2019 BIOLOGICAL SCIENCES HONOURS STUDENTS

Semester 1

Semester 2
WELCOME

A message from A/Professor Chris Greening, Honours Coordinator:

Welcome to the School of Biological Sciences 2020 Honours Projects Handbook, which provides information about Honours projects that are available for Semester 1, 2020.

The Honours year provides an opportunity for high achieving students to participate in the research of the School of Biological Sciences during a fourth year of undergraduate study. The Honours program involves the completion of a research project (BIO4100) and advanced coursework (BIO4200). The areas of study encompassed in Biology Honours are:

- Genetics
- Ecology and Conservation Biology
- Plant Sciences
- Zoology

Honours students work on a research project in collaboration with one or more supervisors from the School of Biological Sciences, or through collaborative partnerships with the School of Psychological Sciences and the Hudson Institute of Medical Research.

Projects within the School regularly attract financial support from the Australian Research Council (ARC), the National Health and Medical Research Council (NHMRC), government agencies, and industry. Our findings, including the results of many honours projects, are reported in some of the world's leading scientific journals.

Entry Requirements:

Students must meet Faculty of Science requirements for entry into Honours, which include:

- being course complete
- having an average above 70 for your top-four Level 3 units
- having the agreement of a supervisor

Students from other universities who wish to pursue Honours research in the School of Biological Sciences are encouraged to apply and should have qualifications comparable to those above.

Please contact the Honours Coordinator for more information.

Honours Information Session (for S1 and mid-year start) and Start Dates:

- Please refer to the School of Biological Sciences Honours page
- Note: Honours training commences on Monday, one week before O week (eg. two weeks before Week 1 of Semester). Students should ensure they are available to attend this two week training period.

For more information or assistance, please contact:

Biology Honours Coordinator (BIO4100 - Research Project)
A/Professor Chris Greening
Email: sci-biohonours.coordinator@monash.edu

Biology Honours Deputy (BIO4200 - Advanced Coursework)
Dr Chris Johnstone
Email: christopher.johnstone@monash.edu

Biology Honours Technical Co-ordinator
Ms Kate Elliott
Email: kate.elliott@monash.edu
HONOURS PROJECTS

SCHOOL OF BIOLOGICAL SCIENCES

Professor Melodie McGeoch - Ecology Research Group

Quantiﬁcation of biodiversity change

Dr Jeremy Barr - Bacteriophage Biology Research Group

Various projects

Dr Francine Marques - Hypertension Research Group

The role of the gut microbiota in the regulation of blood pressure

Dr Sonika Tyagi - Bioinformatics Research Group

Comparative genomics study of Australian mammals

Transcriptomics analysis of antibiotic resistant pathogens

Building an RNA-protein interactome

Dr Mike McDonald - Experimental Evolution Research Group

Using evolution to combat multidrug resistance in H. pylori

Experimental evolution of an artiﬁcial microbiome

Professor Bob Wong - Behavioural Ecology Research Group

Wildlife behavioural responses to a changing world

Dr Matt Piper - Nutritional Physiology and Ageing Research Group

Diet as medicine: investigating how nutrition can enhance health, suppress appetite and extend lifespan in Drosophila

Dr Tim Connall - Biodiversity Research Group

The role of structural variation in the evolution of sex-speciﬁcally selected genes

Topics in theoretical biology

Testing faster-X theory in mosquitoes

A/Professor David Chapple - Evolutionary Ecology of Environmental Change Research Group

Macroeckology of Australian lizards

Conservation, behavioural ecology and evolutionary ecology of Australian skinks

Dr Rohan Clarke - Ornithology and Conservation Management Research Group

Thermal scanning as a tool to monitor for the endangered Plains-wanderer

Various projects

Professor Moira O’Bryan - Male Infertility and Germ Cell Biology Research Group

The function of KATNAL1 in mammalian spermatogenesis

Detoxifying acrosome disassembly in animal sperm during fertilization

Professor Craig White - Evolutionary Physiology Research Group

The effect of size and temperature on energy intake and use

Does experimental manipulation of resting energy expenditure alter growth, locomotor performance, or food intake?

The genetic architecture of rates of metabolism and water loss

A/Professor Martin Burd - Evolutionary Ecology Research Group

The enigma of sex allocation in plants

Dr Jessica Walsh - Conservation Science Research Group

Is recovery of threatened ecosystems possible?

Professor Carla Sgro - Genetics, Evolution, Biodiversity & Climate Change Research Group

Does the nutritional environment of parents affect offspring stress resistance and the potential for climatic adaptation?

Feeding ecology of Drosophila and its impacts on climatic adaptation

The potential for transgenerational effects to increase or reduce climate change risk

The potential for Wolbachia to impact male fertility under climate change

The effects of competition on metabolic rate

Thermal tolerance of Australian native bees

Professor Steven Chown - The Chown Lab

Evolutionary potential of cold tolerance in springtails

Dr Christian Mirth - Developmental Responses to Environmental Change Research Group

Developmental responses to environmental change

Adapting feeding responses to environmental stress

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The School of Biological Sciences has research strengths in four broad discipline areas:

- Ecology and Ecosystems;
- Evolution in a Changing World;
- Form and Function of Life; and
- Genetics, Genomics, and Health.

Research within, and across, the discipline areas of the School addresses key problems in the life sciences that encompass: molecular and cellular genetics; evolutionary genetics, disease causality, adaptation to environmental change and disease resistance; community ecology and ecosystem functioning; the impacts on biodiversity, and strategies to mitigate major environmental challenges. Simply put, we are interested in all forms of life, the interactions between the environment and genetics / genomics and strategies to improve human and environmental health.

This research is undertaken in freshwater, marine and terrestrial environments, from the tropics to the Antarctic, and in state-of-the-art laboratory settings. Investigations span a range of organisms, from unicellular algae and bacteria to plants, invertebrates and vertebrates including humans. The School has a global network of collaborators that includes the university sector, not-for-profit organizations, industry and government agencies. The Members of the School contribute to the work of several international conventions and agreements, and play leading roles in professional societies spanning evolution, ecology, developmental biology, the environment, and human health.
Project Title: Quantifying biodiversity change

Supervisors:
Professor Melodie McGeoch
melodie.mcgeoch@monash.edu
+61 3 9902 0464

Other Supervisors

Location:
Clayton Campus, 18 Innovation Walk

Outline of Project

**Background:** Biodiversity, and specifically the composition of communities, is changing – driven by all forms of global environmental change. Being able to accurately and efficiently measure this change over space and over time is central to understanding the implications of biodiversity change for the services that ecosystems deliver that support human well-being.

**Project Aims:** To be refined in discussion with the Honours student. Broadly, to develop, understand and test measures of biodiversity turnover (i.e. measures of change in species composition).

**Techniques:** Biodiversity Informatics, Statistics and modelling in R; Application of diversity metrics
Background: The Bacteriophage Biology research group studies bacteriophages and their function and role within the human body. Bacteriophage (or phage for short) are viruses that infect and kill bacteria and are the most abundant and diverse microbe found in the body. Phages control and manipulate bacterial populations, prevent infection and disease and have important roles in regulating the microbiome and body that have not yet been fully elucidated. Our group is an experimental biology lab that utilise a range of cross-disciplinary techniques to investigate fundamental and mechanistic bacteriophage biology.

Projects Available: Our research group has a number of on-going research projects that are suitable for Honours students. Some of our research focuses on phage therapy - or the use of phages to combat bacterial infections and disease, particularly those caused by difficult to treat, antibiotic resistant infections. We also investigate the role of bacteriophages within the human gut microbiome, utilise experimental evolution to study phage-bacterial infection and investigate the interaction between phages and human cells.

Interested Honours students should contact Jeremy Barr (jeremy.barr@monash.edu) to discuss research opportunities available in the lab. More information can be found through our lab website - https://thebarrlab.org/
**Project Title**: The role of the gut microbiota in the regulation of blood pressure

**Supervisors**: Dr Francine Marques, francine.marques@monash.edu

**Other Supervisors**: Prof Charles Mackay (Monash)

**Location**: Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background**: High blood pressure (BP), also known as essential hypertension, is responsible for more than 50% of cardiovascular deaths worldwide, being the principal risk factor for global burden of disease. While epidemiological studies show that obesity and a high fat and high sodium intake are clear contributors to hypertension, it is starting to emerge that other dietary components such as fibre might also modulate cardiovascular risk factors. Consumption of a diet high in fibre increases gut microbiota populations that, through fermentation, generate short chain fatty acids (SCFAs), which have a protective role in experimental models of inflammatory diseases. We have recently found that dietary manipulation with fibre or acetate can prevent the development of high blood pressure and heart failure in a model of disease (Marques et al., Circulation 2017; Marques et al., Nature Reviews Cardiology 2018).

**Project Aims**: We have several projects that aim to study the role of gut microbes and SCFAs in the setting of blood pressure regulation, including communication between gut, heart, kidney and other organs, and mechanisms of how SCFAs decrease inflammation and blood pressure. Other projects are available for discussion – come and have a chat!

**Techniques**: Animal handling and surgery, blood pressure measurement, DNA, RNA and protein extraction and (real-time) PCR, flow cytometry, next-generation sequencing, bioinformatics, histology and microscopy.
**Comparative genomics study of Australian mammals**

**Supervisors:** Dr Sonika Tyagi  
sonika.tyagi@monash.edu  
+61 3 9905 6047

**Other Supervisors:**

**Location:** Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background:** We have access to recently completed genome assemblies of more than 80 Australian species. Our group is partnering in annotating these newly sequenced genomes. The project provides a great opportunity to learn from the efforts of international groups in generating this data and related resources and make use of the existing tools and pipelines to add value to new genomic studies.

**Project Aims:** Using comparative genomics approaches to annotate genomes of Australian mammals.

**Techniques:** Existing Bioinformatics tools and pipelines will be used in the project. Required bioinformatics training to use these tools will be provided. It is desired that the students have prior exposure to running bioinformatics application in a web-based and command line environment.

**Transcriptomics analysis of antibiotic resistant pathogens**

**Supervisors:** Dr Sonika Tyagi  
sonika.tyagi@monash.edu  
+61 3 9905 6047

**Other Supervisors:**

**Location:** Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background:** The aim of the project was to study non-coding RNA in pathogenic bacteria. We have sequence data from bacteria that are known to cause sepsis condition in the hospitals. In many cases, these microbes are resistant to an antibiotic. Developing biomarkers and characterizing functional molecules involved in gene regulation of these microbes is of importance in designing targeted drugs for sepsis. We aim to decipher the role of noncoding RNA in gene regulation of these bacteria. The project provides a great opportunity to learn from efforts of research groups in generating this valuable data on Australian antibiotic-resistant pathogens and making use of the existing tools and pipelines to add value to their genomic studies.

