti*

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Cockroaches are among the most recognisable and widespread insects in the world, and include the eusocial termites. There are more than 4000 species (representing 9 families) of cockroaches worldwide, plus a further ≈4000 termites. Despite numerous studies of cockroach phylogenies in recent years, relationships among a number of the major lineages are yet to be resolved. Almost all cockroaches as well as the termite *Mastotermes darwinensis* harbour the obligate endosymbiont *Blattabacterium cuenoti* (hereafter *Blattabacterium*) in highly specialised cells in their fat bodies. These bacteria are vertically transmitted from mother to offspring and their phylogenetic relationships have been shown to match those of their hosts. We obtained new genomic data from *Blattabacterium* strains of 80+ different species of cockroaches, including >100 protein coding genes, and combined them with previously published genomic data for 10 strains. Phylogenetic analyses were performed using these data, as well as mitochondrial genomes from the same taxa. These analyses represent the most comprehensive analyses of cockroach phylogenetic relationships to date. Our results indicate that the cockroach family Corydiidae is sister to a clade containing *Blattidae*, *Cryptocercidae*, termites (*Isoptera*), *Tryonicidae*, *Anaplectidae*, and *Lamproblattidae*. These results have implications for understanding the evolution of social behaviour among *Cryptocercidae* and termites. We found for the first time high support for relationships among a number of *ectobiid* lineages. Two *Blattabacterium* lineages show signs of accelerated sequence substitution rates.

Fabien Aubret, Station d’Ecologie Expérimentale et Théorique du CNRS à Moulis: Climate Change

Altitudinal colonisation and adaptability to hypoxia: an ignored constraint of climate change on biodiversity

Jérémie Souchet*, Gaelle Micheli*, Coralie Bossu* & Fabien Aubret* * SETE CNRS, UMR5321, 09200 Moulis, France

Climate change is driving many species to migrate along the altitudinal gradient of mountainous landscapes. While the impacts of temperature shifts on range expansion are well established, the effects of altitude-related hypoxia on the ability of organisms to colonize and adapt to higher altitudes during warming have, to our knowledge, not received scientific interest. Specifically, the short, medium and long term effects of acute and chronic hypoxia on the growth, survival, reproductive biology and colonization dynamics of animals reaching higher altitude refuges remain unknown. Here we show preliminary results on the effect of altitude related hypoxia on embryo development, hatching success and hatchling phenotype in snake eggs (*Natrix maura*). We incubated 12 clutches (113 eggs) using a split-clutch design either at low altitude (412m; Moulis) or high altitude (2877m; Pic du midi; 30% less oxygen). Hypoxia generated greater egg mass loss, increased embryo metabolic rates (heart beats) and a slightly shorter incubation period. While hatching success was unaffected, hatchling were born smaller in size and body condition. Locomotor performances were also strongly affected. Results will be discussed in the face of climate change, colonisation dynamics and reproductive success along the altitudinal gradient.

Jannike Axelsson, University of Gothenburg: Life History & Physiology

Thermal effects on telomeres in sand lizards

Jannike Axelsson, Mats Olsson, University of Gothenburg, Department of Biological and Environmental Sciences

Telomeres, the protective, terminal parts of the chromosomes, can in many organisms reflect aspects of age and sometimes longevity. Telomere erosion occurs during cell division, or by oxidative damage by ROS and elevated temperatures. Ectotherms rely on ambient temperatures for maintaining their body temperature, regulated through behavioural thermoregulation. Their temperature dependant metabolism, hence also the ROS production, is indirectly regulated through thermoregulation. Consequently, with the potential causal chain temperature-metabolism-ROS production-telomere erosion, ectotherms may constitute good models for analysing thermal (climate) effects on telomere biology. Telomere length was measured on sand lizards (*Lacerta agilis*) through qPCR of blood samples from 1998-2006. Correlative effects of climatological parameters on telomere length where analysed using Proc Mixed in Statistical Analysis Software 9.4. During the lizards' active period, the correlative effects of mean temperature and sun hours on telomere length were significantly negative. This trend was completely opposite during the lizards' inactive period; telomere length covaried positively with both these weather parameters. In conclusion, we found that telomere dynamics are affected by environmental factors, but differently depending on season. Thus, indicating that if there is an optimum in weather conditions for telomere maintenance, this might be influenced by the individual's current activity level.

Julian Beaman, The University of Queensland: Macroevolution 1

Evolution of allometric scaling: limited evolutionary potential for mass-dependence of metabolic rate

Julian Beaman (The University of Queensland); Daniel Ortiz-Barrientos (The University of Queensland); Craig R. White (Monash University)

Most phenotypic traits correlate with body size, the consequences of which permeate levels of biological organisation from physiological rates to ecological interactions. Understanding the mechanistic basis of the allometric relationship between body mass and metabolic rate in particular has been the focus of intense research. Evidence demonstrates that there is significant macro-evolutionary variation in the allometric slope for metabolism. Yet until now there have been no estimates of the evolutionary potential of metabolic scaling relationships. Here we use a quantitative genetics approach and demonstrate for the first time that there is a very small but significant amount of additive genetic variance for the mass-dependence of metabolic rate. Relative to the genetic variance in allometric slope however, there is vastly more genetic variance in growth rate and adult mass. Furthermore, the allometric slope is genetically correlated with growth rate. More work is needed to determine whether the observed patterns of genetic variation and evolution of metabolic scaling have arisen as a consequence of mechanistic constraints, correlational selection, or both.

Julian Beaman, The University of Queensland: Posters

Evolution of plasticity: mechanistic link between development and reversible acclimation

Julian Beaman (The University of Queensland) Craig R. White (Monash University) Frank Seebacher (University of Sydney)

Phenotypic characteristics of animals can change independently from changes in the genetic code. These plastic phenotypic responses are important for population persistence in changing environments. Plasticity can be induced during early development, with persistent effects on adult phenotypes, and it can occur reversibly throughout life (acclimation). These manifestations of plasticity have been viewed as separate processes. Here we argue that developmental conditions not only change mean trait values but also modify the capacity for acclimation. Acclimation counteracts the potentially negative effects of phenotype-environment mismatches resulting from epigenetic modifications during early development. Developmental plasticity is therefore also beneficial when environmental conditions change within generations. Hence, the evolution of reversible acclimation can no longer be viewed as independent from developmental processes.

Perry Beasley-Hall, University of Sydney: Posters

Ecological speciation and the evolution of soil burrowing behaviour in Australian giant cockroaches

Perry G. Beasley-Hall(1), Timothy R. C. Lee(2), Harley A. Rose(1), Nathan Lo(1) 1) School of Life and Environmental Sciences, University of Sydney, Sydney NSW 2006 2) Australian Museum Research Institute, 1 William Street, Sydney NSW 2010

It is not uncommon for separate lineages of organisms to develop similar evolutionary solutions to challenges in their environment. This scenario, termed parallel evolution, has key implications for the debate regarding the predictability of evolution. We have recently discovered an example of parallel evolution across two subfamilies of wood-feeding (*Blaberidae: Panesthiinae*) and soil-burrowing (*Blaberidae: Geoscapheinae*) cockroaches that appears to have been driven by ancient climate change. Here, we construct environmental niche models to investigate if specific environmental factors have contributed the evolution of soil-burrowing behaviour, and whether the speciation mode of geoscapheines from panesthiine ancestors involved niche conservatism or divergence. Our results are consistent with soil-burrowing behaviour evolving in response to ancient aridification events in Australia following the arrival of the *Panesthiinae* from Asia 20 Mya. Our results suggest a scenario of ecological speciation leading to subsequent niche divergence in the *Geoscaphinae*.

Eleanor Beavan, The Australian National University: Macroevolution 2

Understanding rates of molecular evolution in eucalypts

Eleanor Beavan, Robert Lanfear

The rate of molecular evolution varies considerably across the tree of life, but the causes of this variation remain uncertain. We compiled a dataset of over 700 species of eucalypt to investigate links between the rate of molecular evolution and four key life-history traits: height, specific leaf area, seed mass and genome size. We show that the rate of molecular evolution in the chloroplast genome is positively correlated to both height and genome size. We also show that the rate of molecular evolution is negatively correlated with seed mass. These results highlight interesting differences in the correlates of molecular evolution in eucalypts and other angiosperms.

Nick Beeton, University of Tasmania: Ancestral States

Linearising is so PASSÉ: Approximating BiSSE for large trees

Nick Beeton, Larry Forbes, Steve Walters, Greg Jordan, Barbara Holland

Analysing phylogenetic trees using a Binary-State Speciation and Extinction (BiSSE) model is a useful way to test for the presence of trait-based selection in the evolutionary process, and for ancestral state reconstruction. However, calculating likelihoods in BiSSE requires numerical integration along every edge of the tree, meaning that the process is slow, and becomes slower proportional to tree size. We introduce the Perturbation Approximation of State-based Speciation and Extinction (PASSÉ) model. Our approach uses a naÕËve approximation to BiSSE which has a known analytic solution, negating the need for numerical integration but introducing error to the process. We show that despite the error, the model can be used to detect trait-based selection in very large trees (10,000 tips and up) which would be infeasible with BiSSE. We then further explore the advantages, disadvantages and possible uses of the model.

Jacob Berson, The University of Western Australia: Sexual Selection

Sex-dependent evolution of an olfactory display trait: experimental evidence that sexual selection drives the evolution of cuticular hydrocarbons in a dung beetle

Jacob D. Berson(1), Francisco García-González(1, 2) and Leigh W. Simmons(1); Author Affiliations: (1) Centre for Evolutionary Biology, School of Biological Sciences, The University of Western Australia, Crawley, Western Australia 6009, Australia; (2) Present address: Doñana Biological Station, Spanish Research Council CSIC, Sevilla, Spain

Darwin argued that the effects of sexual selection would differ between males and females, leading to divergent evolution of the sexes. This argument is now widely accepted, and multiple studies have found sexual selection to be acting on sexually dimorphic secondary sexual traits. Though the contemporary action of sexual selection implicates its role in the phenotypic divergence of the sexes, it does not exclude the potential influence of natural selection. Experimental evolution studies that control the effects of natural selection, whilst varying the degree of sexual selection, are therefore required to test if sexual selection does indeed lead to divergent evolution of the sexes. We conducted such an experiment using the dung beetle, *Onthophagus taurus*, to examine the role of sexual selection in the sex-dependent evolution of an olfactory display trait, cuticular hydrocarbons (CHCs). Cuticular hydrocarbons are sexually dimorphic in many insect taxa, and male CHCs are subject to sexual selection in at least some species, including *O. taurus*. However, consistent with secondary sexual traits more generally, there is very little evidence that the CHC profiles of the sexes respond differently to sexual selection, and the ultimate cause of the widespread sexual dimorphism in CHCs remains elusive. We measured the CHCs of both sexes after six, 12 and 21 generations of either enforced monogamy or polygamy. We found sex-dependent evolution in response to sexual selection, providing direct evidence for its role in the evolution of sexual dimorphism in this sexual display trait. Interestingly, the divergence under sexual selection was largely due to the evolution of female CHCs, suggesting the operation of sexual selection on both sexes. Males and females responded to the removal of sexual selection by evolving CHC profiles of likely improved water-proofing properties, suggesting the antagonistic action of natural and sexual selection on *O. taurus* CHCs.

Nicole Bezemer, University of Western Australia: Phylogeography

Genetic structure in *Eucalyptus caesia*, a bird-pollinated tree endemic on granite outcrops, revealed by exhaustive microsatellite genotyping of seven populations

Nicole Bezemer1,2, Siegfried Krauss1,2, David Roberts1,2, Ryan Phillips2,3 and Stephen Hopper1,2; 1University of Western Australia, 2Botanic Gardens and Parks Authority,3 Australian National University

Population genetic theory predicts that small, isolated plant populations will undergo a rapid loss of genetic diversity through natural selection, increased genetic drift and inbreeding, as a by product of self-pollination or mating between close relatives. On the other hand, bird pollination is predicted to facilitate genetic connectivity between fragmented populations. The apparently bird-adapted *Eucalyptus caesia* occurs as small, isolated populations in the Wheatbelt Region of Western Australia and is a model system to investigate these issues. Studies have shown that *E. caesia* populations have low genetic diversity and are strongly differentiated, and based on chloroplast and nuclear evidence there is no significant association between population differentiation and geographical distance. We aimed to test whether these conclusions stand, and assess population genetic structure, through exhaustive microsatellite genotyping of all individuals comprising seven populations using 15 polymorphic loci (total $n = 1300$). Heterozygosity varied across populations (H_O = 0.17 $\pm$ 0.07 to 0.54 $\pm$ 0.05), and generally speaking larger populations had higher levels of genetic diversity. Levels of inbreeding assessed by fixation indices were variable between populations (F = -0.295 pm 0.20 to 0.07 pm 0.02) and not clearly related to population size. Analysis of Molecular Variance (AMOVA) revealed that 36 % of variation occurred among populations. Pairwise population F_{st} values ranged from 0.05 - 0.45, and G_{st} ranged from 0.16 - 0.69. Principle Components Analysis supported high differentiation between populations, with Boyagin forming the most discrete cluster in the ordination plot. In contrast to previous research using nuclear RFLP, our microsatellite data show evidence for isolation by distance. Genotypic distance and geographic distance were significantly correlated (R^2 = 0.311, P = 0.001). We also found evidence of genetic structuring within populations. The results of our genetic survey have implications from a conservation management perspective. Strongly differentiated populations may experience outbreeding depression, which could explain the apparent lack of gene flow, despite having highly mobile bird pollinators that demonstrably move pollen between fragmented populations of other plant species. Other mechanisms to cope with low genetic diversity, such as purging of deleterious recessive alleles, enhanced resilience or cytogenetic adaptations, may be in play. For trees such as *E. caesia* with naturally insular population structures, conservation of all populations is likely necessary to conserve species genetic diversity.

Nicole Bezemer, University of Western Australia: Posters

Sex on the Rocks: Recruitment of a Tree Endemic on Granite Outcrops

Nicole Bezemer1,2, Siegfried Krauss1,2, David Roberts1,2 and Stephen Hopper1,2; 1University of Western Australia, 2Botanic Gardens and Parks Authority

Plant communities on granite outcrops are characterised by high biodiversity and endemism, and strong population genetic structuring. The floristic diversity and structure of inselberg flora receives much attention in international conservation research, yet our understanding of how recruitment influences population genetic structure of plants endemic to granite outcrops is limited. To determine the immediate genetic consequences of recruitment and to quantify mating and dispersal patterns by parentage analysis, we conducted an opportunistic study following a wildfire in a stand of the lignotuberous tree *Eucalyptus caesia* (*Myrtaceae*) at Boyagin Nature Reserve. The entire adult stand ($n = 180$) plus seedlings ($n = 115$) were genotyped with 14 microsatellite loci. Compared to adults, seedlings had low heterozygosity and a high inbreeding co-efficient, but similar levels of allelic diversity. There was no evidence of post-germination selection against homozygous seedlings over the 20 month survey period. Seedlings that resulted from cross-pollination were more heterozygous than seedlings resulting from selfing, but could not be distinguished based on height measurements or survivorship. Parentage analysis in CERVUS revealed mostly limited seed dispersal, assuming that candidate parents closest to seedlings were the maternal parent. By comparison, pollen movement was more extensive, yet still restricted to plants within the stand. Recruitment has increased the population size, but appears insufficient to enhance genetic diversity in the Boyagin stand of *E. caesia*. Nonetheless, *E. caesia* appears adept at persisting as extremely small populations.

Isobel Booksmythe, Monash University: Sex

When to make males: the timing of sex and male production in Daphnia

Isobel Booksmythe, Monash University; Nina Gerber, University of Zurich; Dieter Ebert, University of Basel; Hanna Kokko, University of Zurich

Facultative sex avoids many hypothesized costs of sexual and asexual reproduction, while gaining benefits of both. However, this strategy brings with it a suite of additional life history traits to optimize, not least the frequency, timing and duration of sexual periods. These have flow-on effects on traits such as offspring sex allocation, with consequences for sex ratio dynamics that can feed back to affect the relative costs of sexual and asexual reproduction. So when should facultative sexuals invest in sex? We documented the dynamics of sexual reproduction and sex ratios in natural populations of *Daphnia magna* over their growing season, and disentangled the effects of population density and sex ratios on sex allocation with simple experimental manipulations. Sex was more common when its costs relative to asexuality were lowest: when population density was high, mortality rates increased, and asexual fecundity was low. Not unexpectedly, as males are necessary for sexual reproduction, the timing of sex exerted a strong influence on the sex ratio, with male production similarly predicted by high population density. However, sex allocation also responded to the current population sex ratio, with male production declining under more male-biased conditions.

Tom Botterill-James, University of Tasmania: Lightning Talks & Posters

Family aggression in a social lizard

Thomas Botterill-James[1], Ben Halliwell[1], Simon McKeown[1], Jacinta Silince[1], Tobias Uller[2,3], Erik Wapstra[1] and Geoffrey M. While[1*]; [1]University of Tasmania, [2]Lund University, [3]Oxford University

The evolution of family living is underpinned by conflict and cooperation between family members. However, our current understanding of family life is almost exclusively based on studies that only examine parent-offspring interactions. Here, we compared the level of aggressive interactions between siblings and between parents and offspring in the family living skink *Liopholis whitii*. Aggressive interactions occurred much more frequently between siblings and between fathers and offspring than between mothers and their offspring. These results suggest that ecological and social conditions that reduce conflict between siblings and between males and offspring will be fundamental in the evolutionary maintenance and diversification of family living in this and related lizard species.

Matilda Brown, University of Tasmania: Macroevolution 2

Out of place: anomalous conifer fossils

Matilda Brown (University of Tasmania); Nick Beeton (University of Tasmania); Tim Brodribb (University of Tasmania); Greg Jordan (University of Tasmania)

There are several southern hemisphere conifer fossils which have been derived from species that appear to have a different climatic niche to their extant relatives. This suggests that phylogenetic niche conservatism in conifers may be less strong than has been widely assumed. This project uses the Cenozoic fossil record of the southern conifers to develop a framework to quantitatively analyse these anomalies. This method is then used to examine possible associations with assemblage age, niche breadth and bioclimatic variables. To do this, the niches of the extant living relatives of co-occurring fossils were modelled and compared using the `hypervolume` package in R. For each anomaly (a pair of species for which the niches did not overlap), the distance and direction between the niches was extracted, and these data were used to calculate various taxon- and assemblage-based metrics. There was a strong negative correlation between anomalies and niche volume and a positive association with palaeoendemism. The results of this study imply that many anomalies in the southern conifer fossil record are a result of the simultaneous contractions in climatic niche and geographic range of palaeoendemic taxa. Thus, there is no evidence of niche expansion and the conifers included in this study are shown to be unlikely to expand their climatic niche in response to climate change.

David Bryant, University of Otago: Ancestral States

Dinner products and niche evolution

David Bryant, University of Otago

Diversity Inner Products (Dinner products) are an extension of inner products to sets, just as diversities are an extension of metrics. I will introduce dinner products via their axioms and give a complete characterisation of them in terms of inner products in a particular dual space. We have been exploring the geometry implied by these concepts, a geometry where 'lines' involve one shape morphing into another. Applying this mathematics to phylogenies, we show how to parsimoniously assign species niches to ancestral species, given niches at the leaves. We have been studying this problem as part of a general investigation into niche evolution.

Conrad Burden, The Australian National University: Population Genetics & Coalescent

Mutation in Populations Governed by a Galton-Watson Branching Process

Conrad Burden, The Australian National University

A population genetics model based on a multitype branching process, or equivalently a Galton-Watson branching process for multiple alleles, is presented. The diffusion limit forward Kolmogorov equation is derived for the case of neutral mutations. The asymptotic stationary solution is obtained and has the property that the extant population partitions into subpopulations whose relative sizes are determined by mutation rates. An approximate time-dependent solution is obtained in the limit of low mutation rates. This solution has the property that the system undergoes a rapid transition from a perturbation of the model with zero mutation rates to a phase in which the distribution collapses onto the asymptotic stationary distribution. The changeover point of the transition is determined by the per-generation growth factor and mutation rate.

Nathan Burke, University of New South Wales: Social 1 & Posters

Hanging with the wrong crowd? Juvenile exposure to males reduces female investment in asexual reproduction in a stick insect

Nathan W. Burke & Russell Bonduriansky, Evolution & Ecology Research Centre; School of Biological, Earth and Environmental Sciences; University of New South Wales

The rarity of asexual reproduction in animals is an unsolved evolutionary puzzle. One intriguing idea is that males could inhibit the evolution of asexuality by exposing asexual females to detrimental factors that reduce asexual reproduction. However, the effect of male factors on asexual reproduction is poorly understood. We used the spiny leaf stick insect, *Extatosoma tiaratum*, a species capable of both sexual and asexual reproduction, to examine the effect of male factors on asexual performance. We manipulated the developmental age at which females were exposed to male cues, and collected asexual eggs to measure hatching success. We found that eggs produced by females previously exposed to juvenile males during development had lower hatching success than eggs of non-exposed females. But, surprisingly, exposure to adult males at sexual maturity had no effect on hatching success. Our findings suggest that female investment in asexual reproduction is influenced by male factors experienced during development that signal the future likelihood of sex. We suggest that this early-life sensitivity to male cues may be adaptive because responsive females that withhold investment in asexuality may reallocate resources to sexual reproduction instead, thereby producing more offspring with higher genetic diversity.

Nathan Burke, University of New South Wales: Posters

Hanging with the wrong crowd? Juvenile exposure to males reduces female investment in asexual reproduction in a stick insect

Nathan W. Burke & Russell Bonduriansky, Evolution & Ecology Research Centre School of Biological, Earth and Environmental Sciences University of New South Wales

The rarity of asexual reproduction in animals is an unsolved evolutionary puzzle. One intriguing idea is that males could inhibit the evolution of asexuality by exposing asexual females to detrimental factors that reduce asexual reproduction. However, the effect of male factors on asexual reproduction is poorly understood. We used the spiny leaf stick insect, *Extatosoma tiaratum*, a species capable of both sexual and asexual reproduction, to examine the effect of male factors on asexual performance. We manipulated the developmental age at which females were exposed to male cues, and collected asexual eggs to measure hatching success. We found that eggs produced by females previously exposed to juvenile males during development had lower hatching success than eggs of non-exposed females. But, surprisingly, exposure to adult males at sexual maturity had no effect on hatching success. Our findings suggest that female investment in asexual reproduction is influenced by male factors experienced during development that signal the future likelihood of sex. We suggest that this early-life sensitivity to male cues may be adaptive because responsive females that withhold investment in asexuality may reallocate resources to sexual reproduction instead, thereby producing more offspring with higher genetic diversity.

Justin Cally, The University of Melbourne: Lightning Talks

Sexual selection mitigates population fitness decline in stressful environments: A meta-analysis of experimental evolution studies

Justin G. Cally*, Devi Stuart-Fox* and Luke Holman*; * School of BioSciences, The University of Melbourne, Parkville, Vic, Australia

Sexual selection may have positive or negative population fitness consequences. Theoretical studies have shown that sexual selection filters deleterious mutations and prevents population fitness decline under stressful environmental conditions. Alternatively, sexual selection may have negative fitness consequences due to sexual antagonism or maintenance of energetically expensive traits and behaviours. Here, we conduct a meta-analysis on over 60 experimental evolution studies measuring the effects of sexual selection on a range of fitness outcomes. Effect sizes comparing experimental lines that differed in opportunity for sexual selection varied substantially across species, studies and types of fitness outcomes. However, in stressful environments (e.g. elevated mutation load or sub-optimal food source) we find that sexual selection mitigates population fitness decline through improved reproductive success. Our research synthesis shows the population fitness benefits of sexual selection. These results have wide implications for experimental evolution, theoretical evolution and conservation biology.

Hayley Cameron, Monash University: Developmental Plasticity

Does within-brood variation in egg size affect fertilization success?

Hayley Cameron1, Keyne Monro1 and Dustin J. Marshall1; 1 Centre of Geometric Biology, School of Biological Sciences, Monash University, Melbourne, Victoria 3800, Australia.

Why do mothers produce offspring that vary in size? Within a single brood, mothers can produce offspring that vary by several fold in volume. While such variation might be adaptive in species with parental care (e.g. birds), the consequences of within-brood variation have been relatively unexplored in other taxa. In marine broadcast spawners, egg size and sperm concentration interact to affect the probability of sperm-egg collisions. Thus, the local sperm environment can drive selection on mean egg size, yet whether within-brood variation is similarly under selection remains unexplored. Here, we investigate phenotypic selection on within-brood variation in egg size using a broadcast spawning marine tube worm. We conduct laboratory experiments to measure the relationship between within-brood mean and variance in egg size on fertilization success (i.e., maternal fitness) across a range of sperm environments. We find that depending on the mean egg size of the brood, there can be both costs and benefits of within-brood variation for fertilization success (i.e., correlational selection).

Yao-ban Chan, The University of Melbourne: Networks

Inferring incomplete lineage sorting, duplications, transfers and losses with reconciliations

Yao-ban Chan (The University of Melbourne), Vincent Ranwez (Montpellier SupAgro), Celine Scornavacca (Université de Montpellier)

Gene trees and species trees can be discordant due to several processes. Reconciliations explain these discrepancies by mapping the gene tree into the species tree and explicitly accounting for these processes. Standard models of reconciliations consider macro-evolutionary events at the genetic level: gene duplications, losses and transfer. Another common source of gene tree-species tree discordance is incomplete lineage sorting (ILS), whereby gene divergences corresponding to speciations occur “out of order”. However, ILS is seldom considered in reconciliation models. In this talk, we present a unified formal IDTL reconciliation model which includes all of these processes. We show how to properly cost ILS under this model, and then outline a fixed-parameter tractable (FPT) algorithm that calculates the most parsimonious IDTL reconciliation, with guaranteed time-consistency of transfer events. Provided that the number of branches in contiguous regions of the species tree in which ILS is allowed is bounded by a constant, this algorithm is linear in the number of genes and quadratic in the number of species. This provides a formal foundation to the inference of ILS in a reconciliation framework.

Michael Charleston, University of Tasmania: Combinatorics

Tabu Sequences

Michael Charleston (UTAS) and Arndt von Haeseler (University of Vienna and Medical University of Vienna)

We investigate the properties of binary ℓ-sequences in which some motifs are prohibited or ”tabu”. More specifically, we exclude the ”00” motif. We show that the resulting so-called Fibonacci graph is still highly connected, but loses some important symmetries of the hypercube $\{0,1\}^{\ell}$. We provide a description of the *mutability* and steady-state distribution of the sequences in this space, and some initial thoughts on its consequences to the understanding of molecular sequence evolution.

Evatt Chirgwin, Monash University: Developmental Plasticity & Sex

How does parental environment influence the potential for adaptation to global change?

Evatt Chirgwin, Dustin J. Marshall, Carla M. Sgró, and Keyne Monro; School of Biological Sciences, Monash University

Adaptation to global environmental change will depend on genetic variation in traits under selection. While this variation is known to depend on environmental conditions within generations, its sensitivity to conditions in past generations is unclear. Using a marine tubeworm, we examined if the thermal acclimation of parents influenced the expression of additive and/or non-additive genetic variance in offspring fitness across current-day and elevated rearing temperatures during their most vulnerable life stage (survival to hatching). Our results suggest that parental environmental effects on offspring may have important evolutionary consequences as ocean temperatures rise.

Benny Chor, Tel Aviv University: Macroevolution 3

Ultra Conserved Protein Elements

Benny Chor, School of Computer Science, Tel Aviv University

Ultra conserved DNA elements are long segments of consecutive nucleotides in a genomic sequence, that are shared exactly (conserved with 100% identity) among a set of three or more species. In 2004, ultra conserved DNA elements (UCDEs) were discovered, and sparked extensive follow up research. This discovery has challenged a number of accepted views on the relations between conservation, function, and essentiality, as many UCDEs are located in “gene deserts”, away from any protein coding genes, and have no known function.

In this work, we expand the notion of ultra conservation to proteins. Ultra conserved protein elements (UCPEs) are amino acid sequences that are shared exactly (conserved with 100% identity and no gaps) among a set of three or more species. We considered five mammalian species: human, mouse, rat, cow, and dog. We found over 2600 clusters of proteins (one per species) with ultra conserved protein element of length 80 amino acids or more. Proteins containing these elements are enriched for tens to hundreds of (human) gene ontology (GO) terms, for tens of KEGG pathways, and for tens of Pfam domains.

It is not clear how to measure the “surprise” of having that many ultra conserved protein elements.

Tim Connallon, Monash University: Developmental Plasticity & Sex

Coadaptation of mitochondrial and nuclear genes, and the cost of mother’s curse

Tim Connallon (Monash U), M. Florencia Camus (U College London), Edward H. Morrow (U of Sussex), Damian K. Dowling (Monash U)

Strict maternal inheritance renders the mitochondrial genome susceptible to accumulating mutations that harm males, but are otherwise benign or beneficial for females. This “mother’s curse” effect can degrade male survival and fertility if unopposed by counteracting evolutionary processes. Coadaptation between nuclear and mitochondrial genomes – with nuclear genes evolving to compensate for male-harming mitochondrial substitutions – may ultimately resolve mother’s curse. However, males are still expected to incur a transient fitness cost during mito-nuclear coevolution, and it remains unclear how severe such costs should be. We present a population genetic analysis of mito-nuclear coadaptation to resolve mother’s curse effects, and show that the magnitude of the “male mitochondrial load” – the negative impact of mitochondrial substitutions on male fitness components – may be large, even when genetic variation for compensatory evolution is abundant. We also find that the male load is surprisingly sensitive to population size: male fitness costs of mito-nuclear coevolution are particularly pronounced in both small and large populations, and are minimized in populations of intermediate size. Our results reveal complex interactions between demography and genetic constraints during the resolution of mother’s curse, suggesting potentially widespread species differences in susceptibility to mother’s curse effects.

George Cunningham, University of Tasmania: Climate Change

Sex in a warming climate: predicting the influence of climate on offspring sex in snow skinks across Tasmania

George Cunningham (1), Lisa Schwanz (2), Geoff While (1) and Erik Wapstra (1); 1: The School of Biological Sciences, The University of Tasmania; 2: School of Biological, Earth and Environmental Sciences, The University of New South Wales

Species in which offspring sex is influenced by environmental temperature are predicted to be especially at risk from climate change. The magnitude of such responses may, however, vary among populations due to adaptation to local conditions. Understanding how these patterns vary across the landscape is hard to determine in practice, as long-term data are required from populations throughout a species range. Here we use an extensive, 16-year dataset to demonstrate divergence in the response of offspring sex to temperature between two populations of the Tasmanian skink *Niveoscincus ocellatus*. We present the results of an individual-based simulation model, based on a theoretical framework (Pen *et al.* 2010) and parameterised with data from the long-term study, to estimate the probability of a temperature effect on offspring sex in populations throughout the present-day climatic landscape of Tasmania. We extend the results of this model, using fine-scale climatic projections, to predict the likely long-term change in this distributional pattern as the Tasmanian climate continues to warm and populations adapt to new conditions.

Carmen Da Silva, The University of Queensland: Developmental Plasticity

Thermal acclimation in a rapidly fluctuating environment: the intertidal zone

Carmen da Silva (University of Queensland), Cynthia Riginos (UQ), Robbie Wilson (UQ)

Intertidal organisms from temperate and subtropical regions are exposed to wide daily and seasonal variation in temperatures. When daily variation equals or exceeds thermal change among seasons, theory suggests that ectotherms should not acclimate but should evolve wide thermal performance curves, allowing them to maintain performance over a wide range of temperatures. This assumes that daily variation masks seasonal shifts, which is not realistic in intertidal habitats; despite daily variation, mean, minimum, and maximum temperatures shift in predictable ways with season. Therefore, we expect intertidal organisms to maintain their capacity to acclimate. We tested this question using a subtropical intertidal goby, *Bathygobius cocosensis*, which lives in tide pools that vary widely — but predictably — over days and seasons. We exposed *B. cocosensis* to winter (12C - 17C) and summer (30C - 35C) thermal conditions for six weeks and then measured their burst swimming speed, maximum metabolic rate, routine metabolic rate, and ventilation rate over a range of six temperatures (12C - 36C). *Bathygobius cocosensis* exhibited an acclimation response for burst swim speed, maximum metabolic rate and metabolic scope and had wide thermal performance curves for all performance traits. Our data supports the hypothesis that acclimation can occur even where daily temperatures vary widely, as long as seasonal thermal shifts are predictable.

Isabel Damas Moreira, Macquarie University: Coevolution & Conservation

Learning Skills in an Invasive Lizard

Isabel Damas-Moreira (1), Ana Pereira (2), Daniel Oliveira (2), Joana L. Santos (2), Julia Riley (1), David James Harris (2), Martin Whiting (1); (1) Macquarie University, Sydney, Australia; (2) CIBIO InBIO, University of Porto, Portugal

In an era of global transport networks, invasive species are readily translocated. These species are frequently successful because of rapid local adaptation or plasticity. We investigated the potential role of animal cognition in determining invasive ability. Behavioural flexibility (the ability to change behaviour to solve novel problems or to solve existing problems in a novel way) and social learning (the ability to acquire new knowledge from other individuals) are hypothesized to have an important role during invasions, by helping individuals to cope with the challenges inherent to a new environment. We used *Podarcis sicula*, a small lacertid lizard that has successfully invaded multiple countries, as a model species. *P. sicula* has rapid evolution, and a remarkable ability to settle in new environments. We studied a population introduced to Lisbon, Portugal, in 1998, and tested its learning ability. Our preliminary results suggest that *P. sicula* have greater behavioural flexibility than closely related congeneric species that lack such invasive ability. Moreover, we also found that *P. sicula* uses social information from other lizards (both conspecifics and heterospecifics) to solve novel tasks. Collectively, our results highlight the important role of cognition during the invasion process.

Ruth Davidson, University of Illinois Urbana-Champaign: Combinatorics

A combinatorial method for connecting BHV spaces representing different numbers of taxa.

Jingwen Bi (University of Illinois Urbana-Champaign), Ruth Davidson (University of Illinois Urbana-Champaign), Michelle Delcourt (University of Birmingham), Rosemary Guzman (University of Illinois Urbana-Champaign), Cara Monical (University of Illinois Urbana-Champaign), José A. Sanchez (University of Illinois Urbana-Champaign), Yingying Ren (University of Illinois Urbana-Champaign), and Sihan Zha (University of Illinois Urbana-Champaign)

The phylogenetic tree space introduced by Billera, Holmes, and Vogtmann (BHV tree space) is a CAT(0) continuous space that represents trees with edge weights with an intrinsic geodesic distance measure. The geodesic distance measure unique to BHV tree space is well known to be computable in polynomial time, which makes it a potentially powerful tool for optimization problems in phylogenetics and phylogenomics. Specifically, there is significant interest in comparing and combining phylogenetic trees. For example, BHV tree space has been shown to be potentially useful in tree summary and consensus methods, which require combining trees with different number of leaves. Yet an open problem is to transition between BHV tree spaces of different maximal dimension, where each maximal dimension corresponds to the complete set of edge-weighted trees with a fixed number of leaves. We show a combinatorial method to transition between copies of BHV tree spaces in which trees with different numbers of taxa can be studied, derived from its topological structure and geometric properties. This method removes obstacles for embedding problems such as supertree and consensus methods in the BHV treespace framework.

David Duchene, University of Sydney: Macroevolution 3

New statistical criteria for exploring phylogenetic signal across the genome

David A. Duchêne 1, Jason G. Bragg 2,3, Sebastián Duchêne 4, Linda E. Neaves 5, Sally Potter 2,5, Craig Moritz 2, Rebecca N. Johnson 5, Simon Y. W. Ho 1, and Mark D. B. Eldridge 5 1 School of Life and Environmental Sciences, University of Sydney, Sydney, NSW 2006, Australia 2 Research School of Biology, Australian National University, Canberra, ACT 2601, Australia 3 National Herbarium of NSW, The Royal Botanic Gardens and Domain Trust, Sydney, NSW 2000, Australia 4 Centre for Systems Genomics, The University of Melbourne, Melbourne, VIC 3010, Australia 5 Australian Museum Research Institute, Australian Museum, 1 William Street, Sydney, NSW 2000, Australia

Genomic data present valuable opportunities for resolving the evolutionary relationships among taxa. However, complexities in the evolutionary process lead to heterogeneous signals across loci. We explore this heterogeneity by visualising differences among loci and identifying the number of gene-tree clusters in a data set. This approach exposes patterns in the data, such as the expectation from incomplete lineage sorting that there can be a few distinct phylogenetic signals across loci. We find that distinct signals are associated with the overall GC content of loci in a phylogenomic data set of marsupials. Another useful diagnostic for phylogenomic data is the heterogeneity in model performance across loci, because inferences can be biased when the model is incorrect. We turn to methods for assessing model adequacy and find that they can be powerful for describing phylogenetic signal, but determining appropriate thresholds for deeming the model as inadequate can be difficult.

David Duchene, University of Sydney: Posters

PhyloMAd: Efficient assessment of phylogenomic model adequacy

David A. Duchone 1, Simon Y. W. Ho 1 and Sebastian Duhcone 2 1 School of Life and Environmental Sciences, University of Sydney, NSW 2006, Australia, 2 Bio21 Molecular Science and Biotechnology institute, University of Melbourne, Melbourne, VIC 3010, Australia

Statistical phylogenetic inference plays an important role in evolutionary biology. The accuracy of phylogenetic methods relies on having suitable models of the evolutionary process. Various tools allow comparisons of candidate phylogenetic models, but assessing the absolute performance of models remains a considerable challenge. We introduce PhyloMAd, a user-friendly application for assessing the adequacy of commonly used models of nucleotide substitution and among-lineage rate variation. Our software implements a fast, likelihood-based method of model assessment that is tractable for analyses of large multi-locus data sets. PhyloMAd provides a means of informing model improvement, or identifying data that allow acceptable modelling in phylogenomic analyses.

Amy Edwards, La Trobe University: Sex

Maternal effects obscure condition-dependent sex allocation in changing environments

Amy M. Edwards: La Trobe University; Elissa Z. Cameron: University of Canterbury; Erik Wapstra: University of Tasmania; Jo McEvoy: University of Tasmania

Fluctuations in environmental conditions can impact population demography, such impacts are increasing with changing climates. Offspring sex ratios are a key life history characteristic, which respond to environmental conditions. In species with temperature-dependant sex determination, it is clear that changing climates may cause extreme sex ratio skews, however to date there has been little investigation into possible effects on animals with chromosomally determined sex. Here we discuss how vulnerable these species may also be in unpredictable environments. Maternal effects during gestation influence the development of offspring, and can lead to lifelong physiological changes. These changes may be adaptive if the offspring can respond suitably to environmental conditions. However, if the environment changes, a mismatch between the pre- and post-natal conditions may result in the anticipatory maternal effects being detrimental, as the offspring is prepared for a different environment. Maternal effects do alter sex ratios; here we discuss whether this is due to an anticipatory maternal effect, by experimentally manipulating the gestational environment, and then breeding the female offspring in an environment that was either matched or mismatched to her environment during development. Offspring sex ratios are expected to vary with maternal condition where fitness returns are sex-specific. Females with matching environments displayed the predicted positive relationship between body condition and sex ratio, but females breeding in mismatched environments did not. Thus, the predicted condition-sex ratio relationship is obscured by anticipatory maternal effects when the environment changes, which may explain why some studies find unexpected sex ratio effects when developmental history is unknown. This may also explain why biased sex ratios are often seen in captive breeding and reintroduction programs, and presents evidence that such unpredicted effects may become more common with increasing environmental changes.