**Project Aims:** To profile noncoding RNA in antibiotic resistant bacteria in strains specific to Australia.

**Techniques:** Existing Bioinformatics tools and pipelines will be used in the project. Required bioinformatics training to use these tools will be provided. It is desired that the students have prior exposure to running bioinformatics application in a web-based and command line environment.

**Building an RNA-protein interactome**

**Supervisors:** Dr Sonika Tyagi  
sonika.tyagi@monash.edu  
+61 3 9905 6047

**Other Supervisors:**

**Location:** Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background:** We have sequence data from bacteria that are known to cause sepsis condition in the hospitals. In many cases, these microbes are resistant to an antibiotic. Developing biomarkers and characterizing functional molecules involved in gene regulation of these microbes is of importance in designing targeted drugs for sepsis. We aim to decipher the role of noncoding RNA in gene regulation of these bacteria. The project provides a great opportunity to learn from efforts of research groups in generating this valuable data on Australian antibiotic-resistant pathogens and making use of the existing tools and pipelines to add value to their genomic studies.

**Project Aims:** To build RNA-RNA and RNA-protein interaction database for a given list of noncoding RNA.

**Techniques:** Existing Bioinformatics tools and pipelines will be used in the project. Required bioinformatics training to use these tools will be provided. It is desired that the students have prior exposure to running bioinformatics application in a web-based and command line environment.
Background: H. pylori is a class I human carcinogen and WHO priority pathogen that infects 50% of humanity. Antibiotic eradication therapy is vital for reducing the rate of gastric cancer and the global health burden imposed by chronic infection. Current and past therapies for H. pylori were successful in the short term. However, over longer time scales, evolution renders frontline antibiotics useless one by one, and multidrug resistant (MDR) strains of H. pylori have begun to emerge. It is essential that we learn from previous mistakes and employ evolutionary stable strategies that anticipate genetic adaptation of H. pylori to antibiotic treatment.

Project Aims: The goal of this project is to characterise the core network of antibiotic resistance and compensatory mutations in MDR H. pylori. This will be achieved using MDR clinical strains, genomics and a novel experimental evolution approach that exploits H. pylori’s natural capacity for recombination. In a preliminary evolution experiment with H. pylori, we showed that recombining antibiotic resistant H. pylori with an evolving lab strain drew out only those mutations that were required for metronidazole resistance.

Techniques: Short and long-read genome sequencing, bioinformatic genome assembly, experimental evolution and molecular biology.
Background: Humans have brought about unprecedented changes to environments worldwide. For many animals, behavioural adjustments represent the first response to altered conditions. Such behavioural modifications can potentially improve an organism’s prospects of surviving and reproducing in a rapidly changing world. However, not all behavioural responses are beneficial. Human-altered conditions, for instance, can undermine the reliability of sexual signals used by animals to assess potential suitors. Environmental changes can also impair sensory systems or interfere with physiological processes needed to mount an appropriate behavioural response. An understanding of behaviour could therefore be important in helping to explain why some species are able to survive, or even flourish, under human altered conditions, while others flounder.

Project Aims: To understand the pivotal role that behaviour plays in determining the fate of species under human-induced environmental change. Honours projects in the Behavioural Ecology Research Group are developed in close collaboration with students and have covered topics as diverse as the effects of chemical pollutants on sexual selection in fish and the role of behaviour in mediating the success of invasive lizards. If you have an interest in this area, please contact Bob Wong to discuss opportunities. The Research Group is also open to supervising projects on animal behaviour more generally (Please see bobwonglab.org for details of our research interests and expertise).

Techniques: Laboratory and/or field based studies and techniques in behavioural and evolutionary ecology. Specific details of techniques will depend on the project.
Dr Matt Piper - Nutritional Physiology and Ageing Research Group

**Project Title**: Diet as medicine: investigating how nutrition can enhance health, suppress appetite and extend lifespan in Drosophila

**Supervisors**
Dr Matthew Piper
dr.matthew.piper@monash.edu
+61 3 9902 0493

**Outline of Project**

**Background**: My lab uses the fruitfly Drosophila melanogaster to investigate the mechanisms by which nutrition affects long-term health and behaviour. In particular the proportion of amino acids is a potent modulator of growth, fecundity, stress resistance, ageing and satiety. Using new innovations in fly diets and methods for their design, projects are available to investigate each of these interactive effects.

**Project Aims**: To identify and understand the molecular mechanisms by which diet design can be used to modify fly behaviour and health.

**Techniques**: Handling and genetics of Drosophila as well as design and construction of synthetic diets. Basic behavioural assays will be implemented where relevant.
**Background:** Males and females are often subject to widely divergent evolutionary pressures ('sex-specific selection'). In recent years, there has been growing interest in finding sex-specifically selected genes, with two notable genome-wide scans performed in humans (Cheng & Kirkpatrick 2016, PloS Genet.) and fruit flies (Ruzicka et al. 2018, biorXiv). In parallel, theory has also shown that inversions—a type of structural variant that suppresses recombination—are favoured when they capture pairs of genetic variants under sex-specific selection (Connallon et al., in prep.). However, no study has yet examined the relationship between inversions and patterns of sex-specific selection across the genome.

**Project Aims:** This project would bring together recent genomic data on inversions in humans (Martinez-Fundichely et al. 2014, Nucleic Acids Res.) and fruit flies (Chakraborty et al. 2018, Nat. Genet.) to test whether inversions are associated with sex-specifically selected genes. There is also scope to examine the influence of other types of structural variation (e.g. gene duplications) on the evolution of sex-specifically selected genes.

**Techniques:** This project would be suitable for any student interested in applying computational biological methods (genome-wide selection scans, structural variant detection, data mining, statistical analysis) to test fundamental evolutionary theory.
Project Title: Testing faster-X theory in mosquitoes

Supervisors:
Dr Filip Ruzicka  filip.ruzicka@monash.edu  +61 491111042
Dr Tim Connallon  tim.connallon@monash.edu  +61 3 9905 0899

Other Supervisors:

Location:
Clayton Campus, 18 Innovation Walk

Outline of Project

Background: Theory predicts that genes on the X chromosome should evolve faster than on autosomes (‘faster-X’ effect, Charlesworth et al. 1987). This is because the X chromosome is present as a single copy in males, allowing recessive beneficial mutations to be ‘seen’ by selection, whereas recessive autosomal mutations are not. However, testing faster-X theory is difficult because X chromosomes and autosomes carry different sets of genes, which may also influence their rates of evolution in addition to effects of X-linkage per se.

Project Aims: This project would use whole-genome sequences from multiple species of Aedes (zika, dengue) and Anopheles (malaria) mosquitoes to compare rates of gene evolution on the X chromosomes and autosomes. These species provide a unique opportunity to test faster-X theory because they harbour similar sets of genes yet differ in their X-chromosomal copy number (Anopheles species have one X-linked copy in males, while Aedes have two copies).

Techniques: This project would be suitable for any student interested in applying modern computational biological methods (e.g. manipulating big genomic datasets, conducting scans for signals of selection/adaptation) to test a fundamental evolutionary theory.
### Project Title

**Macrocology of Australian lizards**

**Supervisors**
- A/Professor David Chapple  
david.chapple@monash.edu  
+61 3 9905 3015
- Professor Shai Meiri, Tel Aviv University

**Location**
Clayton Campus, 19 Rainforest Walk, Room 113

**Outline of Project**

**Background:** Australia is a ‘land of lizards’. With ~800 described species, Australia is home to 12% of the world’s lizard diversity. Skinks (Scincidae) are the dominant lizard group in Australia, comprising almost 60% of species (~450 species). They have diversified to inhabit every terrestrial environment in Australia, from alpine peaks to rainforests. Skinks have particularly thrived in the arid regions of central Australia, where few other vertebrate groups have prospered. This project will investigate whether morphological innovation has been driving the amazing radiation of skinks in Australia. Available for either a Feb 2020 or July 2020 start.

**Project Aims:** Investigate the ecology, evolution, diversification and ecomorphology of Australian lizards.

**Techniques:** The project will involve collating data from the literature, and visiting several Australian museums to take detailed morphological measurements of preserved specimens.

### Project Title

**Conservation, behavioural ecology and evolutionary ecology of Australian skinks**

**Supervisors**
- A/Professor David Chapple  
david.chapple@monash.edu  
+61 3 9905 3015

**Location**
Clayton Campus, 19 Rainforest Walk, Room 113

**Outline of Project**

**Background:** Skinks (Scincidae) are the dominant lizard group in Australia, comprising ~450+ species. Around 8% of species are listed as Threatened, and a further 6% are listed as Data Deficient or Near Threatened. Potential projects are available examining the conservation of these skink species, or investigating the threatening processes that impact Australian skink species. The projects will be developed in consultation with the student. Available for either a Feb 2020 or July 2020 start.

**Project Aims:** Improve the conservation status and knowledge of Australian skinks.

**Techniques:** The project will involve lab-based experiments investigating aspects of behavioural and evolutionary ecology. The project may also involve field-based studies and collection of lizards for the lab-based experiments.
**Thermal scanning as a tool to monitor for the endangered Plains-wanderer**

**Supervisors**
Dr Rohan Clarke  
rohan.clarke@monash.edu  
+61 3 9905 1968

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

*Background:* This project aims to develop and test survey methods for Plains-wanderers (and other endothermic vertebrates) in the grasslands of north-central Victoria. Specifically, the intent is to compare the results of traditional spotlight surveys with novel methods employing vehicle mounted thermal scanners. This project involves fieldwork that will be conducted at night in collaboration with Zoos Victoria and Parks Victoria. The successful student must have a current driver’s licence.

**Various projects**

**Supervisors**
Dr Rohan Clarke  
rohan.clarke@monash.edu  
+61 3 9905 1968

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

*Background:* Our group are interested in applied ecology, and work especially with birds and marine mammals to identify and respond to threatening processes. Current research in our group includes the conservation management of threatened woodland birds, island conservation, monitoring fur-seal and seabird colonies with drones and interactions between offshore development, seabirds and other marine vertebrates. Notwithstanding the above listed project, honours projects in these broad areas of interest are typically tailored to meet our research objectives and the student’s interests.
SCHOOL OF BIOLOGICAL SCIENCES – 2020 HONOURS PROJECTS

Professor Moira O’Bryan - Male Infertility and Germ Cell Biology Research Group

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### Project Title: The function of KATNAL1 in mammalian spermatogenesis

**Supervisors:**
- Professor Moira O’Bryan
  - moira.obryan@monash.edu
  - +61 3 9905 5650

**Other Supervisors:**
- Dr Jessica Dunleavy
  - moira.obryan@monash.edu

**Location:**
- Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background:** Previous work from our laboratory has shown that mammalian male fertility is critically dependent on the katanin family of microtubule severing proteins. The identity of the katanin involved in male meiosis, however, remains elusive. Within this project, the honours student will use a unique tissue-specific model of Katnal1 gene ablation to test the role of KATNAL1 in spermatogenesis. This research has relevance to the diagnosis and treatment of human male infertility and the definition of the processes underpinning sperm production. Students should have a background in either genetics and/or developmental biology.