Amy Edwards, La Trobe University: Posters

Cryptic male choice: Experimental evidence of sperm sex ratio and seminal fluid adjustment in relation to coital rate

Amy M. Edwards: La Trobe University; Elissa Z. Cameron: University of Canterbury

The differential allocation hypothesis suggests that a mother should adjust the sex of her offspring in relation to her mate's attractiveness, thereby increasing future reproductive fitness when her sons inherit the attractive traits. More attractive males have been shown to sire more sons, but it is possible that the sex ratio skew could be a result of paternal rather than maternal manipulation, which would be a more parsimonious explanation. Sex allocation research in mammals has focused almost exclusively on mothers under the assumption that the male contribution is genetically determined during meiosis and therefore not under adaptive control. However, we have recently challenged this assumption and shown variation under conditions where you would not expect it. Here we manipulated coital rate (an indicator of attractiveness) in laboratory mice and showed that males that mate more often have higher levels of glucose in their semen despite lower blood glucose levels. Since peri-conceptual glucose levels *in utero* increase male conceptus survival, this could result in male-biased sex ratios. The males that mated most also had more remaining X-chromosome-bearing-spermatozoa, suggesting depletion of Y-chromosome-bearing-spermatozoa during mating. We hypothesise that males may alter both seminal fluids and X:Y ratios in an ejaculate to influence subsequent sex ratios. Our results further support a paternal role in sex allocation.

John Endler, Deakin University: Sexual Selection

Visual Contrast and Colour Pattern Evolution in guppy populations

John A. Endler, School of Life and Environmental Sciences, Deakin University, Waurn Ponds, VIC, Australia

Females may use male colour patterns as criteria for mating decisions. Visual contrast may be important to both attract and stimulate females as well as giving them information for choice. Visual contrast is affected by the light environment. We report how visual contrast has changed and increased in 12 guppy mesocosms living under 3 different light environments. Male guppies display a mosaic of colours to females. Some of this change is predictable from the efficiency of the individual colour classes in stimulating the retina, but examination of the visual contrast between adjacent patches reveals some interesting constraints on the geometry of the patch positions which may be a long term effect of visual predation.

Jan Engelstädter, The University of Queensland: Posters

Jumping in trees: modelling the dynamics of parasite spread within clades of host species

Jan Engelstädter & Nicole Fortuna (The University of Queensland)

New infectious diseases often originate from host-shifts, i.e., the successful transfers of parasites to new host species. We present the results of mathematical models and computer simulations aimed at gaining a better understanding of the dynamics of parasite spread through host-shifts on evolving host phylogenetic trees. We focus in particular on the influence of the ‘phylogenetic distance effect’, i.e., the extent to which the success of host-shifts decreases with increasing phylogenetic distance between donor and recipient host species. Our results indicate that under the phylogenetic distance effect, both particular host phylogenies and broad patterns of host diversification have a major impact on the fraction of infected species and the distribution of parasites within the host trees. We also investigated the simultaneous spread of two different types of parasites, demonstrating that ‘specialist parasites’ that form relatively stable associations with their hosts can often out-compete ‘generalist parasites’ that are less stable but can shift more easily to distantly related new host species. Our results should be relevant for a wide range of host-parasite systems, including endosymbiotic bacteria such as Wolbachia.

Jan Engelstädter, The University of Queensland: Macroevolution 2

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Philip Erm, The University of Melbourne: Coevolution 2

Spreading populations and the evolutionary push to be pulled

Philip Erm, The University of Melbourne

Accurately predicting the expansion rates of spreading populations is crucial for managing introduced species and gauging the potential impacts of climate change. Despite these needs, reliable estimates of invasion speeds have proven to be elusive. This may in part be due to an underappreciation of the interaction between the Allee effect (where the fitness of individuals in a population is highest at intermediate, rather than low densities) and evolution during invasions. To examine this interaction, I conduct simulations in which a trait that governs resistance to the Allee effect evolves in invaders spreading across a landscape. I find that invaders rapidly gain resistance to the Allee effect, and that invasions may transition from spreading as pushed waves to pulled waves as a result. These findings underscore the importance of accounting for evolution in predictions of invasion speed, and suggest that it has the capacity to fundamentally alter dynamics of spreading populations.

Jon Evans, University of Western Australia: Lightning Talks

Multivariate sexual selection on ejaculate traits under sperm competition

Jon Evans; Contributing authors: Rowan Lymbery & Jason Kennington

The widespread prevalence of sperm competition means that ejaculates typically face intense sexual selection. However, until now, our ability to investigate sexual selection on gametes has been hampered by the twofold difficulties of (1) deriving estimates of relative fitness from sperm competition trials that are comparable across rival male and female genotypes, and (2) obtaining measures of competitive fertilisation success that are not confounded by post-zygotic (e.g. embryo survival) effects. Here, we exploit the extraordinary experimental tractability of a broadcast spawning marine invertebrate to overcome both of these challenges, enabling us to characterise multivariate sexual selection on ejaculate traits when sperm from multiple males compete for fertilisations. In a series of multi-male spawning events, we tracked the real-time success of sperm from the mussel *Mytilus galloprovincialis* — using fluorescent sperm tags that are visible inside fertilised eggs. We then used multivariate selection analyses to identify complex patterns of linear and non-linear sexual selection on combinations of sperm morphology and motility traits. Directional selection favoured shorter sperm flagella, while we found non-linear selection against divergent combinations of sperm velocity, swimming path linearity and sperm length. These patterns likely reflect the way different swimming strategies allow sperm to successfully find and respond to chemical attractants released by eggs. Our findings provide empirical evidence that selection under sperm competition acts on ejaculate traits as an integrated multivariate phenotype.

Anna Farre Orteu, The University of Melbourne: Social 2 & Posters

Co-option of the sex differentiation cascade for caste determination in social insects

Anna Farre Orteu, Melbourne Integrative Genomics & School of BioSciences, The University of Melbourne; Irene Gallego Romero, Melbourne Integrative Genomics & School of BioSciences, The University of Melbourne; Luke Holman, School of BioSciences, The University of Melbourne

Eusocial insects like ants and bees are characterised by complex societies composed of two ‘castes’ — queens and workers — which can have radically different morphology, lifespan, fecundity and behaviour. This extreme phenotypic plasticity has evolved several times independently, but its genetic underpinnings remain poorly understood. A recent hypothesis proposes that eusocial insects have re-purposed a pre-existing genetic switch to control caste development, namely the the sex differentiation cascade, which normally controls development into a male or female. Using RNA-seq data from queens and workers in 12 social insect species, I investigate the involvement of a major sex differentiation gene in caste fate across bees, ants and wasps.

Will Feeney, University of Queensland: Coevolution 2

Predation drives recurrent convergence of fish-anemone mutualisms

William E. Feeney, Rohan M. Brooker, Lane N. Johnston, James D. J. Gilbert, Marc Besson, David Lecchini, Danielle L. Dixson, Peter F. Cowman, Andrea Manica

Mutualisms are common in nature, yet the circumstances that promote their evolution remain unclear. We report that fish-anemone mutualisms have evolved repeatedly over the past 60 MY and that adult body size is associated with the ontogenetic stage of anemone mutualisms: larger-bodied fish species partner with anemones as juveniles, while smaller-bodied species partner with anemones throughout their lives. Field and laboratory studies show that predators preferentially target smaller prey, that smaller individuals more commonly associate with anemones, and that these relationships confer protection to small fishes. Our results indicate that predation is the most likely pressure driving the recurrent convergent evolution of fish-anemone mutualisms and suggest that similar ecological processes may have selected convergence in interspecies interactions in other animal clades.

Nathalie Feiner, University of Lund: Developmental Plasticity & Sex

How do wall lizard embryos adapt to cool climate

Nathalie Feiner (Lund), Alfredo Rago (Lund), Geoff While (UTAS), Tobias Uller (Lund)

Populations adapting independently to the same environment provide important insights into the repeatability of evolution at different levels of biological organization. In the 20th century, common wall lizards (*Podarcis muralis*) from southern and western Europe were introduced to England, north of their native range. Non-native populations of both lineages have adapted to the shorter season and lower egg incubation temperature by increasing the absolute rate of embryonic development. Here we tested if this adaptation is accompanied by signatures of directional selection in the transcriptomes of early embryos and, if so, if non-native populations show adaptive convergence. Embryos from non-native populations exhibited gene expression profiles consistent with directional selection following introduction, but different genes were affected in the two lineages. Despite this, the functional enrichment of genes that changed their expression following introduction showed substantial similarity between lineages, and was consistent with mechanisms that should promote developmental rate. Moreover, the divergence between non-native and native populations was enriched for genes that were temperature-responsive in native populations. These results indicate that small populations are able to adapt to new climatic regimes, but the means by which they do so may largely be determined by founder effects and other sources of genetic drift.

Renee Firman, University of Western Australia: Lightning Talks

Sociality and sexual dimorphism in Australian endemic rodents

Renee Firman, University of Western Australia; Bruno Buzatto, University of Western Australia; Jessica Moran, University of Western Australia; Dustin Rubenstein, Columbia University

Research on intrasexual competition has, for the most part, focused on male rivalry for access to mates. However, it is now clear that a complete understanding of selective pressures that shape the evolution of competitive traits in both sexes demands that we also consider competition for resources and rank necessary for reproduction, and not just mates. By concentrating individuals in time and space, sociality intensifies intra- and inter-sexual competition for resources that are necessary for survival and reproduction, often increasing the capacity of the most dominant individuals to obtain a disproportionate share and strengthening selection for traits that enhance success in competitive encounters. Variation in the intensity of female-female competition can influence the evolution of sexual dimorphism in body size, where the typical pattern ($M > F$) might be reduced ($M = F$) or reversed ($M < F$). The Australian rodents show a broad spectrum in sociality and cooperative behaviour and represent a powerful system for investigating the degree to which intrasexual competition has been a selective force in the evolution of sexual dimorphism. We incorporated sociality, body size and phylogenetic data of the Australian Muridae in a comparative analysis and found differences in sexual dimorphism correlated with social organisation: a typical “large male, small female” pattern among non-social species and a reversed sexual dimorphism among social species. This result indicates that intrasexual competition has likely been an important evolutionary force shaping sexual dimorphism in our native rodents.

Renee Firman, University of Western Australia: Posters

Cryptic female sex allocation and the local neighbourhood

Renee Firman, University of Western Australia

The theory of sex allocation is clear — it explains why most species produce equal numbers of sons and daughters and highlights situations that select for deviation from this norm. For example, the ability to adjust offspring sex ratios can be advantageous when parents and their non-dispersing offspring remain in the local neighbourhood and compete for resources (local resource competition; LRC) or mates (local mate competition; LMC). I performed a social manipulation experiment on wild-caught house mice to test a prediction of LMC theory: that female sex ratio control is a phenotypically plastic trait. The predictions were: (i) low (L-) LMC (high female density) conditions will favour the production of male offspring, and (ii) high (H-) LMC (high male density) will favour female offspring production. My investigation returned very interesting results: equal offspring sex ratios under L-LMC ($\bar{x} = 0.48$) and skewed sex ratios, in favour of female offspring, under H-LMC ($\bar{x} = 0.36$). The observed sex bias confirms that: 1. sex allocation is a phenotypically plastic trait; 2. females are sensitive to the LMC environment, and adjust offspring sex ratios accordingly; and 3. females use cryptic sex-biasing mechanisms to control offspring sex ratios. This finding leads to an extension of intriguing questions relating to the evolutionary process by which LMC modifies strategies of sex allocation, and the consequences that these modifications have for individual fitness and population structure.

Luisa Fitzpatrick, University of Tasmania: Life History & Physiology

Is ageing hot? Telomere attrition rates in a viviparous reptile.

Luisa Fitzpatrick, Geoffrey M. While, Tiana Pirtle, Laura Parsley, Angela Pauliny, Mats Olsson, Erik Wapstra

One of the most fundamental questions in biology is why and how organisms age. Senescence is associated with changes at a molecular level, specifically length of telomeres; the caps on the end of chromosomes, which slow age-related cell decline. Ectotherms are directly influenced by environmental temperature in many ways and as yet, patterns of ageing in these species are not well-known. This project investigated the effect of temperature on telomere loss in the spotted snow skink (*Niveoscincus ocellatus*), a viviparous ectotherm occurring across a wide climatic range. We examined the causality of climate in mediating the aging process by experimentally manipulating the thermal environment experienced by *N. ocellatus* and examining relative telomere length in blood samples at the beginning and the end of a three-month treatment period. Relative telomere length was found to increase in lizards exposed to both a long basking treatment and a short basking treatment. The most significant predictor of change in relative telomere length was initial telomere length, with short initial telomeres becoming longer and long initial telomeres becoming shorter over the three-month experimental period. These findings provide insights into the effect that temperature has on cellular senescence in ectotherms and this process will be linked to organism level senescence in future studies to determine the importance of climate effects on ageing patterns of populations

Nicole Fortuna, The University of Queensland: Posters

What factors can produce clusters of parasites within host trees? Comparing the phylogenetic distance and clade effects.

Nicole Fortuna, Jan Engelstädter, The School of Biological Sciences University of Queensland

Host-shifting is a major mechanism of parasite diversification across host species. However, the evolutionary dynamics driving the ability to host-shift can be difficult to interpret. The observation that similar parasites tend to exist on clusters of similar hosts has been given two major evolutionary explanations. The first is the phylogenetic distance effect (PDE), where the probability of host-switching declines as the genetic distance increases between host species. The second is the clade effect (CE), where susceptibility and resistance towards parasites can be inherited from an ancestral host species, leading to clusters of hosts with similar tendencies for harbouring parasites. In order to understand how PDE and CE can influence the distribution of parasites across a host clade, a stochastic model was built to simulate the evolution of coevolving host and parasite clades over time. In this model, a host clade evolves where species can mutate to be either susceptible or resistant to parasites. This host clade is invaded by a parasite, which diversifies across it through host-shifting and cospeciation. This model under either PDE or CE resulted in parasite clustering on the host tree. Correlations between the phylogenetic distance matrices of host species and their associated parasites show that CE results in a distribution of correlations indistinguishable from the null model, while PDE can result in strong positive correlations. Furthermore, the effects of PDE and CE can be distinguished by comparing the infection frequencies of a host clade with its subclades. The results also show that PDE has the highest variability in infection frequencies between host subclades. CE results in variability in infection frequencies between host subclades when host mutation rate is low. As the mutation rate increases, variability in infection frequencies diminishes. When PDE and CE were combined, CE disrupted the effects of PDE, reducing the strength of the correlation between the phylogenetic distance matrices of hosts and parasites.

Mathieu Fourment, University of Technology Sydney: Computational Methods

Bayesian variational inference in phylogenetics

Mathieu Fourment and Aaron E. Darling. ithree institute, University of Technology Sydney, Ultimo, NSW, 2007, Australia

Markov chain Monte Carlo (MCMC) algorithms have been the workhorse of Bayesian inference in phylogenetics for almost two decades. Although these algorithms have been successfully used in a wide range of applications they do not scale well to large numbers of sequences. Here we present an algorithm for approximate inference of phylogenetic models on fixed tree topologies using the variational Bayesian framework. Variational inference (VI) poses the problem of approximating probability densities as an optimization task. We developed a prototype of a variational algorithm for phylogenetic inference in the Stan package and compare its accuracy to widely-used MCMC-based algorithms. Our preliminary results show that this new algorithm is very efficient while generating accurate estimates. A phylogenetic VI algorithm can be implemented in a standalone program but could also be used within an MCMC as a proposal mechanism for continuous model parameters.

Mathieu Fourment, University of Technology Sydney: Posters

Effective online Bayesian phylogenetics via sequential Monte Carlo with guided proposals

Mathieu Fourment and Aaron E. Darling. ithree institute, University of Technology Sydney, Ultimo, NSW, 2007, Australia

Modern infectious disease outbreak surveillance produces continuous streams of sequence data which require phylogenetic analysis as data arrives. Current software packages for Bayesian phylogenetic inference are unable to quickly incorporate new sequences as they become available, making them less useful for dynamically unfolding evolutionary stories. This limitation can be addressed by applying a class of Bayesian statistical inference algorithms called sequential Monte Carlo (SMC) to conduct online inference, wherein new data can be continuously incorporated to update the estimate of the posterior probability distribution. In this paper we describe and evaluate several different online phylogenetic sequential Monte Carlo (OPSMC) algorithms. We show that proposing new phylogenies with a density similar to the Bayesian prior suffers from poor performance, and we develop 'guided' proposals that better match the proposal density to the posterior. Furthermore, we show that the simplest guided proposals can exhibit pathological behaviour in some situations, leading to poor results, and that the situation can be resolved by heating the proposal density.

The results demonstrate that relative to the widely-used MCMC-based algorithm implemented in MrBayes, the total time required to compute a series of phylogenetic posteriors as sequences arrive can be significantly reduced by the use of OPSMC, without incurring a significant loss in accuracy.

Andrew Francis, Western Sydney University: Networks

Can we future-proof phylogenetic consensus trees?

Andrew Francis, Western Sydney University; David Bryant, University of Otago; Mike Steel, Canterbury University

Consensus methods are widely used for combining phylogenetic trees into a single estimate of the evolutionary tree for a group of species. But how robust are these methods to future information? If additional species are added to the original set of trees, will the expanded consensus tree simply be an expansion of the original consensus tree? In this talk I will formalise and answer this question. Joint work with David Bryant and Mike Steel.

Chris Friesen, University of Sydney: Sexual Selection

Correlated evolution of sexually selected traits: Interspecific variation in ejaculates, sperm morphology, copulatory mate-guarding and body size in two sympatric species of garter snakes

Christopher R. Friesen[1,2†], Emily J. Uhrig[2,3], Ehren J. Bentz[2], Leslie A. Blakemore[2], Robert T. Mason[2]; [1]School of Life and Environmental Sciences, University of Sydney, Heydon-Laurence Bldg AO8, Science Rd, NSW 2006, Australia. [2]Department of Integrative Biology, Oregon State University, Cordley Hall 3029, Corvallis, Oregon, 97330 3Department of Physics, Chemistry and Biology, Linköping University, 58183 Linköping, Sweden

Male reproductive success is dependent on a correlated suite of traits related to a species' ecology and mating system dynamics. Closely related species differing in their mating systems and ecology, such as the garter snakes (*Thamnophis*), are ideal for studying the correlated evolution of sexually selected traits. Here, we compare the degree of SSD, copulatory behaviour, copulatory plug size, and traits associated with sperm competition between two sympatric and closely related *Thamnophis* species, *T. sirtalis* and *T. radix* with divergent mating aggregation size and density.

Clelia Gasparini, The University of Western Australia: Lightning Talks

It's not all about sperm: cryptic female choice driven by premating male × female interactions

Gasparini Clelia1 & Jonathan P. Evans1; 1 Centre for Evolutionary Biology, The University of Western Australia

When mated multiply, females in many species have the ability to bias paternity towards the preferred male through behavioural, morphological and physiological processes. Despite increasing interest in female choice and its mechanisms at both pre- and post-copulatory level, we still know very little about the extent and role of female choice in determining fertilization success. Using the guppy, an iconic species for sexual selection studies, we analysed paternity distribution of the same pairs of males across two different females and multiple successive broods. One of the females was allowed to mate naturally with the two males, while the other was artificially inseminated with the same amount of sperm from the two competing males. Results show a stronger paternity bias (bimodal distribution) in naturally-mated females compared to those artificially inseminated. This result provides clear evidence that the interaction with the male is of paramount importance for the female to bias the paternity towards the preferred male.

Stephen Gipson, Monash University: Coevolution 2

Sex differences and the condition-dependence of pathogen fitness

Stephen Gipson

Infection is characterized by conflict between a pathogen and host over a host's finite pool of resources. Upon pathogen exposure, hosts are expected to mount costly immune responses while pathogens simultaneously reproduce and directly appropriate host resources. Males and females often vary in many costly traits such as behaviour, physiology, and immune or reproductive investment and may therefore vary in both their pool of exploitable resources, or condition, and the allocation of those resources. An intimate link thus exists between the sex of the host, condition, and the outcome of infection. Previous work has shown that variation in host condition or allocation of resources impact on both the extent of pathogen reproduction as well as the speed in which disease spreads between individuals. Consequentially, condition dependence of disease is implicated in the maintenance of genetic variation as well as the speed of coevolutionary cycles. In this study, we explore how variation in condition and energy use between the sexes impacts on the outcome of disease. Specifically, we manipulate host condition by exposing individuals to dietary variation and measure the resulting impacts on host energy use and pathogen fitness. We find that pathogen fitness is greatest in the female host, corroborating the results of previous studies, but find that host energy use and pathogen fitness are more sensitive to dietary manipulation in the female host. We discuss the role for sex to modulate the condition dependence of disease, adding to the developing evidence about sex differences and their impact on the evolution of infectious disease.

Robert Griffiths, Oxford University and ANU: Population Genetics & Coalescent

Genealogy of Wright-Fisher Bridges

Robert Griffiths, University of Oxford

The path of the frequency of a gene, $X(t)$ at time t, which enters a population and is then lost at time T later is modelled as a bridge in a Wright-Fisher diffusion process beginning at $X(0) = 0$ when the gene enters and ending at $X(T) = 0$ when the gene is lost at time T. The model can be neutral with no selection or mutation; or there can be selection; or there can be mutation away from the genes' type as new types arise. Theoretical results that will be discussed in the talk are the probability distribution of $X(t)$, $0 < t < T$ in the bridge; the coalescent genealogy in the bridge and the maximum attained in a bridge.

Jodie Gruber, University of Sydney: Lightning Talks

Geographic divergence of behaviour in cane toads: rapid evolution or developmental plasticity?

Jodie Gruber 1, Gregory Brown 1, Martin J. Whiting 2, Richard Shine 1; 1. School of Life and Environmental Sciences, The University of Sydney, Australia; 2. Department of Biological Sciences, Macquarie University, New South Wales, Australia

Individuals at the leading edge of expanding biological invasions often show distinctive phenotypic traits, in ways that enhance their ability to disperse rapidly and to function effectively in novel environments. Cane toads (*Rhinella marina*) at the invasion front in Australia exhibit shifts in morphology, physiology and behaviour (directionality of dispersal, boldness, risk-taking). We took a common-garden approach, raising toads from range-core and range-edge populations in captivity, to see if the behavioural divergences observed in wild-caught toads are also evident in common-garden offspring. Captive-raised toads from the invasion vanguard population were more exploratory and bolder (more prone to “risky” behaviours) than toads from the range core, which suggests that these are evolved, genetic traits. Our study highlights the importance of behaviour as being potentially adaptive in invasive populations and adds these behavioural traits to the increasing list of phenotypic traits that have evolved rapidly during the toads’ 80-year spread through tropical Australia.

Matt Hall, Monash University: Developmental Plasticity & Sex

Genetic correlations and sex-specific adaptation in changing environments

Tim Connallon and Matthew D. Hall

Females and males have conflicting evolutionary interests. Selection favours the evolution of different phenotypes within each sex, yet divergence between the sexes is constrained by the shared genetic basis of female and male traits. Current theory predicts that such ”sexual antagonism” should be common: manifesting rapidly during the process of adaptation, and slow in its resolution. However, these predictions apply in temporally stable environments. Here, we analyze models of sex-specific evolutionary divergence under directional and cyclic environmental change, and consider the impact of genetic correlations on long-run patterns of sex-specific adaptation. Our results reinforce recent empirical observations that changing environmental conditions alleviate conflict between males and females. They also generate new predictions regarding the scope for sexually antagonistic selection and its resolution in changing environments.

Ben Halliwell, University of Tasmania: Social 2

Live Bearing Promotes The Evolution of Sociality in Squamate Reptiles

Ben Halliwell, University of Tasmania; Tobias Uller, Lund University; Barbara Holland, University of Tasmania; Geoffrey M. While, University of Tasmania

Identifying factors responsible for the emergence and evolution of social complexity is an outstanding challenge in evolutionary biology. Here we report results from a phylogenetic comparative analysis of over 1000 species of squamate reptile, nearly 100 of which exhibit facultative forms of group living, including prolonged parent offspring associations. We show that the evolution of social groupings among adults and juveniles is overwhelmingly preceded by the evolution of live birth across multiple independent origins of both traits. Furthermore, the results suggest that live bearing has facilitated the emergence of social groups that remain stable across years, similar to forms of sociality observed in other vertebrates. These results suggest that live bearing has been a fundamentally important precursor in the evolutionary origins of group living in the squamates.

Lauren Harrison, The Australian National University: Lightning Talks

Do winners win more mating opportunities?

Lauren Harrison, Megan Head, & Michael Jennions

Animals compete to establish dominance hierarchies, and physical contests can have lasting effects on competitors. These winner and loser effects can influence subsequent contest behaviour, but it is unknown if winner/loser effects directly influence access to resources like mating opportunities. In this study, size-matched *Gambusia holbrooki* males were experimentally manipulated to have a series of either winning or losing experiences before competing for a female. We found that winners spent significantly more time with females, but did not make more copulation attempts, or have more successful attempts, than losers. Additionally, winner/loser effects on the number of successful copulation attempts that males make seem to be size-dependent. This study demonstrates the importance of considering competition context when studying potential winner and loser effects on resource acquisition.

Momoko Hayamizu, The Institute of Statistical Mathematics & JST PRESTO: Networks

A generalisation of the fundamental theorem of phylogenetics

Momoko Hayamizu (The Institute of Statistical Mathematics & JST PRESTO)

The mathematical foundation of distance-based phylogenetic tree reconstruction was established in 1960/70s when the graph realisability of finite metric spaces was actively studied. However, biologists need more general theorems as they believe that phylogenetic “networks” may provide a more accurate description of complicated evolutionary relationships between species. In this talk, I will summarise basic facts around tree metrics and describe how to extend the notion of tree metrics / phylogenetic trees.

Tobias Hector, Monash University: Climate Change

How infectious disease affects thermal tolerance

Tobias E. Hector, Monash University

Climate change is resulting in a rise in extreme weather events around the world. An increase in the severity and frequency of heat waves puts populations and species at risk if they are exposed to temperatures outside their functional range. Co-occurring stressors such as infectious disease have the potential to further impact how organisms cope with extreme temperatures. In this study, we explored how infection success and infection intensity impact upper thermal tolerance. Using bacterial infection in the waterflea, *Daphnia magna*, as a model system, we exposed individuals to multiple pathogen genotypes and then measured upper thermal limits using a range of methodological approaches. We find that exposure to infectious disease lowers upper thermal tolerance. However, we found no evidence to suggest that the intensity of infection, in terms of pathogen load, has any effect on thermal tolerance. We discuss the role that co-occurring stressors, specifically infectious disease, may have in determining the upper thermal limits of animals and the consequences this may have for the adaptation of populations to an increasingly variable and extreme climate.

Michael Hendriksen, Western Sydney University: Networks

Nonbinary Unrooted Tree-Based Networks

Michael Hendriksen, Western Sydney University

There is contemporary debate in biology as to whether evolution of some species is inherently tree-like with some reticulations between the branches (e.g. horizontal gene transfer and hybridisations) or whether there are too many reticulation events to describe these histories as tree-like in any meaningful way. In 2015, Francis and Steel introduced the concept of ‘tree-based’ networks in the rooted, binary network setting to differentiate between these possibilities. Since then there has been a great deal of interest in the area. In particular, Jetten and van Iersel (2017) extended the concept to non-binary rooted networks to allow for rapid speciation events or uncertainty about order of speciation events, and Francis, Huber and Moulton (2017) extended it to binary unrooted networks, to allow for uncertainty about root location. In this talk we present some preliminary results in the area of nonbinary unrooted networks, including characterisations of extensions of both the tree-based property and the related concept of a fully tree-based network.

John Hewson, University of Tasmania: Algebraic Methods

The ring of Markov invariants on two state tripod trees.

John Hewson, Jeremy Sumner

A general model will be introduced to contextualise phylogenetic trees in a mathematical setting. Invariant functions will be derived from the model which form a ring. Different methods of enumeration will be employed to ensure that all such invariant functions have been found.

Peta Hill, University of Tasmania: Developmental Plasticity & Sex

Conserved sex-linked markers in a skink with population divergence in sex determination

Peta Hill, Christopher Burridge, (University of Tasmania), Tariq Ezaz (Institute of Applied Ecology, University of Canberra), Erik Wapstra (University of Tasmania)

Sex determination systems are exceptionally diverse and have undergone multiple and independent evolutionary transitions among species, particularly reptiles. However, the mechanisms underlying these transitions have not been established. Here we tested for differences in sex-linked markers in the only known reptile that is polymorphic for sex determination system, the spotted snow skink, *Niveoscincus ocellatus*, to quantify the genomic differences that have accompanied this transition. In a highland population, sex is determined genetically (GSD), whilst in a lowland population, sex is influenced by temperature (TSD). We found a similar number of sex-linked loci in each population, including shared loci, with genotypes consistent with male heterogamety (XY). However, population-specific linkage disequilibrium suggests greater divergence of sex chromosomes in the highland population. Our results suggest that transitions between GSD and TSD can be facilitated by subtle genetic differences.

Mitchell Hodgson, University of New South Wales: Climate Change

Variation in the thermal behaviour and physiology of ectotherms and its implications for response to novel thermal environments.

Mitchell Hodgson (UNSW); Lisa E. Schwanz (UNSW)

Global predictions of contemporary climate change create a serious imperative to understand the methods and mechanisms animals implement to persist in novel thermal environments. Ectotherms are seriously imperilled by shifts in thermal environment due to the integral role temperature has on daily activity. However, behavioural and physiological plasticity, as well as evolutionary response, may allow organisms to adjust to unique thermal environments. This talk will focus on two ongoing projects using Jacky Lizards (*Amphibolurus muricatus*) as a model organism to investigate: (1) Latitudinal differences in the physiology and behaviour of the species to better understand intraspecific variation of thermal phenotypes and the roles acclimation and adaptation have in dictating observed responses (2) Quantifying heritability in thermal preferences limits using a pedigreed colony of lizards.

Barbara Holland, University of Tasmania: Networks

Where to next for convergence networks?

Jonathan Mitchell[1,2], Barbara Holland[1], Jeremy Sumner[1]; [1]University of Tasmania, [2]University of Alaska Fairbanks

Abstract: Over the last few years we have been working on a class of models we call ‘Convergence-Divergence models’. These allow for traditional speciation events where species diverge from a common ancestor but they also allow species to become more similar again. In this talk I will (1) introduce the model, (2) discuss potential areas of application: morphological convergence, modelling gene content, introgression (3) discuss issues around identifiability with an intriguing link to the molecular clock (4) present some first thoughts on a distance based approximation to the model (joint work with Vince Moulton and Kathi Huber)

Luke Holman, University of Melbourne: Social 2

Conserved transcriptomic effects of queen pheromones in bees and ants

Luke Holman, Heikki Helantera, Kalevi Trontti, and Sasha Mikheyev

Social insects queens produce ‘queen pheromones’: chemical signals that have manifold phenotypic effects on other colony members. Queen pheromones are chemically similar in many ants, wasps and most bees, which is remarkable because these taxa diverged >150MYA, and evolved queens and workers independently. To test hypotheses about the evolution of eusociality and queen pheromones, we measured the transcriptomic effects of experimental exposure to queen pheromones in workers of two ant and two bee species (genera: *Lasius*, *Apis*, *Bombus*) using mRNA sequencing. Queen pheromones affected transcription and splicing at hundreds of loci. The transcriptomic effects were similar in ants and bees, and included genes involved in lipid biosynthesis, oogenesis, metabolism, ageing, and histone modification. Pheromone-sensitive genes tended to be evolutionarily ancient, positively selected, weakly connected, hypomethylated, and differentially expressed between queens and workers. Our results reveal how queen pheromones achieve their effects, and suggest that ants and bees use conserved or convergent genetic modules to achieve reproductive division of labour.

Cameron Hosking, University of Sydney: Macroevolution 3

A Nutritionally Explicit Ecological GPU Model Exploring the Evolution of Life History Traits

Cameron Hosking, Sydney University; Alistair Senior, Charles Perkins Centre; Stephen Simpson, Charles Perkins Centre

Understanding how environments shape the way that organisms have evolved to develop, reproduce, and die, is a fundamental problem in evolutionary biology. Data suggest an intricate link between nutrient intake and the aforementioned traits. We simulated the evolution of life histories and appetites in differing nutritional landscapes using agent-based models. The models are nutritionally explicit in that the intake, expenditure and effects of multiple nutrients on each trait are treated individually based on biological data. The models are implemented using CUDA and are thus highly scalable. We found that, agents adopt nutritional appetites that favour longevity in sparse environments and reproduction in rich environments. The results are observed across a wide variety of other ecological and biological factors such as rates of predation and metabolic costs.

Maider Iglesias-Carrasco, The Australian National University: Coevolution & Conservation

Effect of exotic tree plantations on the sexual behaviour of the palmate newt (*Lissotriton helveticus*)

Maider Iglesias Carrasco[1,2,3], Megan L. Head[1], Michael D. Jennions[1], Carlos Cabido[2]. miglesias15@gmail.com; [1]The Australian National University, Canberra. Australia; [2]Aranzadi Society of Sciences, Donostia. Spain. [3]Museo Nacional de Ciencias Naturales-CSIC, Madrid. Spain

Novel environments due to human habitat disturbance could influence sexual selection by changing the allocation of resources to costly sexual traits or the costs of mate choice. To test this, we explored how the transformation of the natural forest to exotic plantations affected the investment on male condition-dependent sexual traits and female mating preferences in the palmate newt, a common European urodele species. By combining field with mesocosms work, we explored the investment in immune response, body condition and secondary sexual traits of males inhabiting natural forests and exotic tree plantations. We then tested whether being exposed to leachates from exotic trees alter female mate choice. We found that males inhabiting exotic plantations had smaller sexual traits and poorer immune responses than those from the natural forests, probably due to a change in the optimal allocation of resources in each habitat and the effect of water toxicity. We also found a change in female mate choice, since females exposed to eucalypt leachates did not preferentially associate with the best quality males. We conclude that newly created habitats might generate long-term selection for new resource allocation strategies and alter the direction of sexual selection in native species.

Peter Jarvis, University of Tasmania: Algebraic Methods

How to handle trees in phylogenetics

Peter Jarvis (University of Tasmania)

Splits networks and directed acyclic graphs to the contrary, binary trees remain the basic working fabric of phylogenetics. While tree searching is famously hard, binary trees nonetheless possess wonderful combinatorial attributes, and arise in very many contexts. This very universality provides great potential and opportunity for their characterization. This talk will revisit some of the standard enumerative tree counting bijections, with the Catalan numbers playing a central role. To widen the perspective, we will also inject a quantum of algebra into the mix, by exploring the properties of some associated mathematical structures.

Michael Jennions, The Australian National University: Sex

Sex Ratios and Sex Roles

Michael Jennions (Australian National University) and Lutz Fromhage (University of Jyvaskyla)

‘Sex roles’ is shorthand for male–female differences in mate searching, competitive traits that increase mating or fertilization opportunities, mate searching, mate choice and parental care. Theory suggest that biased sex ratios drive the evolution of sex roles. For each sex, the total number of heterosexual matings and thereafter of offspring is identical. Consequently, the mean success of individuals depends on the sex ratio (Fisher condition). But which sex ratio? The Fisher condition only applies to some reproductive measures (e.g. lifetime offspring production or matings) for certain sex ratios (e.g. operational or adult sex ratio, OSR and ASR). We clarify whether a biased OSR, ASR, or sex ratio at maturation (MSR) have a causal or correlational relationship with the evolution of sex differences in parental care and competitive traits. We argue that it is necessary to understand the combined effect of the MSR and mortality rates while caring and competing than to focus on the ASR itself. In short, we make the case that the ASR does not cause the evolution of parental care. However, the ASR can still be a cue for adaptive shifts in how each sex invests in parental care. There is a difference between evolutionary and ecological timeframes.

Greg Jordan, University of Tasmania: Macroevolution 2

Evolutionary niche conservatism and relictual clades

Greg Jordan, University of Tasmania

This talk will consider the role of evolutionary niche conservatism in the distribution of ancient, relictual plant clades (more specifically, palaeoendemics). It will present spatially adjusted analyses of the distribution of such clades both globally and locally, including predictors from both current and past environments (climate and topographic complexity). A set of characteristics predict palaeoendemics in multiple regions, and this talk will argue that this is the consequence of extreme phylogenetic niche conservatism.

Ben Kaehler, The Australian National University: Computational Methods

Distance-Based Tree Building with Rooted Models

Ben Kaehler[1], Teresa Neeman[2], Michael Roper[1], Gavin Huttley[1];

[1]Research School of Biology, Australian National University; [2]Statistical Consulting Unit, Australian National University

A class of biologically relevant models of nucleotide substitution that allow consistent estimation of rooted phylogenies has recently been discovered. For those models, it is possible to estimate the genetic distance from just two extant taxa to their most recent common ancestor. Direct estimation of the moment of divergence between two species opens exciting possibilities for extremely simple distance-based tree-building algorithms. Algorithmic simplicity expedites results regarding rates of convergence. I will present some of the possible algorithms along with their rates of convergence in terms of sample complexity.

Fonti Kar, University of New South Wales: Lightning Talks

Individual variation in thermal plasticity

Fonti Kar, Shinichi Nakagawa, Daniel Noble - All from University of New South Wales

Phenotypic plasticity enables individuals to modify their phenotype in response to changes in environment. Typically, plasticity is represented as a reaction norm where a phenotypic trait is measured as a function of the environment with the slope viewed as ‘plasticity’ (function-valued perspective). However, phenotypic variation in different environments can also be considered as separate traits (character-state perspective). Depending on how evolutionary biologists choose to view plasticity, selection can either act on the entire reaction norm or parts of the reaction norm. Here, I compare and contrast both function-valued and character-state approaches in exploring individual variation in metabolic responses to temperature in delicate skinks (*Lampropholis delicata*). I show that individual slopes were moderately repeatable and that repeatability of MR increased with temperature. I also found that metabolic rate at adjacent temperatures more strongly correlated than with temperature extremes, suggesting that the shape of the reaction norm can only change under certain constraints. I advocate the use of both approaches as they bring different insights in understanding how selection can act on reaction norms which is integral to understanding the evolution of plasticity.