**Project Aims:**
- To determine the consequences of knocking out the Katnal1 gene on male fertility using a unique mouse model
- To determine if KATNAL1 plays an essential role in meiosis in the male and/or haploid germ cell development
- To determine if these roles can be compensated for by other Katanin-related microtubule severing proteins

**Techniques:**
- Working with a mouse model
- Fertility phenotyping – including breeding experiments, sperm function testing, histology
- PCR genotyping and expression analysis
- Immunochemistry and microscopy
- Western blotting

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### Project Title: Detoxifying acrosome disassembly in animal sperm during fertilization

**Supervisors:**
- Dr Nadinath B. Nillegoda
  - nadinath.nillegoda@monash.edu
  - +61 3 9905 3636
- Professor Moira O’Bryan
  - moira.obryan@monash.edu
  - +61 3 9905 5650

**Location:**
- Clayton Campus, 15 Innovation Walk and 25 Rainforest Walk

**Outline of Project**

**Background:** In sperm, a protein dense granule named the acrosomal matrix disassembles upon physiological stimuli (acrosome reaction) to release lytic enzymes that help degrade egg barriers allowing fertilization. The (dis)assembly of this detergent-resistant membrane-free structure is controlled by environmental cues, notably pH changes, but the underlying mechanism remains elusive since its discovery in 1898. We have identified apparent pH-sensitive assembly motifs in key acrosomal proteins, based in part on amyloidogenicity, and hypothesize that these are essential regulators of the self-(dis)assembly. In parallel, we hypothesize that a sperm-specific, acrosome-localized chaperone system orchestrates the clearance of disassembling amyloids to prevent spread of toxic species to fertilized eggs.

**Project Aims:** We will test the hypothesized role of acrosome localized Hsp70 chaperone complex in detoxifying the above identified amyloids during acrosome reaction in rodent sperm. The activity of this chaperone complex will be manipulated using mutants and pharmaco inhibitors to evaluate cytotoxicity, (re)aggregation/seeding and propagation of disassembled amyloids into oocytes after fertilization.

**Techniques:** This project employs multidisciplinary approaches spanning top-down proteomics and functional studies with bottom-up reconstitution experiments to understand the interplay of pH-mediated chemical and structural changes in phase-separated acrosomes and the role of chaperones on a molecular, supramolecular and cellular level, thus filling a mechanistic gap in knowledge in the fertilization process. Initial work includes the analysis of the spatiotemporal dynamics of the Hsp70 chaperone machine and its interaction with amyloids during acrosome reaction using highly sensitive confocal microscopy coupled to an in situ protein interaction assay.
# Project Title: The effect of size and temperature on energy intake and use

**Supervisors:**
- Professor Craig White
- craig.white@monash.edu
- +61 3 9902 0769

**Other Supervisors:**
- Clayton Campus, 25 Rainforest Walk

**Outline of Project:**

**Background:** Many species show dramatic changes in body size through ontogeny. Speckled cockroaches Nauphoeta cinerea, for example, increase in size by around two orders of magnitude as they grow from a mass of around 5 mg at hatching to around 0.5 g as adults. Attempts to understand patterns of growth have a history going back at least a century, but there is an ongoing debate about the physiological validity of the various hypotheses that have been put forward.

**Project Aims:** The aim of this project is to test among the various descriptions of growth patterns by measuring changes in rates of food intake and energy expenditure in cockroaches as they grow.

**Techniques:** The project will make use of respirometry techniques to measure rates of energy expenditure, and will measure rates of ingestion of custom-prepared diets. The project would suit a student with an interest in using experiments to test theory.

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# Project Title: Does experimental manipulation of resting energy expenditure alter growth, locomotor performance, or food intake?

**Supervisors:**
- Professor Craig White
- craig.white@monash.edu
- +61 3 9902 0769

**Other Supervisors:**
- Clayton Campus, 25 Rainforest Walk

**Outline of Project:**

**Background:** Metabolism is the fire of life. Animals expend energy to survive, forage, grow, and reproduce, and measures of metabolic rate integrate these and other processes. Metabolic rate sets the energy demand that organisms exert on their environment, and is therefore central to understanding the flow of energy through organisms, populations, and ecosystems. Because of its fundamental importance, metabolic rate should be mechanistically linked to animal performance, but manipulative tests of this are exceedingly rare.

**Project Aims:** The proposed project will manipulate metabolic rate using a chemical mitochondrial uncoupler, and test for the effects of this manipulation on growth, reproduction, or locomotor performance in a model species (either cockroaches Nauphoeta cinerea or Drosophila melanogaster).

**Techniques:** The project will make use of respirometry techniques to measure rates of metabolism. For students interested in locomotion, a cockroach-sized treadmill is available to measure running speed and endurance.
Project Title: The genetic architecture of rates of metabolism and water loss
Supervisors: Professor Craig White, craig.white@monash.edu, +61 3 9902 0769
Location: Clayton Campus, 25 Rainforest Walk

Background: Much of the biodiversity impact of environmental change is likely to be mediated through physiological responses including energy and water balance, and recognition of this has led to calls for an improved understanding of the evolution of physiological variation. However, single traits, such as metabolic rates and rates of water loss, must not be studied in isolation because evolutionary responses to environmental change will take place in a multivariate space, where both genetic interactions between traits and the direction of selection across multiple traits will dictate the potential for evolution. Rates of respiratory water loss typically increase as rates of metabolism and gas exchange increase, but most insects actually lose more water through their cuticle than through their respiratory system. We therefore know little about how respiratory and cuticular water loss might evolve under selection, and how these might be related to metabolic rate.

Project Aims: This project will use our cockroach model (Nauphoeta cinerea) to test for phenotypic and genetic correlations among respiratory water loss, cuticular water loss, and metabolic rate.

Techniques: The project will make use of respirometry techniques to measure rates of metabolism and water loss, and quantitative genetic analyses to understand the genetic architecture of these traits.
Background: Most familiar animals produce approximately equal numbers of male and female offspring. We know why this balanced reproductive investment in the sexes is an evolutionary optimum in general, and we understand the selective forces that in some cases lead to sex-biased investment. Sex allocation in plants is more interesting because it is less well understood and, in some groups of plants, has not even been measured. Until recently, one of these plant groups was the genus Selaginella, a member of an ancient lineage of free-spore-bearing vascular plants. My students and I measured sex allocation in 14 species of Selaginella from around the world. Thirteen of them had strongly male-biased investment in their spore production. One species in Costa Rica put an average of 93% of reproductive investment into male spores. Most species had an average of more than 70% male investment. This was a completely unexpected result. You can read our report of this work in Annals of Botany 121: 377–383 (2018). The evolutionary basis for such skewed sex allocation remains unknown.

Project Aims: One piece of the puzzle that now needs attention is to see if Selaginella is anomalous. There are only a handful of plants that, like Selaginella, are heterosporous (so that they produce distinct male and female spores) and free-sporing (releasing both male and female spores directly into the environment, rather than retaining female spores and having fertilization occur on the parent plant through pollination, as the seed-producing plants do). The sister lineage of Selaginella, the genus Isoetes, is one such group of plants, and the other free-sporing, heterosporous plants remaining on earth are in two small families of ferns called the water ferns because of their aquatic or semi-aquatic habitat. The aim of the project is to measure sex allocation in these plants. Several appropriate species occur in Victoria.

Techniques: Specimen collection will require some field excursions. Plant dissection, microscopy, and image analysis are needed for volumetric measurement of allocation to male and female spore production. This part of the work requires patience and a delicate touch.
Dr Jessica Walsh - Conservation Science Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Is recovery of threatened ecosystems possible?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Jessica Walsh <a href="mailto:jessica.walsh@monash.edu">jessica.walsh@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>+61 3 9905 9736</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 25 Rainforest Walk</td>
</tr>
</tbody>
</table>

**Background:** There are over 70 threatened ecosystems in Australia that are protected under national legislation. They provide essential habitat for biodiversity and provide ecosystem services for humans. Some of these ecosystems – such as Brigalow and the Cumberland Plain woodland – are threatened due to clearing, leaving only 5-10% of their historic distributions. Effective conservation of these ecosystems requires realistic and quantitative targets for recovery, yet it is unclear what these targets should be. This research is timely and of international significance as the relatively new IUCN Red List of Ecosystems expands.

**Project Aim/s:** This project would quantify whether recovery of threatened ecosystems is feasible given the large wide-scale modification of Australian landscapes, and would develop realistic targets for restoration.

**Techniques:** Students would develop GIS spatial and statistical analysis, literature review methods, cost-effectiveness analysis, scientific writing.

Jessica is also willing to supervise projects on conservation ecology, policy, management, decision making and the science-practice interface (Please see jessicawalshconservation.com for details of her research interests).
**Professor Carla Sgro - Genetics, Evolution, Biodiversity & Climate Change Research Group**

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Does the nutritional environment of parents affect offspring stress resistance and the potential for climatic adaptation?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Professor Carla Sgro <a href="mailto:carla.sgro@monash.edu">carla.sgro@monash.edu</a> +61 3 9902 0332</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td></td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk</td>
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<tr>
<td>Outline of Project</td>
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</tbody>
</table>

**Background:** Studies attempting to understand organismal responses to climate change have focussed on climatic stressors. However food limitation is one of the most common environmental challenges faced by organisms. How energy intake is balanced to optimise fitness under changing climates, and how this affects the capacity of organisms to respond to climate change, is unknown. Parental effects, where the environment experienced by parents affects the fitness of the offspring generation, are widespread, and increasingly predicted to affect adaptation to climate change. Despite this, no studies have yet examined how the nutritional environments of parents will influence offspring fitness under combinations of both nutritional and thermal stress.

**Project Aims:** This project will determine the extent to which the nutritional environment of parents affects offspring fitness under combinations of thermal and nutritional stress likely to be experienced under climate change.

**Techniques:** Drosophila husbandry, experimental design, data analysis, possibly molecular work.

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Feeding ecology of Drosophila and its impacts on climatic adaptation</th>
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</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Professor Carla Sgro <a href="mailto:carla.sgro@monash.edu">carla.sgro@monash.edu</a> +61 3 9902 0332</td>
</tr>
<tr>
<td>Other Supervisors</td>
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<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk</td>
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<tr>
<td>Outline of Project</td>
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</table>

**Background:** On-going global change is resulting in changes in both the thermal and nutritional environments experienced by organisms, Yet, we know very little about how the combined effects of thermal and nutritional stress will affect the ability of animals to respond to changing climatic conditions.

**Project Aims:** This project will track how the nutritional and thermal environments of Drosophila change throughout the summer and spring months in the field in south-eastern Australia. Field-caught individuals will also be assessed for their ability to withstand both nutritional and thermal stress, and this data linked back to the nutritional and thermal environments experienced in nature. This project will shed light on how changes in nutrition and thermal stress influence the sensitivity of animals to climatic change.