Michael Kasumovic, University of New South Wales: Open Session

Video games: How to take science and teaching to the next level

Michael Kasumovic, UNSW Sydney

This will either be a talk about understanding human behaviour using video games, or we will play science video games and collect real-time data to show you how useful they can be in teaching. It’ll depend whether the computer has an internet connection...

Tom Keaney, The University of Melbourne: Lightning Talks

Kinship combats Mother’s curse

Thomas Keaney, Theresa Jones, Luke Holman; The University of Melbourne;

Genetic variation in mitochondrial DNA affects many phenotypic traits, and underlies several human diseases. Because males are an evolutionary dead end for mitochondria, it is widely believed that phenotypic effects on males that result from mtDNA are ‘invisible’ to selection, causing male-harming mutations to build up in the mitochondrial genome (‘mother’s curse’). However, male mtDNA can be selected indirectly whenever the male’s phenotype affects the fitness of his matrilineal relatives (e.g. via altruism or competition). Using sexual conflict in *Drosophila* as a case study, I am empirically testing this hypothesis for the first time, to determine whether mother’s curse is indeed an inescapable reality. I hope to further our understanding of genomic conflict, mitochondrial disease, and endosymbiont evolution.

Vanessa Kellermann, Monash University: Climate Change

Can we predict species plastic responses to climate change?

Ary A. Hoffmann, The University of Melbourne; Johannes Overgaard, Aarhus University; Volker Loeschcke3, Aarhus University; Carla M. Sgró, Monash University; 1School of Biological Sciences, Monash University, Clayton, Melbourne, Victoria, 3800; 2School of BioSciences, The University of Melbourne, Bio21 Institute, 30 Flemington Road, Parkville, Victoria, 3010; 3Department of Bioscience, Aarhus University, DK-8000 Aarhus, Denmark.

Species vulnerability to climate change will be dictated by their capacity to respond via evolutionary responses. Phenotypic plasticity is likely to be the initial response and in the short-term may buffer species from environmental change. But whether some species are more or less likely to respond plastically to climate change is unknown. The seasonality hypothesis predicts species occupying highly variable environments will evolve higher plasticity, leading to the assumption that temperate/sub-tropical species will have higher plasticity than tropical species. The empirical evidence to support this hypothesis is unclear. Here we examined the extent to which 32 Drosophila species, varying in their distribution, could increase their desiccation resistance via phenotypic plasticity involving hardening. Testing the seasonality hypothesis and other plasticity hypotheses we show that phylogeny, environment and trade-offs all helped to explain variation in plasticity for desiccation resistance but in complex ways. These findings suggest some species have the ability counter dry periods through plastic responses, whereas others do not; and this ability will depend to some extent on a species' placement within a phylogeny, along with its basal level of resistance and past history of adaptation.

Ella Kelly, The University of Melbourne: Coevolution & Conservation

Can targeted gene flow be used to save northern quolls of extinction?

Kelly, Ella and Phillips, Ben; School of Biosciences, The University of Melbourne, Parkville, VIC, Australia

Targeted gene flow is an emerging conservation strategy. It involves translocating individuals with favourable genes to areas where they will have a conservation benefit. The applications for targeted gene flow are wide-reaching, including buffering natives from the impact of invasive species. The endangered carnivorous marsupial, the northern quoll, has declined rapidly since the introduction of the cane toad, which fatally poisons quolls that attack them. There are, however, a small proportion of quolls that know not to eat cane toads (termed "toad-smart"), and it is this behaviour that we hope to promote through targeted gene flow. We have shown toad-smart behaviour is a heritable trait in northern quolls. We demonstrated that northern quolls born in captivity to toad-smart parents ignore toads as a prey item — despite never encountering a toad before. This aversion seems to be present in both quolls with one or two toad-smart parents, indicating dominance of the trait. The heritability of toad smart behaviour means it has been rapidly selected for in some populations of northern quolls since toad arrival. Not all quolls have adapted to cane toads however, with around 95% of local populations going extinct after toad invasion. We propose that targeted gene flow could be used to promote toad-smart genes in these threatened populations to improve northern quoll's chances of surviving the cane toads. I will present data from captive breeding experiments, as well as projections from individual based population viability analyses to show that targeted gene flow may be a viable conservation strategy for saving northern quolls from extinction.

Rob Lanfear, The Australian National University: Macroevolution 3

Do plants evolve differently?

Rob Lanfear, ANU; David Kainer, ANU; Amanda Padovan, ANU; Alejandro Morales, Macquarie University; Adam Orr, Arizona State University; Reed Cartwright, Arizona State University

It is often thought that plants and animals should evolve in fundamentally different ways, because animals have a separate germline but plants don't. However, evidence from our lab suggests that this might not be the case. We have developed methods to reliably measure the genome-wide accumulation of new mutations in individual plants. By applying them to individual eucalypts of large stature, we are able to measure both the rate and spectrum of new mutations accumulating within individuals. Our results suggest that plants might not evolve so differently to animals after all.

Clementine Lasne, Monash University: Developmental Plasticity & Sex

The role of intersexual genetic correlations in the evolution of male and female local adaptation

Clementine Lasne, Tim Connallon, Carla Sgró

During the process of adaptation, selection over a trait can differ between: (1) locations, resulting in the evolution of local adaptation, and (2) sexes, resulting in the evolution of sexual dimorphism. Many traits that are expressed by both sexes are positively and strongly genetically correlated, which may lead to correlated patterns of sex-specific trait divergence across a species' range. While such genetic correlations should promote local adaptation when directional selection aligns between the sexes, they will constrain adaptation in cases where selection differs between the sexes. To date, it remains unclear how spatial patterns of selection differ between males and females. We estimated patterns of sex-specific clinal divergence for a set of five traits in *Drosophila melanogaster* that vary in the strength of the cross-sex genetic correlation. We found parallel male and female clines in all traits regardless of their genetic correlation. These results suggest that the direction of local selection is concordant between males and females, resulting in a parallel shift of male and female traits across the species' range. Overall, patterns of spatial selection do not seem to differ between the sexes, and consequently, local adaptation should generally be facilitated in traits with strong genetic correlations between the sexes.

David Liberles, Temple University: Origins of Life

Evaluating the proteinness of amino acid substitution models in the development of new approaches for protein evolution

David A. Liberles, Temple University, Philadelphia, PA, USA

Comparative genomic and molecular evolutionary studies aim to uncover the relationship between selection on mutations in individual genes/proteins, phenotypic evolution, and adaptation. Theory and tools that enable this analysis have mostly not been rooted in underlying biochemical processes. My group has been involved in building this bottom-up approach to understanding the genotype-phenotype map and its behaviour over evolutionary time.
The first layer of this approach is to understand amino acid changes in the context of protein structure and inter-molecular interaction. Many models for characterizing amino acid substitution have been described to date. These models make different sets of assumptions and have mostly been evaluated using statistical approaches that assume that every site in a protein evolves independently of every other site. If one is interested in using amino acid substitution models for functional or biochemical inference, then the degree to which the model actually describes a protein is important. Several different models have been evaluated from this perspective to characterize the retained “proteinness” of a sample SH2 domain structure. Additionally, a new set of models has been developed that enables characterization of amino acid changes in the context of fit within the existing structure and with binding to existing and alternative interacting partners. These models, still in their development, are one path towards extracting additional information about functional change for protein encoding genes under positive selection.

Simone Linz, University of Canterbury: Combinatorics

Are cherry-picking sequences the new agreement forests?

Charles Semple, School of Mathematics and Statistics, University of Canterbury, New Zealand

Throughout the last decade, we have seen much progress towards characterizing and computing the minimum hybridization number for a set of phylogenetic trees. Roughly speaking, this minimum quantifies the number of hybridization events needed to explain a set of trees by simultaneously embedding them into a phylogenetic network. From a mathematical viewpoint, the notion of agreement forests is the underpinning concept for almost all results that are related to calculating the minimum hybridization number for two trees. However, despite various attempts, characterizing this number in terms of agreement forests for more than two trees remains elusive. In this talk, we first discuss the limitations of agreement forests. Subsequently, we establish a new characterization to compute the minimum hybridization number for an arbitrarily large set of not necessarily binary trees in the space of tree-child networks. This new characterization is in terms of cherry-picking sequences.

Gracie Liu, The University of New South Wales: Developmental Plasticity

Hormonal mediators of thermal maternal effects in the jacky dragon (*Amphibolurus muricatus*)

Gracie Liu (The University of New South Wales), Kristal E. Cain (The University of Auckland), Lisa E. Schwanz (The University of New South Wales)

Maternal thermal regime is known to influence numerous offspring phenotypes, including growth and sex ratios. However, mechanisms by which thermal information can be passed onto offspring have been underexplored. Here, corticosterone (an important steroid hormone) was investigated as a potential mediator of thermal maternal effects. Plasma corticosterone levels of jacky dragons (*Amphibolurus muricatus*; $n = 74$) placed in two different thermal regimes (short, 7h, or long, 11h, basking treatments) were quantified and examined for correlations with reproductive and offspring traits. Corticosterone levels were found not to differ between basking treatments and were not associated with maternal reproductive timing or output, or offspring sex, size or growth. This suggests that previously reported thermal maternal effects on sex ratios and growth are mediated by mechanisms other than maternally-derived corticosterone. However, in the post-breeding season, lizards in long bask conditions tended to exhibit higher corticosterone levels than those in short bask conditions and were in significantly worse body condition. Together with the findings that early-breeding season body condition positively predicted reproductive output (clutch sizes and total number of eggs) and offspring size at hatching, these results suggest that thermal opportunities may also have indirect effects on a range of fitness-relevant traits via effects on body condition. However, as there was no association between condition and corticosterone in the breeding season, corticosterone does not appear to be a mechanistic link between condition and reproductive and offspring traits.

Nate Lo, University of Sydney: Coevolution 2

Rampant host-switching shaped the termite gut microbiome

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The gut microbiota of animals exert major effects on host biology, ranging from energy metabolism and immune responses to the development of gut structure and function. Although horizontal transfer is generally considered the prevalent route for the acquisition of gut bacteria in mammals, recent evidence from primates indicates that some bacterial lineages have cospeciated with their host on timescales of over several million years. Termites harbor one of the most complex gut microbiota of any animal group, and their complex social behaviour provides the potential for long-term vertical symbiont transmission, and co-evolution of gut symbionts and host. Despite clear evolutionary patterns in the gut microbiota of termites, a consensus on how the microbial communities have been assembled during the diversification of this lineage has yet to be reached. Although some studies have concluded that vertical transmission has played a major role, others indicate that diet and gut microenvironment have been the primary determinants shaping microbial diversity in termite guts. To address this issue, we undertook the most comprehensive examination of the termite gut microbiota to date, through 16S rRNA metabarcoding of 94 termite species. We analyzed the phylogeny of 211 bacterial lineages obtained from termite guts including their closest relatives from other environments, which were identified using BLAST. The results provided strong evidence for rampant horizontal transfer of gut bacteria between both closely and distantly related termite host lineages. While the majority of termite-derived phylotypes formed large monophyletic groups, indicating high levels of niche specialization, numerous other clades were interspersed with bacterial lineages from the guts of other animals. Our results indicate that “mixed-mode” transmission, which combines colony-to-offspring vertical transmission with horizontal colony-to-colony transfer, has been the primary driving force shaping the gut microbiota of termites.

Anicee Lombal, University of Tasmania: Phylogeography

Genetic divergence between colonies of Flesh-footed Shearwater exhibiting different foraging strategies

Anicee Lombal, Jennifer Lavers, Jeremy Austin, Eric Woehler, Ian Hutton, Christopher Burridge. University of Tasmania & University of Adelaide

Increasing evidence suggests foraging segregation as a key mechanism promoting genetic divergence within seabird species. However, testing for a relationship between population genetic structure and foraging movements among seabird colonies can be challenging. Telemetry studies suggest that Flesh-footed Shearwater *Ardenna carneipes* that breed at Lord Howe Island or New Zealand, versus southwestern Australia or Saint-Paul Island in the Indian Ocean, migrate to different regions (North Pacific Ocean and northern Indian Ocean, respectively) during the non-breeding season, which may inhibit gene flow among colonies. In this study, we sequenced a 858-base pair mitochondrial region and seven nuclear DNA fragments (352-654 bp) for 148 individuals to test genetic differentiation among colonies of Flesh-footed Shearwaters. Strong genetic divergence was detected between Pacific colonies relative to those further West. Molecular analysis of fisheries' bycatch individuals sampled in the Sea of Japan indicated that individuals from both western and eastern colonies were migrating through this area, and hence the apparent segregation of the non-breeding distribution based on telemetry is invalid and cannot contribute to the population genetic structure among colonies. The genetic divergence among colonies is better explained by philopatry and evidence of differences in foraging strategies during the breeding season, as supported by the observed genetic divergence between Lord Howe Island and New Zealand colonies. We suggest molecular analysis of fisheries' bycatch individuals as a rigorous method to identify foraging segregation, and we recommend the eastern and western *A. carneipes* colonies be regarded as different Management Units.

Rowan Lymbery, The University of Western Australia: Sexual Selection

Sperm competition, gamete choice and genetic mechanisms in a broadcast spawner

Rowan A. Lymbery, W. Jason Kennington, Jonathan P. Evans; Centre for Evolutionary Biology, School of Biological Sciences, UWA

In many taxa, multiple mating or multi-individual spawning leads to competition among ejaculates for fertilisation and the opportunity for females (or eggs) to promote fertilisations by sperm from preferred males. There is growing evidence that genotype-by-genotype interactions among rival ejaculates or between ejaculates and females can modify the expression of ejaculate phenotypes, and consequently affect variation in reproductive fitness. However, in most systems we lack an understanding of the mechanisms underlying these interactions. Here, we exploit a range of powerful experimental techniques in a broadcast spawning marine invertebrate to investigate a putative mechanism of differential gamete-level mate choice. We demonstrate that chemoattractants released by eggs, which differentially modify sperm swimming behaviour and sperm physiology, allow females to mediate fertilisation success among competing ejaculates. Moreover, we test whether the differential effects of egg chemoattractants on ejaculate phenotypes are underlain by functional changes in sperm RNA profiles, which would represent the first evidence for differential transcription in mature sperm. Uncovering these processes in the ancestral reproductive condition of broadcast spawning has broad implications across animal taxa.

Erin Macartney, University of New South Wales: Lightning Talks

Condition dependent post-copulatory traits: A meta-analysis

Shinichi Nakagawa, Russell Bonduriansky (all UNSW)

The amount of metabolic resources available to an individual through diet (which influences condition) can significantly affect the ability to invest in costly sexual traits, resulting in condition-dependent expression of such traits. This has consistently been applied to male signalling traits, and more recently to post-copulatory traits. However, while high condition males with highly expressed signalling traits are expected to achieve high mating success, mating does not necessarily translate into fertilisation success. The post-copulatory environment is a harsh and complicated place where no single trait determines fertilisation success, and males may invest in multiple, costly post-copulatory sperm and semen traits to gain fertilisation. These traits may vary in their degree of condition-dependence, but the patterns of male investment in such traits are poorly understood. Are some post-copulatory traits more condition-dependent than others? Is post-copulatory condition-dependence more prevalent in some taxa? Are specific nutrients particularly important for the expression of post-copulatory traits? And how does condition-dependence of post-copulatory traits compare to condition-dependence of body size? We carried out a meta-analysis to address these questions, providing a clearer picture of how post-copulatory traits evolve to express variation in male condition.

Erin Macartney, University of New South Wales: Posters

Can condition-dependence theory be extended to cryptic non-genetic paternal factors?

Erin L. Macartney UNSW, Angela Crean (the University of Sydney), Russell Bonduriansky (UNSW)

The theory of condition-dependence has been extensively applied to costly sexual traits such as displays and weaponry, sperm and spermatophores. But can this theory be extended to the more ‘cryptic’ components of the ejaculate that can influence offspring quality such as trace amounts of proteins, non-coding RNAs, DNA methylation and chromatin structure? I consider the conditions under which selection may act on these factors, and suggest ways to test for differential costs and condition-dependence. This will enable the condition-dependence literature to be extended to fitness enhancing factors that have largely been overlooked.

Martino Malerba, Monash University: Macroevolution 1

The Eco-Evolutionary Dynamics of Body Size

Martino E. Malerba and Dustin J. Marshall (Centre of Geometric Biology, Monash University)

Size imposes physiological and ecological constraints upon all organisms. Theory abounds on how traits covaries with body size, yet causal links are often elusive. As a more direct test, used artificial selection to evolve the green microalga *Dunaliella teriolecta* (Chlorophyta) toward different mean cell sizes, while monitoring changes in all major traits. Within 220 generations (c. 18 months), we generated a 600% difference in cell volume among selected lineages. Overall, large-selected populations produced more energy than small-selected populations of equivalent total biovolume, but at the cost of much higher volume-specific respiration. These differences in energy utilization between large (more productive) and small (more energy-efficient) individuals were used to successfully predict ecological performance (i.e., max. growth rate and carrying capacity of the population) across novel resource regimes. In this talk I will describe how physiological and ecological characteristics change as a consequences of cell size evolution.

Dustin Marshall, Monash University: Macroevolution 1

Why are big things big? Why are small things small?

Dustin Marshall, Monash University; Craig White, Monash University

Callum McDiarmid, University of Sydney: Lightning Talks

Sperm form and function in the north American red-sided garter snake *Thamnophis sirtalis*

Callum S. McDiarmid, Christopher R. Friesen, both The University of Sydney

Female polyandry resulting in post-copulatory sexual selection is now considered to be the norm across most taxa, and this exerts strong selection for high quality ejaculates. Specifically, selection on sperm morphology is often suggested to occur, at least partially, via selection for fast swimming sperm that are more likely to successful achieve fertilisation in both competitive and non-competitive scenarios. While there is evidence for relationships between sperm morphology and velocity in a few species, this is yet to be examined in any snake. This lack of understanding is problematic because the incredibly high variability of sperm cells across taxa means that do sperm cells differ in their morphology (e.g. what a sperm head looks like varies considerably among taxa). Thus, sperm cells also swim in quite different ways (with different 'strokes') across taxa, so we would expect different aspects of morphology to be important. Here we assess this relationship for the first time in a snake species, comparing sperm morphology and velocity measures across individual red-sided garter snakes *Thamnophis sirtalis* during the spring breeding season in Manitoba, Canada. Understanding the relationship between form and function of sperm is vital to gain a fuller appreciation of this phenomenon across taxa, but is also important to support future evolutionary research as snake study systems offer valuable opportunities to investigating both pre- and post-copulatory sexual selection.

Marcus Michelangeli, Monash University: Developmental Plasticity

Integrating thermal physiology within a syndrome: locomotion, personality and habitat selection in an ectotherm

Marcus Michelangeli, Celine Goulet, Hee Sung Kang, Bob B. M. Wong, David G. Chapple

Individuals within animal populations often differ from one another in a range of behaviours, and exhibit consistent personalities. How and why these animal personalities are maintained remain key evolutionary questions. Physiology and temperature are known to have a profound influence on behaviour, yet thermal physiology has rarely been considered within the animal personality framework. However, it could be a mechanism that constrains individuals into exhibiting predictable personalities. This may be particularly true for ectothermic species that must behaviourally thermoregulate in order to reach their optimal body temperatures for ecological performance. Here, we present evidence for a novel behavioural syndrome, the Thermal Behavioural Syndrome (TBS), and how it is linked to variation in microhabitat selection in an Australian lizard. The TBS predicts that an individual's thermal traits will correspond with their personality traits. We firstly tested the TBS by measuring the thermal preferences and optimal performance temperature of individual skinks and linking it to their activity, exploratory, social and boldness behaviours. We then monitored the skink's microhabitat selection in an environment containing three substrates differing in thermal characteristics. Our results, among the first to link behaviour and physiological syndromes, will highlight how such variation, both within and between populations, can promote niche specialisation in a lizard species.