**Techniques:** Field sampling of Drosophila feeding and breeding sites; animal husbandry, experimental design and data analysis. There are no pre-requisites for this project, although a real interest in evolutionary ecology/evolutionary biology would be an advantage.
<table>
<thead>
<tr>
<th>Project Title</th>
<th>The potential for transgenerational effects to increase or reduce climate change risk</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Belinda van Heerwaarden <a href="mailto:belinda.vanheerwaarden@monash.edu">belinda.vanheerwaarden@monash.edu</a> +61 3 9902 0449</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Professor Carla Sgro <a href="mailto:carla.sgro@monash.edu">carla.sgro@monash.edu</a> +61 3 9902 0332</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk, Level 4</td>
</tr>
<tr>
<td>Outline of Project</td>
<td>Background: Understanding which organisms will be most vulnerable to climate change remains a crucial challenge in conservation biology. Models predicting which species will be most at risk of future warming typically compare estimates of CTmax, a trait which measures the ability of adults to survive high temperature stress, to temperatures currently experienced in nature to estimate warming tolerance. However, this measure ignores the fact that many species are no longer fertile at temperatures much lower than the temperatures adults can withstand, and thus, may be underestimating climate change risk. Transgenerational or carry-over effects, such as maternal and/or epigenetic effects, can increase or decrease fitness and heat tolerance due to beneficial phenotypic plasticity or the accumulation of cellular damage across generations respectively. Nonetheless, studies that examine reproductive fitness across temperature, typically measure fitness on organisms exposed to different temperatures for one generation only. The extent to which transgenerational or carry over effects (maternal and/or epigenetic effects) might lead to over or underestimating climate change risk remains to be explicitly examined.</td>
</tr>
<tr>
<td>Project Aims: This project aims to investigate the extent to which transgenerational effects may alter estimates of climate change risk in tropical and temperate species of Drosophila.</td>
<td>Techniques: Drosophila husbandry, experimental design, data analysis.</td>
</tr>
</tbody>
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<table>
<thead>
<tr>
<th>Project Title</th>
<th>The potential for Wolbachia to impact male fertility under climate change</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Belinda van Heerwaarden <a href="mailto:belinda.vanheerwaarden@monash.edu">belinda.vanheerwaarden@monash.edu</a> +61 3 9902 0449</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Professor Carla Sgro <a href="mailto:carla.sgro@monash.edu">carla.sgro@monash.edu</a> +61 3 9902 0332</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk, Level 4</td>
</tr>
<tr>
<td>Outline of Project</td>
<td>Background: Wolbachia are endosymbionts that infect many species of arthropods and nematodes. They have been shown to alter the fitness of their insect hosts (e.g. cytoplasmic incompatibility) and have recently been used as a biological control agent to try to eliminate Dengue fever and other mosquito borne diseases. Empirical studies suggest that the fitness effects of Wolbachia on their hosts may be influenced by temperature, but whether the presence of Wolbachia may alter male fertility at higher temperatures predicted under climate change is unknown. Male fertility is emerging as a key trait that may underlie the susceptibility of insects to climate change, as temperatures that induce male sterility, and thus limit reproduction and ultimately survival under climate change, are much lower than the ability to survive a heat stress in adults.</td>
</tr>
<tr>
<td>Project Aims: To examine whether Wolbachia influences male fertility under warmer temperatures in Drosophila.</td>
<td>Techniques: Drosophila husbandry, PCR, DNA extraction, experimental design, data analysis.</td>
</tr>
</tbody>
</table>
Background: Current methods for estimating the threat of climate change to biodiversity primarily focus on abiotic drivers such as temperature, but this approach fails to incorporate a key component of the natural world: a species does not exist in isolation but interacts with others, competing for resources to fuel survival, growth and reproduction. Despite the clear expectation that climate change will have both abiotic (e.g. temperature) and biotic (e.g. competition) effects, we actually know very little about how abiotic and biotic factors will interact to shape species distributions and extinction risk under climate change.

Project Aims: To examine the combined effects of temperature and competition on the physiological capacity of three model insect species (Drosophila melanogaster, D. simulans, and D. sulfurigaster) to survive, grow and reproduce. Survival, growth and reproduction are important components of Darwinian fitness and the rate at which animals can allocate energy to these functions is set by their rate of energy metabolism (metabolic rate).

Techniques: This project will utilise techniques including animal handling and estimation of metabolic rates.

Background: Bees are keystone species in many ecosystems due to their role as pollinators. Any changes in the abundance and distribution of bees will have significant knock-on effects on biodiversity and ecosystem services. This includes agro-ecosystems all over the world, where local wild bee fauna make an important contribution to crop fruit set, in addition to that provided by managed and feral Western honey bees (Apis mellifera). Indeed, the importance of wild native bees for crop pollination may be on the increase, given recent declines in honey bee populations. Despite their outsized ecological role, we know very little about climatic adaptation in bees, or even which climatic factors drive bee distributions.

Project Aims: To examine how the thermal tolerance and activity temperature of native bees varies across species and link this to bee distributions.

Techniques: Animal handling, experimental design, data analysis.
**Background:** Warming is expected to weaken climatic barriers that currently offer cold regions, such as the sub-Antarctic, a degree of protection from biological invasions. As invasions by temperate species become more likely, the potential for these species to evolve improved cold tolerance will become an important determinant of their invasion success. Yet, the capacity of temperate species to evolve cold tolerance under selection is unknown for many organisms. This project will use the facilities of the main supervisor’s lab (www.chownlab.com) to apply directional selection to a range of springtail (Collembola) species over a number of generations and identify which temperate species could invade against a cold climatic gradient.

**Project Aims:** To identify the effects of directional selection on the cold-tolerance of springtails and so quantify their capacity to invade a colder region.

**Techniques:** This project will involve a small component of fieldwork to collect the founding populations of springtails. Truncated selection methods will be applied to springtail populations in the laboratory, which will develop a range of skills including maintenance and rearing of springtail lines and thermal phenotyping assays. This project will suit an evo/eco focused honours student with interests in thermal biology.
### Developmental Responses to Environmental Change Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Developmental responses to environmental change</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Christen Mirth <a href="mailto:christen.mirth@monash.edu">christen.mirth@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>+61 3 9905 1147</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 25 Rainforest Walk</td>
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</table>

#### Outline of Project

**Background:** Changes in environmental conditions affect a wide range of developmental processes generating an impressive array of phenotypic variation. One such example is the developing ovaries in fruit flies of the species Drosophila melanogaster. Ovary size limits the number of eggs a female can produce and is determined by both nutrition and temperature. How these environmental conditions regulate ovary growth and patterning has yet to be explored.

**Project Aims:** This project will explore how nutrition and temperature modify the growth and patterning of the developing ovary. Using cutting-edge protein tagging tools that mark stages of ovary development, we will rear larvae across two thermal and two nutritional conditions. We will then examine how temperature and nutrition affect the rates of growth and patterning in the ovary. This project could be adapted for either an honours or a PhD student.

**Techniques:** This project will use transgenic fly lines with protein tags for the developing ovary, immunocytochemistry, and advanced microscopy to visualise the growth and development of this tissue. Students will also gain expertise in fly husbandry and genetics, and some basic molecular biology.

### Adapting Feeding Responses to Environmental Stress

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Adapting feeding responses to environmental stress</th>
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</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Christen Mirth <a href="mailto:christen.mirth@monash.edu">christen.mirth@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>+61 3 9905 1147</td>
</tr>
<tr>
<td>Location</td>
<td>Professor Carla Sgro <a href="mailto:carla.sgro@monash.edu">carla.sgro@monash.edu</a></td>
</tr>
<tr>
<td></td>
<td>+61 3 9902 0332</td>
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<tr>
<td></td>
<td>Dr Lesley Alton <a href="mailto:lesley.alton@monash.edu">lesley.alton@monash.edu</a></td>
</tr>
<tr>
<td></td>
<td>+61 3 9905 1185</td>
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<td>Clayton Campus, 25 Rainforest Walk</td>
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</table>

#### Outline of Project

**Background:** Our rapidly changing climate will alter not only the temperature but also the abundance and quality of many food resources for many organisms. To understand how prolonged exposure to combined changes in the thermal and nutritional environment, the Sgro and Mirth labs have undertaken an experimental evolution approach using the fruit fly Drosophila melanogaster. We have exposed flies to nine combinations of nutritional and thermal environments, allowing the animals to adapt to these conditions for a year. This project focusses on how adaptation to these new environments affects how larvae cope with thermal and nutritional stress the foraging behaviour and food preference of developing D. melanogaster larvae.

**Project Aims:** This project will explore how adaptation to novel environments affects foraging strategies in D. melanogaster larvae. Using feeding assays developed in the Mirth lab, we will use the lines generated by experimental evolution to explore how adaptation changes the way larvae balance their food intake across different diet types and thermal regimes. This project could be adapted for either an honours or a PhD student.

**Techniques:** This project will make use of lines of flies that have been experimentally evolved to altered nutritional and thermal conditions and will involve conducting behaviour assays and spectrophotometer analysis to quantify food intake. Students will also gain expertise in fly husbandry, some basic molecular biology, and statistical analysis.
**SCHOOL OF BIOLOGICAL SCIENCES – 2020 HONOURS PROJECTS**

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Growing up in a changing world: how does adaptation to novel environments affect larval tolerance to thermal and nutritional stress?</th>
</tr>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Professor Carla Sgro</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Christen Mirth</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 25 Rainforest Walk</td>
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</tbody>
</table>

**Background:** Climate change will alter not only the thermal environment, but also the abundance and quality of many food resources for many organisms. To understand how prolonged exposure to combined changes in the thermal and nutritional environment, the Sgro and Mirth labs have undertaken an experimental evolution approach using the fruit fly *Drosophila melanogaster*. We have exposed flies to nine combinations of nutritional and thermal environments, allowing the animals to adapt to these conditions for a year. This project focuses on how adaptation to these new environments affects the ability of larvae to cope with thermal and nutritional stress.

**Project Aims:** This project will explore how adaptation to novel environments affects stress resistance in *D. melanogaster* larvae. This project will make use of lines of flies that have been experimentally evolved to altered nutritional and thermal conditions. It will involve raising animals from egg to adult over a range of dietary and thermal conditions to explore how adaptation affects the animal’s ability to survive. This project could be adapted for either an honours or a PhD student.

**Techniques:** Through the course of this project, students will learn how to implement the geometric framework for nutrition and how to assay larval life history traits. Students will also gain expertise in fly husbandry and statistical analysis.