Jonathan Mitchell, University of Alaska Fairbanks: Population Genetics & Coalescent

Hypothesis Testing of Species Trees Under the Multispecies Coalescent

Jonathan D. Mitchell, University of Alaska Fairbanks

Under the multispecies coalescent model with incomplete lineage sorting, species trees can be inferred from unrooted gene tree topologies. A statistical hypothesis test can be constructed to test whether a set of gene tree topology frequencies is consistent with the null hypothesis of the proposed species tree topology. For unrooted quartets, the three gene tree topology frequencies are expected to be close to equal when the internal edge is short. When the internal edge is short the infinite sample size limiting distribution of the log-likelihood ratio statistic and Pearson's χ^2 statistic is not a usual χ^2 distribution. We derive the limiting distribution for an arbitrary length internal edge, providing a robust statistical test even when gene tree topology frequencies are close to being equal. Work is under way to develop a statistical test for n-taxon species trees.

Jonathan Mitchell, University of Alaska Fairbanks: Posters

Quartet Test Statistics Under the Multispecies Coalescent

Jonathan D. Mitchell, John A. Rhodes, Elizabeth S. Allman, University of Alaska Fairbanks

The multispecies coalescent model describes the process of incomplete lineage sorting, which can lead to gene trees having differing topologies. Given a sample of gene trees, how can we test whether they might have arisen from the multispecies coalescent model? Our approach will be to focus on displayed quartets.

Jessica Moran, University of Western Australia: Sexual Selection

Rival accessory gland secretions increase sperm velocity in the European honey bee (*Apis mellifera*)

Jessica Moran, University of Western Australia; Renee Firman, University of Western Australia; Ryan Dosselli, University of Western Australia; Boris Baer, University of California

Sperm motility has been repeatedly demonstrated to be a major determinant of fertilization success in various taxa, both in the presence and absence of sperm competition. Surprisingly, sperm motility remains understudied in insects. In the European honey bee (*Apis mellifera*), previous studies have shown that accessory gland secretions (AGS) mediate sperm competition outcome by reducing the viability of rival sperm, but whether these secretions also affect sperm motility remains unknown. I investigated the effects of AGS on honey bee sperm motility and found that sperm exposed to a rival's AGS increased their swimming velocity by an average of 13%. By increasing their swimming velocity, honey bee sperm are likely increasing their chances of reaching the queen's sperm storage organ, ultimately enhancing the male's fitness. The pattern of sperm motility over time suggests that this enhanced motility comes with a cost, and may be traded-off with sperm-viability and motility longevity. This result is consistent with studies of sperm motility in vertebrates and broadcast spawning invertebrates.

Craig Moritz, The Australian National University: Plenary

Phylogenomics, cryptic diversity and evolution of north Australian lizards

Craig Moritz, Research School of Biology & Centre for Biodiversity Analysis, The Australian National University

Applying phylogenomics to widespread, low-dispersal, tropical species often reveals morphologically cryptic but genetically divergent lineages. This is the “dark matter” of diversity — largely invisible to current taxonomy, yet important. Uncovering this diversity, and combining the resulting lineage/species level phylogenies with phenotypic data, yield new insights into patterns of diversity, evolutionary processes and conservation priorities. Focusing on our recent work from northern Australia, I will touch on (i) when and how to recognize cryptic lineages as species, (ii) implications for understanding speciation and morphological evolution in complex communities, and (iii) progress towards mapping and prioritizing areas for conservation, given the inevitably imperfect match of taxonomy to lineage diversity.

Kirke Munch, University of Tasmania: Lightning Talks

Maternal effects impact decision-making in a viviparous lizard

Kirke L. Munch, Daniel W. A. Noble, Erik Wapstra, Geoffrey M. While

Stressful conditions experienced during early development can have deleterious effects on offspring morphology, physiology and behaviour. However, few studies have examined how developmental stress influences an individual’s cognitive phenotype. Using a viviparous lizard, we show that the availability of food resources to a mother during gestation influences a key component of her offspring’s cognitive phenotype; their decision-making. Offspring from females who experienced low resource availability during gestation did better in an anti-predatory task that relied on spatial associations to guide their decisions, whereas offspring from females who experienced high resource availability during gestation did better in a foraging task that relied on colour associations to inform their decisions. To our knowledge, this represents the first evidence that the prenatal environment can influence decision-making in animals, a cognitive trait with functional implications later in life.

The consequences of population dynamics on the invasion of infectious of disease

Louise Solveig Nørgaard, Monash University

At the front line of an invading population, ecological conditions are fundamentally different from the core, and coincides with low population density, low intraspecific competition and high resource availability. All of these factors may make evolution proceed at different rates at the front versus the core of an expanding population. But, what about evolution of a pathogen that invades a host population undergoing different rates of expansion and growth? In this study, I address how population growth dynamics can affect pathogen evolution and whether host density or growth rate can select for specific pathogen virulence strategies. Using experimental populations of the waterflea, *Daphnia magna*, I manipulated growth the phases of a host population (exponential, stationary or in decline) and then experimentally invaded different genotypes of the bacterial pathogen, *Pasteuria ramosa*. Shortly, I found evidence that population dynamics favour the evolution of different pathogen strategies, since not all of the tested pathogens showed decreases in the probability of infection, invasion success, and transmission, once populations had reached their carrying capacity. I discuss how the dynamics of expanding populations are likely to affect the epidemiology and evolution of infectious disease.

Daniel Noble, University of New South Wales: Lightning Talks

Early developmental temperatures and phenotypic plasticity: a meta-analysis

Daniel Noble (University of New South Wales), Vaughn Stenhouse (Victoria University), Lisa Schwanz (University of New South Wales)

Early developmental environments can impact organisms in ways that persist over their life. In reptiles, nest temperatures can affect offspring phenotype and survival in important ways, yet we still lack an understanding of whether general trends exist and the magnitude of impact. We compiled data from 175 reptile studies to examine, and quantify, the effect of incubation temperature on phenotype and survival. Using meta-analytic approaches (standardized mean difference between incubation treatments, Hedges g), we show that across all trait types examined there is, on average, a moderate to large magnitude of effect of incubation temperatures (absolute effect: $|g| = 0.75$). Unsurprisingly, this influence was extremely large for incubation duration, as predicted, with warmer temperatures decreasing incubation time overall ($g = 8.42$). Other trait types, including behaviour, physiology, morphology, performance, and survival experienced reduced, but still mostly moderate to large effects, with particularly strong effects on survival. Effects of incubation temperature were also persistent one-year post-hatching, suggesting they have the potential to impact fitness in the long term. The magnitude of effect increased as the change in temperature increased between treatments (e.g. 6°C versus 2°C) for nearly all traits, and tended to decrease when temperatures of the treatments fluctuated around a mean temperature compared to when they were constant. The effect also depended on the mid-temperature of the comparison, but not in consistent ways, with some traits experiencing the greatest effects at extreme temperatures, while others did not. The heterogeneous nature of the effects we observe, along with a large amount of unexplained variability, indicates that the shape of reaction norms between phenotype and temperature, along with ecological and/or experimental factors, are important when considering general patterns. Our analyses provide new insights into the effect of incubation environments on reptile phenotype and survival and allow general, albeit coarse, predictions for taxa experiencing warming nest temperatures under climatic change.

Terry Ord, University of New South Wales: Macroevolution 1

Diversifying versus stabilizing selection on body size in Southeast Asian gliding dragons (genus *Draco*)

Terry J. Ord1, Joan Garcia-Porta2, and David C. Collar3; 1 Evolution and Ecology Research Centre, UNSW Sydney; 2 Institute of Evolutionary Biology, Barcelona, Spain; 3 Department of Organismal and Environmental Biology, Christopher Newport University, USA

Evolutionary innovations and ecological competition are two factors that can drive adaptive diversification: in the first instance, by opening up new ecological opportunities that result in adaptive differentiation; in the second instance, by pushing co-existing species to diverge in resource use that promotes character displacement. Yet some innovations could result in stabilizing selection that limits phenotypic diversification. If competition also occurs among co-existing species, such limits could have important implications for the extent to which competing species can diverge and adequately adapt to a shift in resource use. We studied the evolution of gliding in Southeast Asian dragon lizards (genus *Draco*). Gliding has classically been identified as a key innovation that should herald accelerated evolutionary diversification. However, it is also an innovation that is likely associated with important constraints, especially on body size: smaller, lighter animals are better gliders than larger, heavier animals. There is also evidence of ecological competition among sympatric species, which would normally be expected to result in character displacement in body size. We compiled extensive data on body size and species co-occurrence, developed a phylogeny for *Draco* and other agamids, and applied a range of phylogenetic comparative methods to investigate the consequences of evolving to glide on body size evolution and the likelihood of character displacement among sympatric species.

Rebecca Pacey, University of New South Wales: Life History & Physiology

Heritability of colour pattern and physiological colour change in jacky dragons

R. S. Pacey, L. E. Schwanz, J. L. Riley, N. McCarthy, K. D. Umbers

The underlying sources of variation in colour pattern of animals can be genetic, non-genetic or more likely, a combination of both. Using recently developed methods in data collection and analysis, this project examined the genetic and non-genetic sources of colour pattern variation and physiological colour change in a captive population of jacky dragons. Quantitative measurements of dorsal colour pattern were obtained for each jacky dragon of which full pedigree information was available for. I found evidence that dorsal colour pattern metrics of elongation and contrast were heritable in this captive population of jacky dragons. Colour pattern metrics elongation and contrast returning significant values of heritability, indicating genetic factors significantly contribute to the variation in these variables. I also found evidence that external stimuli induced rapid physiological colour change in the dorsal colour pattern in jacky dragons, with elongation and contrast colour pattern metrics significantly affected by external stimuli. This thesis contributes new data on colour pattern heritability and describes physiological colour change in a species of which colour pattern has not been studied or quantified before.

Laura Parsley, University of Tasmania: Posters

Impacts of Prenatal Stress on Male Reproduction: Implications for Sex Allocation

Laura Parsley[1], Terry Pinfold[2] , Tiana Pirtle[1], Paul Scowen[2], Keri Smith[2], Amy Edwards[1,3], Elissa Cameron[1,4]; [1]School of Biological Sciences & [2]Medical Sciences Precinct, University of Tasmania, [3]Latrobe University, [4]University of Canterbury

Offspring sex ratios in mammals are often unpredictable despite predictions that ratios should vary with according to the potential reproductive success of sons compared to daughters, in relation to factors such as population density, social status, stress and body condition. The role of males in influencing offspring sex ratios has been largely overlooked, despite being the heterogametic sex. Recent studies have demonstrated a departure from the assumed 50:50 ratio of Y: X chromosome bearing sperm (CBS),which may result from factors such as the conditions males experience in utero, the extent of oxidative stress in X and Y CBS, and the amount of glucose to which the sperm are exposed. In this study we tested the effect of prenatal exposure to the stress hormone cortisol on sex ratios, the amount of reactive oxygen species (ROS), and the concentration of glucose in the reproductive tract and seminal fluid in virgin, sexually exhausted and old male mice. There was no significant effect of treatment on sex ratios, however, cortisol significantly reduced the amount of ROS, in X and Y sperm in old male mice. Furthermore, cortisol treatment reduced the concentration of glucose in the reproductive tract and in seminal fluid in old male mice. These findings suggest that prenatal exposure to stress hormones can inhibit a males capacity to influence offspring sex ratios.

Amanda Pettersen, Monash University: Life History & Physiology

Competition mediates selection on metabolic rates in the field

Pettersen, A. K., White, C. R., and D. J. Marshall; School of Biological Sciences/Centre for Geometric Biology, Monash University, Victoria 3800, Australia

Metabolic rates reflect the ‘pace of life’ in every organism and provide a measure of an organism’s capacity for essential maintenance, growth and reproduction — all of which interact to affect fitness. While thousands of measures of metabolic rates have been made, the underlying microevolutionary forces that shape variation in metabolic rates throughout ontogeny have been poorly resolved. Metabolic rate varies throughout ontogeny - selection on metabolic rate early in development is unlikely to reflect selection on metabolic rate during late-stage development. Furthermore, selection on metabolic rates throughout the life history are likely to vary across environments. Despite the importance of metabolic rate in shaping processes from the individual to community level, empirical studies have mainly been confined to the laboratory, with very few estimates of selection on metabolic rate under realistic field conditions. Here we combine laboratory measures of metabolic rate throughout ontogeny with field measures of fitness (reproductive output) across three levels of competition (intra-specific, inter-specific, and no competition) for a marine bryozoan. We also measure key components of fitness throughout the life history including survival, growth rate and age at the onset of reproduction. We find that the strength and direction of selection on metabolic rate depends on both the stage of development, and environment to which individuals are exposed. Metabolic rates have long been associated with the pace of the life history. We show the complex nature of context-dependent selection that likely generated these patterns, and the potential evolutionary and ecological consequences of variation in metabolic rates.

Ben Phillips, The University of Melbourne: Coevolution & Conservation

Using connectivity to identify environmental axes associated with local adaptation

Ben Phillips, University of Melbourne

Reciprocal transplant experiments clearly demonstrate that local adaptation is a real phenomenon. What these experiments cant do, however, is show us which environmental variables are the primary drivers of local adaptation. This knowledge gap matters when we look to apply the notion of local adaptation to management actions under climate change such as assisted colonisation and targeted gene flow. For these actions we need to find pairs of sites where the current climate of site A matches the future climate of patch B. But making this match requires us to know which axes of climate matter for fitness. Is a difference of 0.5 degrees Celsius more important than a difference of 50mm in annual rainfall? Here I describe a new approach to identifying the axes of climate associated with local adaptation. The method leverages the expectation that gene flow erodes local adaptation to winnow out trait-environment relationships with a fixed genetic basis versus those due to plasticity or habitat selection.

Joel Pick, University of New South Wales: Social 1

Shopaholic house sparrows: understanding parental care form the parent's point of view

Joel Pick1,2, Michael Spence2, Malika Ihle2 & Shinichi Nakagawa1; 1 Evolution and Ecology Research Centre, University of New South Wales; 2 Department of Animal and Plant Science, University of Sheffield

Typically we think of parental care in terms of the outcomes relevant to the offspring, for example, the total resources provisioned. However this view ignores the parental behaviour that resulted in that particular level of investment, and so obscures the costs and constraints underlying parental care. Through the use of novel statistical techniques, we take a step back to try and understand parental care from the parent's point of view, and so the factors constraining parental investment and the costs of compensating for these constraints.

Federica Poli, University of Western Australia: Lightning Talks

Effects of females reproductive fluids on sperm motility in zebrafish

Federica Poli1, Simone Immler2 and Clelia Gasparini1; 1 Centre for Evolutionary Biology, School of Biological Sciences, University of Western Australia, Crawley, Australia 2 School of Biological Sciences, University of East Anglia, Norwich, United Kingdom

Female reproductive fluids (FRF, the fluid surroundings the eggs also known as ovarian fluid), have been recently shown to affect sperm performance and mediate sperm choice in both internal and external fertilizers. Here, we studied the effect of FRF in the zebrafish (*Danio rerio*). We first investigated to what extent FRF affects sperm motility and longevity, important determinants of ejaculates fertilization ability in many fish species. We then used a North Carolina II design, to explore female, male and female x male effects by testing sperm motility of two males in the FRF of two females (i.e. 2x2 blocks). Results indicate that FRF affects sperm motility, and preliminary results from the NCII design provide evidence that FRF differentially affects sperm from different males, thus suggesting the potential for cryptic female choice mediated by FRF.

Iva Popovic, University of Queensland: Coevolution 2

Evolution in hot waters: Comparative genomics reveals divergent thermal selection in invasive and non-invasive marine mussels

Iva Popovic and Cynthia Riginos; School of Biological Sciences, University of Queensland

Investigating the history of natural selection among closely related species can help delineate how genomes diverge in response to disparate environmental pressures, and how these evolutionary outcomes may affect ecologically important traits such as species' distribution limits and invasive species success. Here, we integrate transcriptome-wide sequence data with a priori knowledge of thermal tolerance candidate genes to assess the contributions of thermal selection to the divergence of the warm-tolerant and invasive marine mussel *Mytilus galloprovincialis*, from three cold-tolerant, non-invasive *Mytilus* congeners. We combine codon model tests with polymorphism and divergence data to infer whether signatures of positive selection for species divergence correspond to lineage-specific shifts in warm-temperature tolerance in *M. galloprovincialis*. We identified a subset of thermal tolerance candidate genes among loci under selection, although a priori genes were not significantly enriched. Transcriptome-wide analyses, however, revealed evidence that the strongest signatures of positive selection are limited to loci involved in protecting the cell from oxidative stress, primarily through pathways regulating sulfur metabolism. This result is consistent with functional gene categories strongly associated with species-specific responses to thermal stress in physiological studies. These findings, coupled with functional concordance among positively selected a priori and non a priori genes, are consistent with a contribution of temperature-dependent selection in the divergence of the *M. galloprovincialis* lineage. Our results support the hypothesis that differential strategies in coping with intracellular reactive oxygen species are an important factor explaining differences in thermal limits among *Mytilus* congeners that may mediate their different propensities for invasiveness.

Venkatesh Radha, Monash University: Life History & Physiology

Genetic variation in the mitochondrial genome exerts sex-specific effects on metabolic rate of fruit flies

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Over the past two decades, studies across taxa has convincingly shown that mitochondrial mutations, which were once thought to be neutral to selection, can sex-specifically alter organismal life-history trait expression. However, the influence of mitochondrial mutations and their sex-specificity on the expression of a core physiological trait, standard metabolic rate, remains an open question in evolutionary biology. To test this, we measured metabolic rates in both sexes across an array of 13 ‘mitochondrial lines’, which differed only in their mitochondrial genomes, but harnessed a common, isogenized w1118 nuclear genome. Four days old, fully fed, adult non-mated flies were assayed for the amount of CO2 released per min, in a flow through respirometry setup, within a dark, temperature and humidity controlled environment. Throughout the experiment, grandparental and parental age and population density effects were controlled. Metabolic rate estimates from each fly were adjusted for their body mass and physical activity. Our results suggest that mitochondrial genetic variation affects standard metabolic rate in both sexes, but more so in males, across all mitochondrial lines. However, much of the metabolic rate variation in males across the lines was strongly tied to diurnal effects. From an evolutionary standpoint, changes in physiological phenotypes between sexes is interesting, because this could explain much of the sex-dependent phenotypic variation across life-history traits, underpinned by mitochondrial genetic variation.