<table>
<thead>
<tr>
<th>Project Title</th>
<th>The effect of food availability and temperature on metabolic rate and feeding behaviour in fruit fly larvae</th>
</tr>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Lesley Alton</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Christen Mirth</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk</td>
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</table>

**Background:** The net amount of energy available for survival, growth and reproduction depends on how an animal manages its energy balance. The energy balance of an ectothermic animal is determined by energy supply and demand, which are influenced by food availability and temperature, respectively. Energy supply decreases with decreasing food availability, whereas an ectotherm’s metabolic rate, and thus energy demand, increases exponentially with increasing temperature. If ectothemers are confronted by the opposing challenges of reduced food availability and increased temperature they will have a negative energy balance and be threatened with starvation. Since climate change and habitat destruction are predicted to cause increases in temperature and lead to reduced food availability respectively, it is important that we investigate the capacity for animals to respond to these challenges by adjusting their energy requirements through physiological and behavioural changes.

**Project Aims:** To determine the physiological and behavioural mechanisms by which animals adjust their energy requirements in response to changes in food availability and temperature.

**Techniques:** This project will involve maintaining populations of animals that have evolved in selective environments that vary in food availability and temperature. Students will learn how to measure rates of carbon dioxide production as a proxy for metabolic rate using flow-through respirometry. They will also learn how to quantify different behavioural traits and rates of food intake.
A/Professor Richard Reina - Ecophysiology and Conservation Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Reproduction and foraging of penguins</th>
</tr>
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<tbody>
<tr>
<td>Supervisors</td>
<td>A/Professor Richard Reina</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td><a href="mailto:richard.reina@monash.edu">richard.reina@monash.edu</a></td>
</tr>
<tr>
<td>Location</td>
<td>Phillip Island and Clayton Campus, 19 Rainforest Walk</td>
</tr>
<tr>
<td>Outline of Project</td>
<td>Mid-year start only</td>
</tr>
</tbody>
</table>

**Background:** Little penguins, Eudyptula minor, live and breed in a large colony at Phillip Island southeast of Melbourne. As part of an ongoing program of the Phillip Island Nature Park (PINP) studying the population dynamics and biology of these penguins, a project opportunity exists to study the reproductive biology, behaviour and/or foraging of the penguins in the colony. Studies of parenting and foraging success are possible to understand the relationships between allocation of time and resources to food acquisition and reproduction. Other topics may be negotiated depending on student interests.

**Project Aims:** To better understand the foraging and reproductive ecology of penguins.

**Techniques:** A variety of field techniques, including animal handling. Analysis of a large automatically collected dataset.

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<thead>
<tr>
<th>Project Title</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>A/Professor Richard Reina</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td><a href="mailto:richard.reina@monash.edu">richard.reina@monash.edu</a></td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 19 Rainforest Walk and possible field sites</td>
</tr>
<tr>
<td>Outline of Project</td>
<td>Background: I will consider projects suggested by students in the areas of ecological physiology of vertebrate animals in any environment. Let me know if you have your own project ideas.</td>
</tr>
</tbody>
</table>

**Project Aims:** Dependent on project.

**Techniques:** Will vary with project.
A/Professor Sureshkumar Balasubramanian - Phenotypes to Genes and Mechanisms Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Genes regulating thermal responses in plants</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>A/Prof Sureshkumar Balasubramanian <a href="mailto:mb.suresh@monash.edu">mb.suresh@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>+61 3 9905 1373</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk</td>
</tr>
</tbody>
</table>
| Outline of Project                                | Background: How do the plants know that it is spring and flower at that time? How do they recognize that it is too hot and react? How do they sense temperature and respond? These are the key fundamental questions about which we know very little at present and my group addresses these questions using molecular genetic approaches in the model organism Arabidopsis thaliana. Potential candidates are encouraged to look at Tasset et al, PLoS Genetics, 2018 for background on the proposed project.
| Project Aims: To characterise genetic suppressors that modulate POWERDRESS, a gene involved in epigenetic regulation of thermal response in plants. The specifics of the project will be decided after discussions with the prospective candidate. |
| Techniques: This project will utilise techniques including: ChIP assays, qRT-PCR, molecular biology techniques such as cloning, sequencing as well as phenotyping and genetic analysis. This project would require you have strong skills/interest in genetics and molecular biology. Research Methods is not a pre-requisite for this project. |

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Triplet Repeat Expansions – translational genetics from plants to human cell lines</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>A/Prof Sureshkumar Balasubramanian <a href="mailto:mb.suresh@monash.edu">mb.suresh@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>+61 3 9905 1373</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk</td>
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</table>
| Outline of Project                                | Background: Trinucleotide repeat expansions underlie several human genetic diseases such as Huntington disease, Friedreich ataxia and Fragile X syndrome. Of these diseases such as Friedreich’s ataxia occur due to expansions in intronic regions, which lead to transcriptional downregulation of the gene. Our group have deciphered the molecular pathway through which repeat expansions lead to transcriptional downregulation. Potential candidates are encouraged to look at Eimer et al. Cell, 2018 for background on the proposed project.
| Project Aims: To analyse the molecular mechanism that mediate phenotypic consequences of triplet repeat expansions in diverse organisms. The specifics of the project will be decided after discussions with the prospective candidate. |
| Techniques: This project will utilise techniques including: ChIP assays, qRT-PCR, molecular biology techniques such as cloning and sequencing, cell culture techniques as well as standard genetic analysis. This project would require you have strong skills/interest in genetics and molecular biology. Research Methods is not a pre-requisite for this project. |
Background: Organisms are highly sensitive to environment and express plasticity in response to environmental changes. One of the key mechanisms that modulate environmental/developmental/tissue-specific response is alternative splicing. Alternative splicing not only generates protein diversity, but also can be used to regulate gene expression by coupling with the mRNA surveillance pathway known as Nonsense-Mediated mRNA Decay (NMD). How splicing is regulated is unknown. We have a new method that changes the way one studies splicing. Interested candidates are encouraged to look at Sureshkumar et al. Nature Plants, 2016 for background on the proposed project.

Project Aims: To determine the molecular basis of how splicing decisions are made and to identify factors and rules that govern splicing decisions in organisms.

Techniques: This project will utilise techniques including: next generation sequencing approaches, computational approaches to analyse splicing, genome-wide analysis of splicing. Programming skills will be great, but you would also learn standard molecular genetic techniques such cloning, sequencing etc. This project would require you have strong skills/interest in computational genetics and molecular biology. Research Methods is not a pre-requisite for this project.
Dr Carly Cook – Conservation Management Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>What is the role of small protected areas in biodiversity conservation?</th>
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</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Carly Cook <a href="mailto:carly.cook@monash.edu">carly.cook@monash.edu</a> +61 3 9905 5642</td>
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<tr>
<td>Other Supervisors</td>
<td>Clayton Campus, 17 Innovation Walk</td>
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<td>Location</td>
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<tr>
<td>Outline of Project</td>
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**Background:** Protected areas are the primary tool for biodiversity conservation, preserving species and habitats in perpetuity. Yet 50% of Australian protected areas are less than 1 km², raising questions about what these areas are contributing to the National Reserve System. If areas are too small or isolated, they may be unable to support viable populations, creating real challenges for the sustainability of these areas into the future. This project will explore the role of the many small protected areas in Australia in contributing to the conservation of mammalian species.

**Project Aims:** The aims of this research would be to:
- Document the contribution of small protected areas to the National Reserve System
- Assess the contribution of these areas to representing mammal species
- Determine the degree to which these areas can support viable populations of the species they contain
- Assess the degree to which small protected area contribute to connectivity among protected areas

**Techniques:** GIS spatial analysis, minimum viable population modelling.
Dr Susie Ho - Course Coordinator, Master of Environment and Sustainability

**Project Title**
Enhancing sustainability education

**Supervisors**
Dr Susie Ho  susie.ho@monash.edu  +61 3 9905 9782
Dr Bronwyn Isaac  bronwyn.isaac@monash.edu

**Other Supervisors**

**Location**
Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background:** Many undergraduate science students aspire to sustainability careers that align with or contribute to the UN Sustainable Development Goals. These roles may be in government, corporations, consultancy, and NPOs/NGOs like the United Nations or World Bank. In a competitive employment landscape, it is crucial students develop a suite of both technical and transferrable skills during their studies. This will foster cross-sector and international employability and the integration of science in decision-making for a more sustainable world. When it comes to careers in sustainability, are technical skills enough? How do science students perceive their undergraduate training in relation to their aspirations in sustainability careers?

**Project Aims:** The project aims to explore students’ perceptions of their education in relation to their aspirations, as a springboard into informing the enhancement of undergraduate sustainability curriculum. The main research question is:
How do science students, who aspire to careers in sustainability fields, perceive their undergraduate training?

**Techniques:** This study will use mixed-methods to explore students' perceptions of their degree in relation to their career goals. Surveys and interviews may form part of the qualitative and quantitative methods. Students without a background in these methods will be provided with training. The methods above are commonly used in psychology, marketing, social sciences and a broad range of other academic and work fields and are therefore relevant to a range of careers.
Project Title: Chloride transport in the function of intracellular organelles and human disease
Supervisors: Dr Richard Burke
Other Supervisors: None
Location: Clayton Campus, 18 Innovation Walk
Outline of Project:

**Background:** Members of the CIC gene family encode antiporter proteins that control the transport of chloride ions across the membrane of organelles such as endosomes and lysosomes. Mutation of these genes can result in human diseases such as Dent’s disease (affecting kidney function), X-linked Intellectual Disability, Osteopetrosis and early-onset Neurodegeneration. We have generated null mutations in the Drosophila orthologues of these mammalian genes and are using these mutations to characterise the functional requirement and cellular role of these important chloride transporters.

**Project Aims:**
1) To determine the cellular defects that arise due to mutation of the Drosophila intracellular chloride transport proteins CIC-b and CIC-c;
2) To screen for genetic modifiers of CIC-b and CIC-c function.
3) To model the effect of human CIC pathogenic mutations in Drosophila

**Techniques:** Targeted gene knockdown and overexpression in various Drosophila tissues; in vivo genetic interaction experiments; examination of gene expression patterns and protein localisation in various Drosophila tissues by conventional and confocal fluorescence microscopy; mosaic analysis to examine the phenotypic effects of lethal loss-of-function alleles; molecular cloning and generation of transgenic Drosophila strains; proteomic analysis of normal and mutant brain tissue.

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Project Title: Male germline development and infertility in Drosophila
Supervisors: Dr Richard Burke
Other Supervisors: Professor Moira O’Bryan
Location: Clayton Campus, 18 Innovation Walk
Outline of Project:

**Background:** The research group of Prof. Moira O’Bryan has identified numerous candidate genes for human male infertility through whole exome sequencing of patients. These genes now need to be tested for their potential role in male germline development. This project will harness the genetic advantages of Drosophila to carry out a rapid functional characterisation of the best male fertility candidate genes.

**Project Aims:**
1) To examine the functional consequences of targeted knockdown and over expression of candidate male infertility genes on: a) Drosophila male fertility; b) Drosophila testis morphology; and c) expression of testis cell-type specific markers
2) To examine the expression pattern and protein localisation of candidate male infertility genes.

**Techniques:** Targeted gene knockdown and overexpression in the Drosophila male germline; male adult fly fertility assays; in vivo genetic interaction experiments; examination of gene expression patterns and protein localisation in the larval and adult male germline by conventional and confocal fluorescence microscopy; possible use of electron microscopy to examine the morphology mutant adult fly testes.
### Project Title
*Regulation of copper transport and homeostasis*

### Supervisors
Dr Richard Burke  
richard.burke@monash.edu  
+61 3 9905 9531

### Other Supervisors

### Location
Clayton Campus, 18 Innovation Walk

### Outline of Project

**Background:** Copper is an essential yet toxic micronutrient required as a co-factor for numerous vital enzymes. Mutation of the human ATP7A gene results in the lethal, untreatable X-linked disorder Menkes disease. We have mutated the sole Drosophila Menkes gene orthologue, ATP7, and found it to be essential for early fly development in the intestine and brain. Together with collaborators at the Florey Institute, we have also found members of the Ubiquitin Proteasome System (UPS) that bind and mediate cellular responses to copper. We now wish to identify which UPS genes modify ATP7 activity and copper transport, with the aim of finding novel targets for therapeutic intervention in Menkes disease.

**Project Aims:**
1) To characterise the effect on copper transport and homeostasis of members of the proteasomal and lysosomal protein degradation pathways;
2) To screen for compounds capable of restoring function to mutated ATP7 copper transport proteins.

**Techniques:** Targeted gene knockdown and overexpression in various Drosophila tissues; in vivo genetic interaction experiments; examination of gene expression patterns and protein localisation in various Drosophila tissues by conventional and confocal fluorescence microscopy; mosaic analysis to examine the phenotypic effects of lethal loss-of-function alleles; molecular cloning and generation of transgenic Drosophila strains; proteomic analysis of ubiquitinated proteins in vivo.

![Image of gATP7WT:GFP, α-DLG, and Merge](image_url)
A/Professor Chris Greening - Integrative Microbiology Research Group

Project Title: Tasting the air: How do soil bacteria sense and respond to trace gases as an energy source?

Supervisors:
Dr Chris Greening - chris.greening@monash.edu +61 3 9905 1692
Dr Rhys Grinter - rhys.grinter@monash.edu +61 403 896 767

Location: Clayton Campus, 18 Innovation Walk

Outline of Project:

Background: It was recently discovered, by our research group and others, that soil bacteria are able to capture and utilise the trace quantities of hydrogen (H2) and carbon monoxide (CO) in the atmosphere as an energy source. This discovery resolved the long-standing mystery of how large numbers of bacteria survive in polar and temperate deserts, where there is no other ‘food’ source. It also highlighted the major role that soil bacteria play in regulating the composition of the atmosphere, showing that soil bacteria consume vast quantities of H2 and toxic CO, purifying the very air we breathe. While we know that soil bacteria utilise specific enzymes (Hydrogenases and CO-dehydrogenase) to ‘burn’ H2 and CO as an energy source, very little is known about how these bacteria turn on these enzymes, when they are required for survival or when they sense that these gases are available. This exciting project will investigate the function of genes encoding two candidate regulators of H2 and CO scavenging enzymes in the model soil bacterium Mycobacterium smegmatis. This project will use a combination of bacterial genetics, molecular biology, cellular microbiology and biochemistry to determine how these regulators sense and respond to different growth conditions and to the presence of H2 and CO.

Project Aims: This project aims to determine the role of regulatory proteins DcpA and MSMEG_2260 in coordinating the expression of H2 and CO consuming enzymes in M. smegmatis. Deletion mutant strains of the genes encoding these proteins have been constructed and the honours student will characterise these mutants using the techniques listed below.

Techniques: Bacterial genetics: gene deletion and complementation analysis; Molecular biology: quantitative real time PCR, transcriptomics, DNA-protein interaction analysis; Cellular Microbiology: Bacterial cell culture, mutant phenotyping, gas chromatography; Biochemistry: cellular proteome analysis.

Project Title: Understanding life on the edge: Microbial trace-gas oxidation in extreme soil environments

Supervisors:
Dr Eleonora Chiri - eleonora.chiri@monash.edu +61 3 9902 0123
Dr Chris Greening - chris.greening@monash.edu +61 3 9905 1692

Location: Clayton Campus, 18 Innovation Walk

Outline of Project:

Background: Bacteria can make a living in environments otherwise incompatible with life thanks to their ability to enter dormant states, or to ‘hibernate’, in response to extreme environmental conditions. Although dry and nutrient-poor environments are hostile places to live in, they surprisingly harbour rich microbial communities. For example, microbial communities from Antarctic desert soils can oxidise atmospheric trace gases to persist in this dry environment. While soil-water content (percentage range) is difficult to control and measure at extremely low values, water activity is a parameter used to determine the limits of life because it describes water availability on the cellular level. Thus, water activity could represent a great tool to study microbial processes in extreme environments such as hot- and cold-desert soils.

Project Aims: The aim of this project is to determine how water activities affect microbial oxidation of the atmospheric trace gas hydrogen, carbon monoxide, and methane in hot- and cold-desert soils. The milestones of the project are: Method optimisation to measure and manipulate water activity in the controlled environment of soil incubations; Manipulative experiments to study trace gas oxidation at different water activities (from well-hydrated to severely dry soils); - Comparison between soil trace-gas oxidation and soil respiration; - Analysis of the microbial communities responsible for trace gas oxidation.

Techniques: Laboratory soil incubations; Gas chromatography; DNA and RNA isolation from soil samples: Analysis of composition and structure of microbial community (Metagenomics/metatranscriptomics analyses; real-time PCR assays).
A/Professor Robert Bryson-Richardson - Neuromuscular Disease Research Group

<table>
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<tr>
<th>Project Title</th>
<th>Characterisation of potential muscle disease genes</th>
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<tr>
<td>Supervisors</td>
<td>A/Professor Robert Bryson- <a href="mailto:richardson@monash.edu">richardson@monash.edu</a></td>
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<td></td>
<td>Richardson</td>
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<td>Other Supervisors</td>
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<td>Location</td>
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**Background:** Whilst more than 200 hundred genes are known to cause muscle disease when mutated, approximately 50% of patients remain without a genetics diagnosis. This indicates that there are many more genes to be identified. We suggest that genes encoding proteins that localise to the sarcomere, the contractile unit of muscle, and that are restricted in expression to the muscle, represent good candidates for potential muscle disease genes.

**Project Aims:** To examine zebrafish strains carrying mutations in candidate muscle disease genes to determine the consequence of loss of function mutations and the potential for these genes to cause muscle disease.

**Techniques:** This project will utilise techniques including: zebrafish handling, immunohistochemistry, in situ hybridisation, genotyping, muscle function assays, confocal microscopy. This project would ideally suit a student interested in molecular genetics, health, and disease.
**Background:** Congenital myopathies are a group of muscle disorders, resulting in muscle weakness, and in some cases, death during early life. Most myopathies are considered rare conditions, however, when the prevalence of heritable myopathies is combined, they affect approximately 1 in 2000 individuals. We are interested in developing zebrafish models for many different myopathies to understand disease pathogenesis and uncover the causes of muscle weakness.

**Project Aims:** To understand how mutations in myosin binding protein, a core component of the skeletal muscle fibre, cause disease. We will overexpress mutations found in patients, in the zebrafish skeletal and cardiac muscle and analyse the effect on muscle pathology and function.

**Techniques:** This project will utilise techniques including: zebrafish handling, immunohistochemistry, *in situ* hybridisation, genotyping, muscle function assays, confocal microscopy. This project would ideally suit a student interested in molecular genetics, health and disease.

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**Background:** Harmful mutations arising in the human genome cause disease, in some cases leading to death in early development. Recent whole-genome sequencing of a number of different human populations has identified mutations, expected to result in loss of gene function, in genes that are critical for survival, and yet these individuals carrying these mutations are unaffected. Therefore, individuals are able to survive despite carrying the harmful mutation, and can compensate for the loss of the important gene function.

**Project Aims:** To understand how genetic variation in affects the penetrance of disease-causing mutations. We will create a number of mutations in zebrafish, in genes that are known to cause human muscle disease, and determine whether they affect muscle structure or function.

**Techniques:** This project will utilise techniques including: zebrafish handling, immunohistochemistry, *in situ* hybridisation, genotyping, muscle function assays, confocal microscopy, morpholino injections. This project would ideally suit a student interested in mechanisms of gene expression and regulation.
A/Professor Damian Dowling - The Experimental Evolutionary Biology Research Group

**Project Title**: Does mitochondrial evolution “curse” males to shorter lifespans?

**Supervisors**
- A/Professor Damian Dowling
damian.dowling@monash.edu
- Dr Rebecca Adrian
rebecca.adrian@monash.edu
- +61 3 9902 0479

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background**: We have recently discovered that mitochondrial genomes act sexually antagonistically—some haplotypes work well in females, but are relative duds in males. Evolutionary theory can explain this phenomenon, which has become known as “Mother’s Curse” (as mitochondria are maternally inherited). Evidence to date suggests that Mother’s Curse may explain a widespread pattern across the life-histories of animals: that females tend to outlive males. We have developed a new set of genetic strains of fruit flies that will enable us to answer this question by exploring the mitochondrial and nuclear genetic contributions to lifespan and other physiological traits in both sexes. New equipment opens up an exciting new opportunity to test lifespan in large sample sizes with minimal time investment (a high-throughput longevity assay).

**Project Aims**: This project will 1) elucidate the role that the mitochondrial and mitochondrial-nuclear genotypes play in determining lifespan and to 2) examine whether genotypes that benefit females are harmful to males. Exploring these questions in the model system of the fruit fly is a critical step toward understanding the means through which our tiny mitochondrial genomes have big effects on our lives.

**Techniques**: This project will utilise lab-based techniques to quantify lifespan and to maintain and phenotype laboratory populations of fruit flies. This involves working extensively with stereomicroscopes, collecting, sexing, and crossing fly populations, and using equipment developed for behavioural and physiological phenotyping. The project requires a good working understanding of key concepts in evolutionary ecology and in the analysis of data using statistical approaches such as linear modelling. Accordingly, it is well suited to a student who has completed BIO3011, and at least one of BIO2022, BIO3070, BIO3052 or GEN3062.