Emily Remnant, University of Sydney: Coevolution & Conservation

Changing viral landscapes in honeybee populations exposed to an ectoparasitic mite

Emily J. Remnant (1), Laura Brettel (2,3), Jessical Kevill (2), Tjeerd Blacquiè (4), Stephen Martin (2) and Madeleine Beekman (1); (1) Behaviour and Genetics of Social Insects Laboratory, School of Life and Environmental Sciences, University of Sydney, Sydney, Australia; (2) School of Enviroment and Life Sciences, University of Salford, Manchester, UK; (3) Hawkesbury Institute for the Environment, Western Sydney University, Sydney, Australia; (4) Wageningen University & Research, Wageningen, The Netherlands

The viral landscape of honey bees (*Apis mellifera*) has changed since the emergence of the ectoparasitic mite, Varroa destructor. The worldwide spread of Varroa caused decreased honey bee health and increased colony loss due to the spread of viruses that Varroa harbours and transmits to bees upon feeding. One strain of a particular virus, strain A of Deformed wing virus (DWV-A), seems to have a close association with Varroa and has been linked with colony deaths. Indeed, wherever honey bee colonies succumb to Varroa, DWV-A is found. It is therefore tempting to conclude that DWV-A is the real culprit and Varroa is simply the vector. So far, the only strategies to prevent colony loss rely on managing Varroa levels with chemicals, or by breeding Varroa-resistant bees. A number of Varroa-resistant honey bee populations currently exist that survive mite infestations without chemical intervention. If honey bee deaths are due to particular viral strains, we would expect Varroa-resistant bee populations to either lack DWV altogether, or carry different DWV strains compared with susceptible populations. We used next-generation sequencing and viral metagenomics to compare viral variants between Varroa-resistant and susceptible honey bee populations from diverse locations around the world. We find that in multiple locations, DWV strain A has been replaced by DWV strain B. In populations that are resistant to Varroa, novel recombinant DWV strains prevail, while in some isolated populations DWV levels remain low or absent despite the presence of Varroa.
Clearly the association between Varroa and DWV is more complex than initially suggested. Instead of Varroa vectoring a single strain of DWV we find that long-term presence of Varroa can lead to replacement of certain viral strains, and particular recombinants could be somehow linked to Varroa tolerance. The question remains if the observed pattern is purely correlational or if the different strains actually differ in their virulence. In other words, how influential is DWV — accidental passenger or key to Varroa resistance?

Emily Remnant, University of Sydney: Posters

Recombinant Deformed Wing Virus strains in Varroa-resistant honey bees

Emily Remnant[1], Stephen Martin[2], Laura Brettel[2], Tjeerd Blacquiére[3] and Madeleine Beekman[1]; [1]The University of Sydney, Sydney, Australia; [2]The University of Salford, Manchester, UK; [3]Wageningen University & Research, Wageningen, The Netherlands

The viral landscape of honey bees (*Apis mellifera*) has changed dramatically since the emergence of the ectoparasitic mite, *Varroa destructor*. The global spread of Varroa caused decreased honey bee health and increased colony losses throughout the beekeeping world. It is now clear that the pathology caused by mites is largely due to the spread of virulent viruses that Varroa harbours and transmits to bees upon feeding. In particular, the spread of one RNA virus, Deformed Wing virus (DWV) has been described as a global pandemic: DWV titres increase dramatically upon infestation with mites. However, multiple DWV strains exist, and specific strains are apparently associated with increased virulence. Furthermore, recombination between DWV strains frequently occurs, generating novel viral haplotypes.

In most cases, chemical miticides are necessary to prevent colony loss. However, multiple honey bee populations have naturally evolved or been selected for Varroa-resistance. While these populations can withstand Varroa infestation, it is unclear whether the bees also differ in their response to viruses. Therefore, we examined the viral landscape of Varroa-resistant honey bee populations from Europe, Africa and the Pacific. We find that DWV titres can be extraordinarily high, similar to levels found in collapsing, Varroa-sensitive colonies. However, we see multiple instances of similar DWV recombinant strains that have occurred in different populations of Varroa-resistant bees. These results indicate that the relationship between honeybees, Varroa mites and DWV is constantly evolving, and subtle differences in viral genomes could alter the balance between colony survival and mortality.

Shane Richards, University of Tasmania: Sex

Investigating mate opportunity cost as the driver of protandry for a butterfly

Shane A. Richards (UTAS), Bethan Hindle, Stephen G. Willis (Durham University)

Mate opportunity cost is usually suggested as the driver of protandry in insects but testing the theory in the field is difficult. Here we apply a mark-recapture analysis that estimates both survival and patterns of emergence for male and female marbled white butterflies (*Melanargia galathea*). We show statistical evidence of protandry in a field population and show that times of peak emergence are consistent with predictions from an evolutionary model. Data on the main nectar source suggests a phenological cascade linking flower production, female emergence and male emergence.

Julia Riley, Macquarie University: Social 1

Early experience impacts social plasticity of the family-living tree skink

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An animal's social environment can be both dynamic and complex. Thus, social species are often highly plastic in their social behaviour to garner fitness benefits. Yet, behavioural plasticity can be constrained by an individual's social experience. We examined the influence of social environment on social behaviour in the family-living tree skink (*Egernia striolata*). In this study's first phase, we reared juveniles in two different social environments for 1.5 years: either in isolation or an unrelated pair. We also quantified each lizard's sociability at four-month intervals using a standardized laboratory assay, and found that isolated lizards were more sociable than socially-reared lizards. In this study's second phase, we released all lizards into a semi-natural environment, observed their associations, and used social network analysis to quantify their social behaviour. During the following six months, isolated lizards were at first more sociable than socially-reared lizards. Then, over time, isolated lizards became less sociable, potentially converging with the lower sociability of socially-reared lizards that was stable over time. Our findings suggest that social experience influences how *E. striolata* associate with conspecifics, but isolation rearing did not constrain their ability to adapt to a novel social environment.

Ben Rohrlach, University of Adelaide: Population Genetics & Coalescent

Quantifying Demographic Structure in Single-copy Alignment Data via Generalised PCA

Ben Rohrlach[1], Nigel Bean[1], Jono Tuke[1] and Barbara Holland[2]; [1]University of Adelaide, [2]University of Tasmania

Identifying demographic structure in alignment data can be of interest to researchers. For example, conservationists may wish to explore the geographic distribution of genetic diversity of an endangered species. Similarly, we may be interested in exploring the historical migration routes of extinct species.
In this talk I will show how single-copy sequence data can be transformed into continuous coordinate information. We can use these coordinates to visualise the data in lower dimensions in gene-space, and how we can explore and quantify the relationship between these coordinates and any qualitative, or quantitative, information about the sequences.
In particular I will show how we can apply these methods to show the risk posed by blast mining to Ghost Bats in Western Australia.

Emily Roycroft, University of Melbourne: Macroevolution 2

Conflict and confidence in phylogenomics: an example from a recent and rapid radiation

Emily J. Roycroft (1, 2), Adnan Moussalli (1), Kevin C. Rowe (1); 1 Sciences Department, Museums Victoria; 2 School of BioSciences, The University of Melbourne

Characterising the evolutionary history of rapid radiations is non-trivial, and often hindered by lack of phylogenetic signal and/or discordant genealogies. Phylogenomic data provide the ability to investigate relationships that have previously been difficult to resolve. One such example is the rapid and recent radiation of “old endemic” murine rodents of Australia and New Guinea. The old endemic rodents have an origin into New Guinea via a single over-water colonisation event from Southeast Asia 6 million years ago, and have since diversified into $\approx$160 species within 34 genera. Topological support around rapid bursts of lineage accumulation, coinciding with ecological opportunity, has been spurious in previous multilocus studies ($<$ 10 loci). To attempt to resolve these relationships, we develop and apply a novel exon capture design, targeting $\approx$1400 protein coding loci. Using these phylogenomic data, we interrogate the strength of phylogenetic signal and genealogical conflict at previously poorly supported nodes. We find that standard metrics of confidence (from both concatenated and summary coalescent-based methods) do not adequately capture uncertainty at short internodes in phylogenomic data, and we thus apply recently described, alternate methods for exploring latent, genome-wide conflict and/or lack of signal.

Fabian Rudin, University of Western Australia: Lightning Talks

The effects of the social environment on the heritability, evolvability and repeatability of behaviour

Fabian S. Rudin (Centre for Evolutionary Biology, School of Biological Sciences, The University of Western Australia); Joseph L. Tomkins (Centre for Evolutionary Biology, School of Biological Sciences, The University of Western Australia); Leigh W. Simmons (Centre for Evolutionary Biology, School of Biological Sciences, The University of Western Australia)

The social environment is expected to have substantial effects on behaviour and its heritability and evolvability through indirect genetic effects and interacting phenotypes. We investigated these effects by exposing Australian field crickets (*Teleogryllus oceanicus*) to silence or recordings of male acoustic sexual signals. By employing a full-sib/half-sib breeding design with elements of a pedigree design we assessed the heritability and evolvability of behaviours related to boldness, exploration and activity. Additionally we were able to estimate the repeatability of behaviours by measuring them at two time points. We found no difference in repeatabilities between the silent and the acoustic environment but did find significant differences in heritabilities and different measures of evolvability between environments. We detected significant genotype-by-environment interactions for most behaviours measured. Additionally, we found a high degree of similarity between the phenotypic covariance matrices in the two environments while the genotypic covariance matrices were highly dissimilar. Lastly, we found that the repeatable aspect of behaviour (‘personality’) was significantly heritable for most behaviours. We discuss the evolutionary implications of our findings light of the social environment and explore hypotheses such as the phenotypic gambit and Cheverud’s conjecture.

Mara Ruiz, University of Tasmania:

Unravelling geographic and climatic barriers to introgression of a sexually selected syndrome in wall lizards

Mara Minano, Geoffrey M. While, Tobias Uller

Recently, it has been shown that geographic phenotypic variation in both plants and animals can be a result of genetic exchange between species and subspecies. The rate and direction of genetic exchange is strongly influenced by patterns of selection and thus mediated to some degree by aspects of 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. The common wall lizard, *Podarcis muralis*, exhibits considerable phenotypic and genetic divergence across its species range with distinct evolutionary lineages that have come naturally into secondary contact in northern Italy. Previous data collected in this species has shown that a) there is a strong asymmetric introgression driven by sexual selection, b) introgression of a small part of the genome is responsible for large shifts in phenotype, c) introgression is widespread geographically and has occurred into multiple genetic backgrounds. However, preliminary data demonstrates that introgression is limited at high altitude, suggesting that climatic factors may be mediating the spread of genes within these regions through relaxed sexual selection or, alternatively, natural selection against sexually selected characters. In this project I will investigate (I) patterns of introgression across the Italian landscape (II) differences in introgression between sexes and (III) possible factors limiting introgression in wall lizards. I will combine a broader approach — landscape genetics — to investigate patterns of introgression and a finer approach — cline analysis — to investigate differences between sexes within lineage and between lineages.

Alistair Senior, University of Sydney: Open Session

Is Fertility Selection the Key to the Double Puzzle of Diabetes?

Alistair M. Senior[1,2] & Stephen Corbett[3,4]; [1]The University of Sydney, Charles Perkins Centre. [2]The University of Sydney, School of Mathematics and Statistics; [3]Centre for Population Health, Western Sydney Local Health District; [4]University of Sydney, Western Clinical School.

Diabetes has been labelled a double evolutionary puzzle: 1) why is such a highly heritable but debilitating condition so common and 2) why is diabetes less common in people of European descent than almost all other peoples. A number of largely unsatisfactory evolutionary explanations have been advanced. We model the plausibility of the fertility first hypothesis (FFH): purifying fertility selection against an ancestral insulin resistant phenotype, triggered by demographic and nutritional changes linked to the Industrial Revolution, has reduced frequency of the phenotype among Europids. The physiological basis of the model is that insulin resistance reduces the time to return to menses after nutritional or lactational amenorrhoea.

Pre-industrially, the duration of lactational amenorrhoea was 30-32 months and births followed a strong seasonal pattern linked to agricultural and food cycles. An insulin resistant phenotype could have historically increased lifetime reproductive success by shortening the inter-birth interval, an advantage that has since been lost. A question raised by FFH is whether such fertility selection is strong enough to induce significant changes in genotype frequency in just 300 years, around 15 human generations. We use disposable soma theory to model the evolution of insulin resistance in a population undergoing nutritional and demographic transition. Our models were parametrized using UK birth and death records from the last 175 years, estimates of the heritability of insulin sensitivity from twin studies and cohort studies on the effects of insulin resistance on reproduction. We find that the prevalence of insulin-resistance could fall from 50% in a pre-industrial population to around 10% in a post-industrial environment in 10 to 15 generations under FFH.

Carla Sgró, Monash University: Plenary

Responding to environmental change: plasticity or evolution?

Carla M. Sgró

Climate change threatens biodiversity, with many animals thought to be at risk of extinction. Global change will also alter the distribution and abundance of species of direct concern to human health and food security, such as disease vectors and agricultural pests. The extent to which evolution and phenotypic plasticity might mediate specie responses to climate change remains largely unknown. We use a combination of experimental evolution and environmental manipulations to address this gap in our understanding.

I will discuss how we have used intra- and inter-specific studies of invertebrates to understand the physiological and evolutionary processes that limit, and enable, adaptive responses to rapid environmental change. I will also discuss our efforts to have evolutionary theory explicitly incorporated into biodiversity management and planning.

William Sherwin, University of New South Wales: Macroevolution 3

Information Theory Broadens the Spectrum of Molecular Ecology and Evolution

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Information or entropy analysis of diversity is used extensively in community ecology, and has recently been exploited for prediction and analysis in molecular ecology and evolution. Information measures belong to a spectrum (or 'q-profile') of measures whose contrasting properties provide a rich summary of diversity, including allelic richness ($q = 0$), Shannon information ($q = 1$), and heterozygosity ($q = 2$). We present the merits of information measures for describing and forecasting molecular variation within and among groups, comparing forecasts with data, and evaluating underlying processes such as dispersal. Importantly, information measures directly link causal processes and divergence outcomes, have straightforward relationship to allele frequency differences (including monotonicity that $q = 2$ lacks), and show additivity across hierarchical layers such as ecology, behaviour, cellular processes, and non-genetic inheritance.

Heejung Shim, University of Melbourne: Posters

BayesCAT: Bayesian co-estimation of alignment and tree

Heejung Shim[1], Bret Larget[2]; [1]School of Mathematics and Statistics, Melbourne Integrative Genomics, University of Melbourne, Melbourne, Australia, [2]Departments of Statistics and of Botany, University of Wisconsin, Madison, Wisconsin, USA

Traditionally, phylogeny and sequence alignment are estimated separately: first estimate a multiple sequence alignment and then infer a phylogeny based on the sequence alignment estimated in the previous step. However, uncertainty in the alignment is ignored, resulting, possibly, in overstated certainty in phylogeny estimates. We develop a joint model for co-estimating phylogeny and sequence alignment which improves estimates from the traditional approach by accounting for uncertainty in the alignment in phylogenetic inferences. Our insertion and deletion (indel) model allows arbitrary-length overlapping indel events and a general distribution for indel fragment size. We employ a Bayesian approach using MCMC to estimate the joint posterior distribution of a phylogenetic tree and a multiple sequence alignment. Our approach has a tree and a complete history of indel events mapped onto the tree as the state space of the Markov Chain while alternative previous approaches have a tree and an alignment. A large state space containing a complete history of indel events makes our MCMC approach more challenging, but it enables us to infer more information about the indel process. The performances of this joint method and traditional sequential methods are compared using simulated data as well as real data. Software named BayesCAT (Bayesian Co-estimation of Alignment and Tree) is available at https://github.com/heejungshim/BayesCAT.

Julia Shore, University of Tasmania: Origins of Life & Posters

Substitution matrices recapitulate amino acid specificity of aaRS phylogenies

Jeremy Sumner, Barbara Holland (both from University of Tasmania) and Peter Wills and Kay Nieselt (University of Auckland)

Enzymes called amino-acytyl tRNA synthase (aaRS) are responsible for attaching amino acids to tRNA during the process of gene expression. In total there are 20 aaRS, one for each amino acid, and their structures strongly suggest that they can be divided into two classes: class I and class II (each class containing 10 aaRS). This has inspired a hypothesis for the origin of life: initially there were only 2 aaRS the first giving rise to class I and the second giving rise to class II.
I will present the results of a study that tested this theory by comparing empirical amino acid substitution rate matrices such as PAM1 and BLOSUM62 to rate matrices generated by the hypothesis. The results of this study show that hypothesised aaRS-class rate matrices do indeed fit empirical models significantly better than rate matrices generated by (random) alternative hypotheses. Further studies show that the polarity of amino acids is also an important factor in these lines of inquiry and that a rate matrix that takes into account both aaRS class and amino acid polarity fits empirical models better than any other method tried.

Mike Steel, University of Canterbury: Combinatorics

Triplet covers and phylogenetic flexibility ("to be slim it helps to be thin")

Mike Steel (University of Canterbury)

Patchy taxon coverage across loci leads to some interesting questions in phylogenetic combinatorics. In this talk, I discuss two. One concerns reconstructing phylogenies from leaf-to-leaf distances when these distances are known for only certain pairs of leaves. I describe the treacherous path that led finally to a proof of the 'triplet cover conjecture'. A second question concerns the notion of 'phylogenetic flexibility' arising when taxon coverage is sufficiently 'thin' or, more generally, 'slim'. We show that phylogenetic flexibility relates to classical combinatorial concepts such as matchings and sub-modularity, from which a polynomial time algorithm for flexibility can be given. This is joint work with Katharina Huber, Vincent Moulton and (for the first topic) Stefan Grünewald.

Jeremy Sumner, University of Tasmania: Algebraic Methods

Newfangled results and musings on Lie-Markov models

Jeremy Sumner (University of Tasmania)

Over the last 5 years+ members of the UTAS Theoretical Phylogenetics Group have worked on what we refer to as "Lie-Markov models". These are a class of continuous-time Markov chains that have the pleasing property of producing substitution matrices that are closed under matrix multiplication. Our primary focus thus far has been on applications to phylogenetic modelling, but the general concept ushers in a multitude of only partially resolved mathematical questions. In this talk I will discuss various mathematically-focused aspects of the Lie-Markov models: a recently obtained proof that multiplicative closure implies a Lie algebra structure; using finite semigroups to derive novel Lie-Markov models; the so-called "generalized pulley principle"; the relationship between the rate matrices of a given Lie-Markov models and the resulting substitution matrices; and a tentative conjecture regarding modification of AIC (Akaike Information Criteria) for phylogenetic models that are not multiplicative closed.

Janan Sykes, University of Tasmania: Macroevolution 2

Analysing Protein Structure Alignment Methodologies

Janan Sykes, University of Tasmania; Barbara Holland, University of Tasmania; Michael Charleston, University of Tasmania

In order to map and understand the protein universe we must have a reliable and robust method of defining which proteins belong to which structures (or 'folds'). This can be done through protein structural alignment and comparison. Dozens of different methodologies for this task have been put forward. Seventeen of these were be used to compare proteins known to share different levels of structural similarity in an attempt to compare them and analyse their effectiveness.

Venta Terauds, University of Tasmania: Algebraic Methods

Maximum likelihood distances for circular genomes

Venta Terauds and Jeremy Sumner, University of Tasmania

Evolution of circular genomes is most commonly modelled via gene rearrangement, with evolutionary distance taken to be the minimum number of rearrangements needed to convert one genome into another. Recent work has suggested that maximum likelihood estimates (MLEs) of time elapsed are a better proxy for true evolutionary distance. We present results to support this claim. By considering potential symmetries of rearrangement models, along with that of the genomes, and by applying techniques from group representation theory, we significantly reduce the combinatorial complexity of the distance calculations. This allows us to compare the properties of minimum distances to MLEs for genomes with up to eleven regions under several distinct rearrangement models.

Joshua Thia, The University of Queensland: Phylogeography

Marine connectivity in time and space: Insights from an intertidal fish

Joshua Thia (UQ), Katrina McGuigan (UQ), Libby Liggins (Massey), Cynthia Riginos (UQ)

In contrast to terrestrial systems, connectivity and genetic structure within marine metapopulations may be highly variable in space and time — a phenomenon coined 'chaotic genetic patchiness'. Historically, it has been largely presumed that planktonic dispersal during the larval phase of many marine organisms would facilitate high connectivity among populations and create genetic homogeneity within a species. However, stochastic forces in the marine environment are becoming increasingly recognised as significant causes of spatiotemporal variability in the distribution of genetic variation through their impact on larval supply and/or variability in local selection. It is therefore important to consider both adult and juvenile cohorts when studying chaotic genetic patchiness, yet few studies to date have replicated sampling across space and time to make full assessments of the: (1) variability in genetic connectivity and structure, and (2) processes that drive this variability. We achieve this by considering spatiotemporal replicates of adult and juvenile *Bathygobius cocosensis* (an intertidal fish) along the east coast of Australia. These individuals were sequenced using restriction associated DNA markers (RADseq) to obtain a large number of polymorphic loci for population genetic analyses. We consider how spatial distance, directionality in ocean currents, and larval retention rates, dictate connectivity through their impact on larval delivery. Furthermore, we test the potential for variability in local selection to impact genetic diversity by contrasting outlier loci across cohorts, sampling sites, and time.