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**Project Title**: From cell to system: mitochondria as mediators of physiological quality

**Supervisors**
- A/Professor Damian Dowling
damian.dowling@monash.edu
- Dr Rebecca Adrian
rebecca.adrian@monash.edu
- +61 3 9902 0479

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background**: Recent hypotheses have proposed that variation in mitochondrial performance underlies much of the variation in physiological performance we observe in animals. Such variation has important implications for our understanding of differences between individuals we observe in nature: within any population, some individuals generally seem healthier, stronger, and more attractive to males (higher "quality"). Complementing a current project that is exploring mating displays in our flies, this honours project will use a targeted subset of our new mito-nuclear genetic lines to explore one of the key physiological processes predicted to be mediated by mitochondrial function: immune response. Fruit flies have a wound-healing response that is easily quantified visually, enabling a relatively simple test of how mitochondrial variation affects individual quality.

**Project Aims**: This project will test how mitochondrial genetic variation may drive variation in innate immune defense in Drosophila fruit flies. The results of this study will be a key step toward testing the hypothesis that variation in mitochondrial quality underlies variation in individual quality.

**Techniques**: This project will utilise lab-based techniques to quantify immune response and to maintain and phenotype laboratory populations of fruit flies. This involves working extensively with stereomicroscopes, collecting, sexing, and crossing fly populations, and using equipment developed for behavioural and physiological phenotyping. The project requires a good working understanding of key concepts in evolutionary ecology and in the analysis of data using statistical approaches such as linear modelling. Accordingly, it is well suited to a student who has completed BIO3011, and at least one of BIO2022, BIO3070, BIO3052 or GEN3062.
**Dr Kay Hodgins - Plant Ecological Genomics Research Group**

<table>
<thead>
<tr>
<th>Project Title</th>
<th>When is hybridisation helpful or harmful to invasive species?</th>
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<tr>
<td>Supervisors</td>
<td>Dr Kay Hodgins</td>
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<tr>
<td>Other Supervisors</td>
<td><a href="mailto:kathryn.hodgins@monash.edu">kathryn.hodgins@monash.edu</a></td>
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<td>Location</td>
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**Background:** The Hodgins’ laboratory studies the genetic basis for adaptation in plants. We are particularly interested in using introduced species as a model for studying rapid adaptation. We also study adaptation to climate change in forest trees and other foundation species. To address evolutionary questions relating to these topics, we use a combination of genomics, ecological fieldwork and experimental approaches. Several projects are available but two examples are listed below.

**Project Aims:** Why some introduced species become invasive while others do not spread has long puzzled biologists. Hybridisation between species has been thought to aid some invaders by introducing genetic novelty, which can facilitate adaptation to novel environments or mask the effects of deleterious alleles. We have identified a remarkable and repeated pattern of invasion and hybridization between two species of sea rocket introduced to multiple areas of the globe. Using common garden analysis and an expansive genomic dataset of samples derived from these replicate invasive hybrid zones (Australia and North America) we are systematically evaluating the role of hybridization during invasion in this group.

**Techniques:** This project would involve lab work and genome analysis, and can be tailored to the interests and background of the student.

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<tr>
<th>Project Title</th>
<th>Repeatability in the genetic basis of behavior</th>
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<tr>
<td>Supervisors</td>
<td>Dr Kay Hodgins</td>
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<tr>
<td>Other Supervisors</td>
<td><a href="mailto:kathryn.hodgins@monash.edu">kathryn.hodgins@monash.edu</a></td>
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**Project Aims:** Why are some genes involved repeatedly in independent bouts of evolution? Are there only a small number of genes that could facilitate adaptation to similar environments or are there many ways to construct an adaptation but only changes in certain genes that are favoured by selection? The Caenorhabditis nematodes offer a unique experimental platform to connect phenotypic variation to genetic differences. Starting with the keystone model organism, C. elegans, and existing data, we are characterizing and classifying genetic variation across wild isolates from three species of Caenorhabditis - C. briggsae, C. elegans, and C. tropicalis. Whole-genome genotype data combined with high-throughput, high-content imaging of behaviors from these same wild isolates are being used to create high-resolution genotype-phenotype map for a range of natural behaviors. This map will be queried for signatures of convergence at orthologous genes to identify which variants are most important evolutionarily. The result will provide the first systematic glimpse into the genomic “knobs” that control behaviors at single-variant resolution across species and insights into the repeatability of the evolution of behaviors.

**Techniques:** This project would involve a comparative analysis of nematode genomes or the development of computer simulations to assess alternative mechanisms contributing to repeatability in the genetics of adaptation. The project can be tailored to the interests and background of the student.
### Project Title: The consequences of marine urbanisation on the growth of invasive species

**Supervisors:**
- Dr Giulia Ghedini, giulia.ghedini@monash.edu
- Professor Dustin Marshall, dustin.marshall@monash.edu

**Other Supervisors:**
- Hayley Cameron, hayley.cameron@monash.edu

**Location:** Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background:**
Marine artificial structures, such as marinas and breakwalls, are becoming more abundant along the coastline due to urbanisation and need for coastal protection. These structures create new habitat for communities of marine invertebrates, but are often associated with the establishment of invasive species, threatening local biodiversity. Changes in water flow are one the proposed mechanisms to explain the abundance of invasive species within these artificial habitats. Marine invasive species can tolerate lower levels of oxygen relative to native species (figure below). Therefore the low oxygen habitats associated with manmade habitats may create niche opportunities for invasive species.

**Project Aims:**
The aim of the project is to test how changes in water flow affect the resource use of invasive communities to help identify alternative 'green' structures that would discourage the establishment of these invasive species.

**Techniques:**
This project will have both a field and laboratory component. It will combine experimental techniques to grow invertebrate communities in the field (marinas) with resource use assays in the laboratory. The project would suit a student with an interest in community and applied ecology.

![Graph showing CO2 levels](Lagos et al. 2017 Global Change)

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### Project Title: Do eggs compete for sperm

**Supervisors:**
- Professor Dustin Marshall, dustin.marshall@monash.edu
- Hayley Cameron, hayley.cameron@monash.edu

**Location:** Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background:**
Most marine organisms reproduce by shedding sperm into the water, whereupon they meet and fertilisation occurs. While sperm competition for eggs is intense and well recognised, the degree to which eggs compete for sperm is much less understood. Yet egg competition could be an important driver of egg characteristics such as size and could even lead to the evolution of internal fertilisation.

**Project Aims:**
The aim of the project is to examine how egg size affects egg competition in a broadcast spawning marine invertebrate.

**Techniques:**
This project will have both a field and laboratory component. It will combine in vitro fertilisation techniques, field collections and various laboratory assays. The project would suit a student with an interest in ecology or evolution.
**Background:** Basalt Grasslands of the Victorian Volcanic Plain have been extensively lost or degraded through conversion to agriculture, urbanisation and grazing. Less than 5% remain with many in degraded condition.

**Project Aims:** The aim of this project is to examine how land-use history affects plant, fungal and microbial diversity and composition and consider the implications of this for restoration.

**Techniques:** The student will undertake DNA extractions of soil (already collected) from 38 sites and use this to generate soil microbial and fungal diversity information. Information on soil physical and chemical properties and plant composition have already been collected. Undertake a range of statistical analyses to examine correlations between soil, microbial, fungal and plant composition across a gradient of land use history.

**Background:** Joslin’s research group is focused on using quantitative methods, ecological models and decision analysis to better understand and manage plant communities and populations. We combine field experiments, observations and modelling to address fundamental questions in plant community ecology, and develop methods and applications that can be directly implemented by managers.

**Project Aims:** Joslin’s research group is focused on using quantitative methods, ecological models and decision analysis to better understand and manage plant communities and populations. We combine field experiments, observations and modelling to address fundamental questions in plant community ecology, and develop methods and applications that can be directly implemented by managers.

**Techniques:** Projects predominantly focus on analysis of existing data (e.g. using R) and/or the development and analysis of simulation models (e.g. using Matlab) including using optimisation to find efficient resource allocation. Projects including limited fieldwork in the Victorian alps or peri-urban grasslands are also possible for mid-year intake.
**Project Title:** Sex, diet, and infectious disease  
**Supervisors:** Dr Matt Hall  
**Other Supervisors:** Dr Matt Hall  
**Location:** Clayton Campus, 18 Innovation Walk

**Background:** Sex differences in the prevalence, course, and severity of infection are widespread, yet the evolutionary consequences of these differences remain unclear. Understanding how male-female differences affect the trajectory of infectious disease requires connecting the contrasting dynamics that pathogens might experience within each sex, to characteristics of the broader population or environment that a host or pathogen inhabits. This project will consider how food availability and quality differentially influence the nature of infectious disease in males and females, using the model system of the water flea Daphnia magna.

**Project Aims:** To understand how the differential nutrient requirements of males and females relates to the onset and intensity of infectious disease. This project could be adapted to a range of topics concerning the interplay between sex, ageing, and infectious disease.

**Techniques:** This project will utilise techniques including: cross-infection experiments, animal handling and culturing, evolutionary genetics, and dietary manipulations. This project would suit to a student with an interest in evolutionary biology, behavioural ecology or health and disease.

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**Project Title:** Sexual conflict and the evolution of sex  
**Supervisors:** Dr Isobel Booksmythe, Dr Matt Hall  
**Other Supervisors:** Dr Matt Hall  
**Location:** Clayton Campus, 18 Innovation Walk, and Jock Marshall Reserve

**Background:** Sex is an evolutionary paradox. Although recombination is beneficial in the long term, in the short term asexual reproduction is more efficient and avoids many costs associated with sex. One potential cost arises from sexual conflict: selection favouring different trait values in males and females may reduce the fitness of sexual populations relative to asexual lineages. Facultative sexual organisms (which use both sexual and asexual reproduction) can be used to test this prediction: is increasing sexual conflict associated with lower rates of sex?

**Project Aims:** To investigate the relationship between sexual conflict and the rate of sexual reproduction in a facultative sexual model system. The student will measure rates of sex across multiple genotypes of Daphnia carinata waterfleas, and measure sex-specific selection on shared life history traits in high-sex and low-sex genotypes.

**Techniques:** Sampling natural populations, animal handling and culturing, phenotyping and fitness assays, microsatellite genotyping, evolutionary genetics. This project would suit to a student with an interest in evolutionary biology and behavioural ecology.
**Project Title:** Genomics studies for precision medicine in irritable bowel syndrome  
**Supervisors:**  
Professor Mauro D'Amato  
Dr Sonika Tyagi  
**Location:** Clayton Campus, 19 Rainforest Walk  
**Outline of Project**

**Background:** Irritable bowel syndrome (IBS) affects one in seven Australians, and consumes 0.5% of the healthcare annual budget. It manifests in women more than men with symptoms including abdominal pain, bloating, constipation, and diarrhoea. The aetiology of IBS is unknown, as there is no causative “organic” abnormality that may be used for diagnostic or prognostic purposes, hence therapy is mostly inefficient. Major insight into IBS pathophysiology is needed, and increasing hope has been put in genetic research for the identification of pathogenetic mechanisms.