Vicki Thomson, University of Adelaide: Lightning Talks

Epigenetics of Tiger Snakes

Carlos Rodriguez-Lopez, Moumouni Konate, Kate Sanders, Vicki Thomson

While research on changes in phenotypic plasticity within wild animal populations is centuries old, very few studies have empirically demonstrated a role for epigenetic variation in the response of natural populations to environmental change. Here we identify a region of biogeographic complexity that houses unique genetic diversity in the wild tiger snake (*Notechis scutatus*) and examine how adaptation to island environments can occur through epigenetic divergence. These snakes have been isolated on a mosaic of offshore islands where they show a variety of phenotypic adaptations, including differences in skin colour, sexual dimorphism, scale counts, aggression levels and levels of plasticity in body and head size linked to the ability to ingest large prey. We have generated methylation sensitive amplified polymorphism (MSAP) data and found that, in general, tiger snakes on island groups that share an evolutionary history and environmental niche are more distinguished by methylation status than genetic differences. Tiger snakes on each island group in South Australia have a distinctive epigenetic signal, suggesting local adaptation to these environments. This is also supported by the strong positive relationship between differences in epigenetic profile and population isolation age, temperature in winter and precipitation level in summer.

Tobias Uller, University of Lund: Plenary

Causes and Consequences of Hybridization: From Behaviour to Evolution

Tobias Uller

Geographic patterns of genetic and phenotypic variation demonstrate that hybridization is common in animals. But rarely do we understand how those patterns come about. Our work on common wall connects individual behaviour to evolutionary processes. In this talk, I will focus on (i) how phenotypic divergence in allopatry shapes individual interactions following secondary contact, (ii) what this means for the patterns of hybridization, and (iii) the implications of hybridization for genetic and phenotypic diversity in native and non-native populations of wall lizards. The results demonstrate an important role for sexual selection and suggest rapid introgression of phenotypes following secondary contact

Belinda van Heerwaarden, Monash University: Climate Change

Limited scope for plasticity to increase upper thermal limits

Belinda van Heerwaarden, Vanessa Kellermann and Carla M. Sgró, Monash University

Increases in average temperature and the frequency of extreme temperature events are likely to pose a major risk to species already close to their upper physiological thermal limits. The extent to which thermal phenotypic plasticity can buffer these changes and whether plasticity is constrained by basal tolerance levels, remains unknown. We examined the effect of developmental temperature under both constant and fluctuating thermal regimes (developmental acclimation), as well as short-term heat hardening on upper thermal limits (CTmax) in a tropical and temperate population of *Drosophila melanogaster*. We found evidence for thermal plasticity in response to both developmental acclimation and hardening treatments; CTmax increased at warmer developmental temperatures and with a prior heat hardening treatment. However, hardening and acclimation responses were small, improving CTmax by a maximum of 1.01°C. While plasticity in CTmax was evident in both populations of *D. melanogaster* we studied, plastic increases in upper thermal limits, particularly at warmer temperatures, may be constrained and be insufficient to keep pace with temperature increases predicted under climate change.

Regina Vega-Trejo, The Australian National University: Developmental Plasticity

Inbreeding depression and a poor start in life

Regina Vega-Trejo, Megan L. Head, Loeske E. B. Kruuk, Michael D. Jennions; The Australian National University

Inbreeding is a widespread phenomenon that decreases fitness and inbreeding depression occurs because matings between relatives lead to an increase in homozygosity. Inbreeding is a pervasive force in evolutionary ecology driving the evolution of different traits, mating systems, and influencing population dynamics. It is generally assumed that the negative effects of inbreeding are exacerbated in stressful environments. We conducted experimental studies that explore whether life history, morphological, and sexual traits show inbreeding depression, and if this effect is increased by an interaction with an early stressful environment. The present study highlights the need to look at the interplay between the many different factors that can affect an individual's fitness. Additionally, we show that inbreeding depression might not be evident based on the phenotype of individual traits, and only become apparent when looking at key fitness components.

Arndt von Haeseler, University of Vienna and Medical University of Vienna:

Computational Methods

Fast Bootstrap approaches in IQ-Tree

joint work with Diep Thi Hoang, Olga Chernomor Bui Quang Minh Sy Vinh Le

The standard bootstrap (SBS), despite being computationally intensive, is widely used in maximum likelihood phylogenetic analyses. We recently proposed the ultrafast bootstrap approximation (UFBoot) to reduce computing time while achieving more unbiased branch supports than SBS under mild model violations. UFBoot has been steadily adopted as an efficient alternative to SBS and other bootstrap approaches.
Here, we present UFBoot2, which substantially accelerates UFBoot and reduces the risk of overestimating branch supports due to polytomies or severe model violations. Additionally, UFBoot2 provides suitable bootstrap resampling strategies for phylogenomic data. UFBoot2 is 778 times (median) faster than SBS and 8.4 times (median) faster than RAxML rapid bootstrap on tested datasets. UFBoot2 is implemented in the IQ-TREE software package version 1.6 and freely available at http://www.iqtree.org.

Geoff While, University of Tasmania:

Social 1

The Evolutionary Ecology of Family Living in Lizards

Geoff While - School of Biological Sciences, University of Tasmania; Tobias Uller - Department of Biology, University of Lund; Erik Wapstra - School of Biological Sciences, University of Tasmania

Social behaviour can be relatively simple such as an interaction between two individuals that briefly meet or it can result in the formation of larger social groups, where multiple individuals interact over extended periods of time. Such stable social groups emerge as the result of either family members remaining together (fraternal societies) or through the non-random association between unrelated individuals (egalitarian societies). In both cases, this can result in individuals becoming mutually dependent on one another, forgoing their own personal reproduction and assisting with the reproduction of others. The evolution of such complex behaviour and societies has been highlighted as a major evolutionary transition. Thus, understanding the factors responsible for the evolutionary origins of such societies has been a major challenge for biologists. To date lizards have played a relatively minor role in our understanding of what triggers and maintains the evolution of such stable complex social behaviour, as they have been assumed to exhibit limited, if any, evidence of stable social groups. However, recent research has begun to question this with the realisation that long-term stable social aggregations are both functionally and taxonomically diverse. Here we outline the evidence for stable social groupings across lizards and provide a detailed discussion of the factors which may have led to their emergence, maintenance and diversification. We argue that lizards offer potential to be outstanding systems for understanding the evolution of complex sociality and anticipate that they will feature more prominently in the social evolution literature in the future.

Michael Whitehead, The University of Melbourne: Coevolution 2

Linking pollinator behaviour and floral evolution

Michael Whitehead (The University of Melbourne), Steve Johnson (University of KwaZulu-Natal)

The majority of flowering plants engage animals to carry out the essential service of pollination. Through mate-selection, the behaviour of animals therefore exerts a profound influence on the evolution of flowering plants. I discuss these links between pollinator behaviour and the evolutionary biology of flowers in studies on two different systems.

The remarkable long-tongue fly is a keystone South African pollinator and provides an empirical system to test the influence of floral communities on pollinator visual ecology. Using artificial flowers, I show that flies' colour preference is flexible in response to the colour of the local flowering community. This evidence for learned preference suggests that the unusually high number of deceptive orchids pollinated by *P. ganglbaueri* have evolved true advergent Batesian mimicry of signalling in the food plants of this fly species. These findings also emphasize the importance of co-flowering community context for the evolution of floral colour via pollinator-mediated selection.

In Australia, we lack basic information on the pollination of most of our native plants. Nevertheless, it is clear that we have an unusually high number of bird-pollinated species. I present a preliminary view of my new study designed to collect novel plant-pollinator ecological data and answer the question: From a plant's perspective, what's the difference between being pollinated by a bee or a bird?

Camilla Whittington, University of Sydney: Open Session

The genetic basis of vertebrate pregnancy and birth

Camilla Whittington (University of Sydney), Denis O'Meally (Beckman Research Institute of City of Hope, USA), Melanie Laird (University of Sydney), Kathy Belov (University of Sydney), Michael Thompson (University of Sydney), Bronwyn McAllan (University of Sydney)

Complex traits such as eyes and live birth (viviparity) are dramatic, adaptive novelties that have shaped the evolutionary trajectories of animals. Viviparity is an important biological innovation that has required a set of complex phenotypic changes to allow internal incubation of embryos, radically changing the way in which organisms interact with their environment and transmit their genes to the next generation. As viviparity has evolved convergently hundreds of times in mammals, reptiles, fish, amphibians, and invertebrates, it is an ideal model to study complex traits, offering the opportunity to compare and contrast naturally replicated evolutionary experiments.

We are using transcriptome profiling coupled with physiological and morphological studies to examine gene expression in the gestational tissues of viviparous animals, and determine the genetic controls underpinning pregnancy in animals in which viviparity has independently evolved. We have identified transcriptional changes associated with nutrient transport, gas exchange, and immunological protection of developing embryos at conception, development and parturition in a range of vertebrates. Key transcripts share homology across pregnant mammals, reptiles, and fish, suggesting a common toolkit of genes regulating pregnancy in divergent evolutionary lineages. Our work shows that common mechanisms may underpin the development of evolutionary innovations across divergent species.

Heidi Wong, The University of Melbourne: Lightning Talks

The fitness cost of being selfish

Heidi Wong, Luke Holman, University of Melbourne

Meiotic drive genes break Mendel's law of segregation to ensure they are preferentially transmitted to the next generation. Segregation Distorter (SD) is a chromosome-sized meiotic drive element in *Drosophila melanogaster*. Even though heterozygous males transmit SD to more than 95% of their progeny, SD is found at low, stable frequencies (0-8%) in wild populations. To understand why SD does not spread, we evaluated the fitness of individuals that carry 0, 1, or 2 copies of SD, at both juvenile and adult stages. We also searched for maternal and paternal effect of SD on offspring fitness. This project will confirm whether SD is kept at low frequency by direct or indirect fitness costs, and reveal whether still other factors are at play.

Michael Woodhams, University of Tasmania: Computational Methods

What makes a good DNA mutation model?

Michael Woodhams*, Michael Charleston*, Jeremy Sumner*, David Liberles+, Barbara Holland*. * University of Tasmania, + Temple University

We analyse 16 DNA alignments with 171 DNA mutation models, selected from both the traditional time reversible models, and the Lie-Markov models. The models can be classified according to various binary properties, such as does this model allow transition and transversion rates to differ? How do these various properties influence the likelihood of the model? How does the relative ranking of DNA models change with different rates across sites models?

Zac Wylde, University of New South Wales: Lightning Talks

Self-perceived dominance hierarchy effects on Cuticular hydrocarbon profiles in *Telostylinus angusticollis* (Diptera)

Wylde, Z.

Most research into the effects of dominance hierarchies is focused on eusocial species of insect, yet little is known about how these hierarchies manifest in species lacking true sociality. Epicuticular hydrocarbons have been implicated in chemical communication in the context of mate choice, sex recognition and intraspecific group recognition in many insect species. The expression of these contact pheromones has been shown to be plastic with respect to age, diet and social environment, but little is known about how these blends of chemicals respond to dominance structures, and whether individuals can perceive their own status within a group. We manipulated self-perceived dominance status and investigated effects on cuticular hydrocarbon profiles (CHCs) in both males and females of *Telostylinus angusticollis* (Diptera) to determine how they respond to 'dominant' and 'subordinate' roles in intrasexual contexts.

Zac Wylde, University of New South Wales:

Male condition and mating sequence effects on ejaculate storage and use in the Neriid fly, *Telostylinus angusticollis*

Wylde, Z.

Traits such as male body size are mostly examined in the context of male-male combat, however recent evidence suggests that these size effects might also have important consequences on the strength and direction of post-copulatory sexual selection. Males may differentially allocate more or less ejaculate and sperm to a given female which is known to be dependent on factors such as age, mating status and health. Nevertheless, we still know very little as to how male condition and mating sequence effect patterns of ejaculate and sperm storage to ultimately impact male fitness. We also know very little as to whether female insects can non-randomly utilise sperm storage organs for fertilisation and if so, how far this control extends. Here we use a species of fly; *Telostylinus angusticollis* (Diptera) which demonstrates highly condition-dependent body size and secondary sexual traits. We examined the effects on mate sequence and male condition on ejaculate storage patterns between spermathecae. We expected that male condition might affect the composition and amount of ejaculates, and therefore the way in which these ejaculates are stored and utilised by the female. Further study aims to examine the fitness effects on offspring viability and male paternity share. Additionally we present a new method for the quantification of competing male ejaculates within the female sperm storage organs.

Boris Yagound, University of Sydney: Sexual Selection

Male honey bees produce semen with unique DNA methylation profiles

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Kin-selected conflicts are an inherent feature of social evolution. Queen honey bees are extremely polyandrous; they mate with numerous males, each fathering a different worker subfamily. This increases the genetic diversity within the colony, but also paves the way for genomic conflicts. Genes favouring worker reproduction are indeed predicted to be over-expressed when paternally inherited, while under-expressed when derived from the queen. Furthermore, worker subfamilies differ markedly in their reproductive traits and show context-dependent reproductive strategies. Epigenetic modifications of the genome such as DNA methylation have the potential to regulate gene expression in a parent-of-origin manner. The existence of sperm-specific methylome profiles could lead to subfamily-dependent reproductive traits. However, the individual specificity of epigenetic marks has never been investigated in social insects. In this study, we compared genome-wide methylation profiles of the semen of three individual males. We found approximately 20,000 methylated sites in over 4,000 genes in each semen sample. While a large number of core methylated sites were common to all individuals, about one third were variable between each individual semen methylome. Average methylation levels at each site were over 95%, suggesting that methylation remains consistent in all individual spermatozoa within each male's semen. We saw between 200 to 500 differentially methylated genes (DMGs) in pairwise comparisons between semen methylomes. Further, we found a number of single nucleotide polymorphisms (SNPs) in regions with methylated sites. DMGs were twice as likely to contain SNPs compared to other genes, suggesting the importance of allele-specific methylation. Our results indicate that males harbour individual-specific DNA methylation patterns that are often associated with genotypic variation. This suggests that pooling samples of workers derived from different subfamilies could introduce biases in methylome sequencing projects. Overall, our study shows that male honey bees differ widely in their methylomes, with epigenetic specificity being strongly linked with genotype. We discuss the evolutionary implications that this double layer of genetic and epigenetic variability could have for the expression of kin-selected conflicts in insect societies.

Toshihisa Yashiro, University of Sydney: Sex

Lost males in mixed-sex termites societies

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Males contribute to increased heterogeneity among individuals through sexual reproduction and sexual dimorphism. In termites, the ubiquitous presence of both male and female workers and soldiers indicate that males play a critical role in colonies of these insects. To date, the loss of males from advanced social animal lineages has been reported only from ants and honey bees, whose males display no helping behaviour. Here, we report the first example of loss of males from mixed-sex animal societies. We found an asexual lineage of the termite *Glyptotermes nakajimai*, demonstrating a transition from mixed-sex to all-female asexual societies. We showed that a unique combination of several traits in the ancestors of the asexual lineage may have allowed the multiple barriers to male-loss to be overcome. Our results demonstrate that males are not indispensable for the persistence of termite societies, and provide important insights into the impact of males on animal societies.

Felix Zajitschek, Monash University: Lightning Talks

Does senescent maladaptiveness unite the sexes? Age effects on male-female fitness correlation in *Drosophila melanogaster*

Susanne Zajitschek (Monash University / Donana Biological Station), Francisco Garcia-Gonzalez (Donana Biological Station / University of Western Australia), Felix Zajitschek (Monash University) & Damian K. Dowling (Monash University)

Well adapted populations frequently harbour substantial amounts of sexually antagonistic genetic variation for fitness. The between-sex genetic correlation for fitness integrates over all traits that are correlated with fitness and expressed in both sexes. It indicates sexual antagonism when negative negative (rMF < 0), since selection on fitness is by definition positive, independent of the sex it is measured in. When phenotypic optima are shifted in both sexes, or, when male and female genotypes become less adapted, the direction of selection can re-align, dampening overall sexual antagonism (resulting in a larger between-sex correlation for fitness). This has been corroborated in novel environments. Age should have a similar effect through an increasingly less adapted genome with increasing age predicted by evolutionary theories of aging. We provide theoretical results in support of this effect. While age-specific genetic correlations were not significantly different from one another and from zero, their point estimates differed as predicted, with negative young age and positive old age between-sex fitness correlations. We further found that genetic variance increased with increasing age only in females, not in males. In summary, we can show an indication of the predicted age-dependent maladaptation leading to dampened sexual conflict over fitness at older age. Statistical non-significance of these changes could be due to the assymmetric response in sex-specific changes in genetic variation with age, with genetic variation for fitness increasing with age in females, but not in males.

Susi Zajitschek, Monash University & Donana Biological Station Sevilla, Spain:

Life History & Physiology

Experimental evolution of sexual conflict in *Drosophila melanogaster*

Felix Zajitschek, Susanne RK Zajitschek, Carla Sgró, Damian Dowling, Tim Connallon

Sexual interactions between males and females often result in suboptimal outcomes for each of the sexes. In fruit flies, females with elevated mating rates often incur fitness costs such as reduced survival, but readily mate with multiple mates. Varying the opportunity and intensity for the sexes to engage in sexual interactions, by use of experimental evolution, can offer insights into the fitness consequences of sexual conflict and male harmfulness. While high conflict environments are expected to produce harmful males that are efficient at securing mating opportunities, and at the same time may exert more detrimental effects on females, the females in these environments are expected to develop counter-adaptations, such as increased resistance to mating attempts. Low conflict environments are expected to lead to relaxed levels of female harassment and decreased stress levels, and potentially less active or competitive males. Our project investigates the costs and benefits of sexual conflict in experimentally evolved *Drosophila melanogaster* populations, under either low or high levels of sexual interaction (>400 generations). We aim to gain an insight on maternal vs paternal contributions for reproductive success in sons and daughters produced from parental crosses, and to identify if indirect benefits of sexual selection and positive net fitness payoffs to females or whether sexual conflict adaptations maximise fitness at the expense of net female fitness shape the evolution of harmful male traits.

Dany Zemeitat, University of Melbourne:

Coevolution & Conservation

Food reward mutualisms: matching macronutrient synthesis with macronutrient preference

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Butterfly larvae of the family Lycaenidae are often found in mutualistic associations with ants; a relationship that is largely mediated through food rewards provided by the larvae through a specialized gland, the Dorsal Nectary Organ (DNO). Optimising ant attendance requires a balance between providing a cocktail of secretions that meet the nutritional preferences of the ant mutualists against the costs of synthesising those secretions, which depends upon their composition. We investigated the nature of the DNO secretions in lycaenid-ant associations, by asking three questions: (1) What is the chemical composition of the food rewards produced by larvae of three species of the Australian genus *Jalmenus*; (2) what are the macronutrient preferences of the workers of ants associated with *J. evagoras* and *J. ictinus*, and; (3) what is the level of congruence between production and preference of macronutrients, and is it linked with the nature of the mutualistic relationship?

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