**Project Aims:** We have pioneered IBS genetic research in the past few years, still large-scale studies have been lacking. We are now exploiting very large international resources and existing genetic and epidemiological data from worldwide biobanks and cohorts, corresponding to a target population exceeding 800,000 people. Our genetic analyses will lead to the identification of i) DNA variants (genotypes) that can inform patients stratification for improved therapeutic precision and ii) key pathophysiological mechanisms that may be later targeted for alternative, improved treatment options in IBS.

**Techniques:** Genome wide association studies (GWAS), functional genomics, computational biology, bioinformatics.

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**Project Title:** The interplay between carbohydrate malabsorption, sucrase-isomaltase genotype and gut microbiota in IBS predisposition  
**Supervisors:**  
Professor Mauro D'Amato  
**Location:** Clayton Campus, 19 Rainforest Walk  
**Outline of Project**

**Background:** Irritable bowel syndrome (IBS) affects one in seven Australians, the aetiology is unknown, as there is no causative “organic” abnormality that may be used for diagnostic or prognostic purposes. My group has pioneered IBS genetic research in the past few years identifying, among others, risk genes involved in the digestion of carbohydrates (malabsorption of disaccharides), linked to changes in the gut microbiome. DNA variants coding for hypomorphic (dysfunctional) sucrase-isomaltase (SI) enzymes (disaccharidases involved in the digestion of sucrose and starch) increase risk of IBS and affect the response to a low-FODMAP diet.

**Project Aims:** We aim to identify all SI protein residues that are important for full enzymatic (disaccharidase) activity, via in vitro mutagenesis and high-throughput screening. We plan to correlate this information with sequencing data from IBS patients, and their response to carb-restricted (SI-targeted) dietary interventions. These results will lay the foundation for larger screening programs of IBS patients and the identification of genotype-driven “IBS carb-malabsorbers”.

**Techniques:** In vitro molecular and cell biology model systems, site-directed mutagenesis, high-throughput screening, targeted NGS sequencing, enzymatic assays.
**A/Professor Anne Peters - Behavioural and Evolutionary Ecology of Birds Research Group**

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Nest defense in superb fairy-wrens (second semester)</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>A/Professor Anne Peters</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td><a href="mailto:anne.peters@monash.edu">anne.peters@monash.edu</a></td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 19 Rainforest Walk, Fieldwork at Lysterfield Lake Park</td>
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<tr>
<td>Outline of Project</td>
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**Background:** Superb fairy-wrens, Malurus cyaneus, are cooperatively breeding birds with an unusual mating system, characterized by extreme levels of extra-pair mating. Nonetheless, despite low relatedness to nestlings, all males in a cooperative group help with feeding nestlings. This project aims to address if they also assist with nest defense against nest predators and cuckoos (brood parasites).

**Project Aims:** Using experimental presentations of mounted specimens, this project will address male participation in nest defense activities such as predator mobbing, and if and how they modulate their assistance relative to their individual risk.

**Techniques:** This fieldwork will involve nest finding, experimental model presentations and behavioural observations. Enthusiasm for the outdoors, patience, a strong work ethic and a valid drivers licence are required.

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Colour diversity in birds</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>A/Professor Anne Peters</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td><a href="mailto:kaspar.delhey@monash.edu">kaspar.delhey@monash.edu</a></td>
</tr>
<tr>
<td>Location</td>
<td>Melbourne Museum and possibly other national avian collections</td>
</tr>
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</table>

**Background:** Differences in coloration between newly diverged taxa are common and may act as prezygotic mating barriers. How do these differences in coloration arise? Are differences in colour between subspecies caused by patterns of colour elaboration or by evolutionary innovations?

**Project Aims:** In order to understand these issues the student will measure colour variability of selected species of Australian birds using museum specimens.

**Techniques:** This project will involve fieldwork, colour analysis by psychophysical models, and statistical analysis. Enthusiasm for the outdoors and a valid drivers licence are required.

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Metabolic adaptation of superb fairy-wren nestling (start mid-year)</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>A/Professor Anne Peters</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td><a href="mailto:andreaz.dupoue@monash.edu">andreaz.dupoue@monash.edu</a></td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 19 Rainforest Walk, Fieldwork at Lysterfield Lake Park</td>
</tr>
</tbody>
</table>

**Background:** This project aims to quantify how nestlings of a native bird will respond to global warming, by determining how vulnerable nestling birds are to high temperatures. Although growing animals are most sensitive to heat, and although stress during early-life often has irreversible negative effects, we know very little about how capable young birds are at dealing with a range of temperatures.

**Project Aims:** This project will investigate how altricial nestlings respond to variation in temperature before and after they become thermoregulatory competent, and whether this changes throughout the season, as environmental temperatures change. The project will involve finding nests, measuring nest temperature and testing metabolic performance of young (downy) nestling and older (feathered) nestlings.

**Techniques:** This project will involve fieldwork and analysis of metabolic rate by respirometry. Enthusiasm for the outdoors and a valid drivers licence are required.
Dr Travis Johnson - Developmental Cell Signalling Research Group

**Project Title**
Tuning growth factor activity for localised cell signalling

**Supervisors**
Dr Travis Johnson
travis.johnson@monash.edu
+61 3 9905 5620

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation walk, Ground floor laboratories

**Outline of Project**

**Background:** During development growth factors are released from cells to communicate critical information to direct processes such as proliferation, differentiation, and death. However, we understand very little about the mechanisms that control these signals. One such growth factor is Trunk, a secreted molecule required in the early fly embryo for initiating development of heads and tails (the termini). Trunk activity is therefore tightly controlled to avoid heads and tails developing in unwanted places, and as yet, we do not understand how this occurs. Our knowledge of Trunk, its receptor Torso, and the embryo system in which these work together make for a powerful paradigm to understand the fundamental nature of growth factor signalling control.

**Project Aims:** This project aims to determine how levels of the Trunk protein influence the pathway leading to head and tail development in the fly embryo. Specifically, it will look at Trunk degradation and its role in keeping signalling localised to the embryo ends. This work will contribute valuable insight into our understanding of growth factor control, its evolution, and diseases such as cancer where growth factors play an important role.

**Techniques:** This work will involve the use of mutant fly lines, expression of Trunk transgenes including fluorescently tagged and mutant forms, advanced imaging (incl. live imaging) of developing embryos, biochemical assays such as immunoprecipitation and western blot, cell biology using fly cell lines, and chemical blockers of protein degradation.

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**Project Title**
Multiple ligands, one receptor: how do cells deal with complex signals during development?

**Supervisors**
Dr Travis Johnson
travis.johnson@monash.edu
+61 3 9905 5620

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation walk, Ground floor laboratories

**Outline of Project**

**Background:** During development cells receive a complex array of information that directs them to proliferate, differentiate, change shape, or even die. Growth factor receptors play a key role in this process and are often capable of receiving and integrating multiple different signals at once, yet how they achieve this remains poorly understood. In flies, the highly conserved Pvr receptor functions in a variety of contexts in response to one or more of its three growth factor ligands (Pvf1-3). During blood cell development, for example, Pvr responds to PfV2, but not PfV1, to induce proliferation. Thus, understanding how Pvr can differentially integrate information from its multiple ligands will give us new insights into the ways that cells use to make critical developmental decisions.

**Project Aims:** This project aims to determine whether or not the ligand-specific responses of Pvr are determined by different Pvr isoforms. A major part of this includes developing new genetic tools to visualise Pvr/Pvf expression.

**Techniques:** This work will involve sophisticated genetic techniques such as the generation and use of mutant and transgenic fly lines, including fluorescently tagged lines, and advanced imaging of developing blood cells. It will also involve characterising Pvr transcripts by flow cytometry and RT-PCR from blood cell RNA, and molecular cloning.
Please note: The availability of this project is dependent upon whether we have a suitable gene for testing at the time of commencement.

**Background:** Identifying genes that underlie disease is a major challenge in modern medicine and requires the ability to test the effects of candidate mutations on gene function. This work is slow and costly when performed using patient cells or in genetic models such as the mouse. Seventy-five percent of human genes that underlie known disease are conserved between the fly and man, suggesting that flies could contribute significantly to this effort. Recently, our lab has helped to develop a rapid pipeline for functional testing of variants in conserved genes in flies. We are now applying this pipeline in collaboration with local clinical geneticists whose patients have rare genetic diseases in order to determine their underlying genetic bases.

**Project Aims:** This project aims to determine whether a patient’s form of a particular candidate disease gene is pathogenic, and therefore contribute evidence for or against the gene/variant being responsible for the disease. Sub aims include testing whether the candidate gene and predicted fly ortholog are functionally equivalent, and expression of the patient variants in place of the fly gene to assess their functionality.

**Techniques:** This work will involve bioinformatic analysis of the candidate gene, molecular cloning techniques to isolate and mutate the human gene of interest, advanced fly genetics including production of transgenic flies, fly crosses to express human genes, basic characterisation of fly gene mutants, and imaging of the expression patterns using advanced microscopy techniques.
**Project Title**: Evolution and development of land plants

**Supervisors**
Professor John Bowman  
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Dr John Alvarez  
john.alvarez@monash.edu
Dr Tom Dierschke  
tom.dierschke@monash.edu

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background**: We are studying the evolution and development of land plants, one of the several independent evolutions of multicellular organisms, and one that dramatically shaped the terrestrial environment. Land plants evolved from an ancestral freshwater alga. We utilize two model systems, both amenable to genetic and genomics approaches: Arabidopsis, a diminutive flowering plant that is a model; and Marchantia, a complex thalloid liverwort representing a basal lineage of land plants.

**Project Aims**: We are particularly interested in the genetic control of pattern formation, focusing on the roles of families of transcription factors and hormone mediated signalling pathways that provide insight into how major changes in body plan evolved in the land plants. In addition, genetic pathways facilitating adaptation during the transition to a terrestrial environment from an ancestral aquatic environment.

**Techniques**: Our approach is genetic, with loss- and gain-of-function alleles created via CRISPR-Cas9 genome editing and transgenic molecular biological approaches. Gene expression patterns are monitored by in vivo expressed fluorescent proteins and as well as genomic approaches. These skills are broadly applicable to any biological system.

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**Project Title**: Post-transcriptional RNA modification its role in gene expression

**Supervisors**
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Dr Eduardo Flores-Sandoval  
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Dr John Alvarez  
john.alvarez@monash.edu
Dr Tom Dierschke  
tom.dierschke@monash.edu

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background**: Regulation of gene expression can occur at both the transcriptional and post-transcriptional levels. At the transcriptional level it is known that ‘epigenetic’ marks on histones, in particular methyl and acetyl groups added to lysines in the N-terminal region of histone 3 influence how much transcript is produced from a locus. It is now becoming clear that mRNA molecules themselves can be marked with methyl groups and this may influence the stability or translatability of mRNAs.

**Project Aims**: To investigate the role of the single YTH ortholog in Marchantia polymorpha. YTH proteins have been demonstrated to bind RNA, specifically to adenine residues with methyl groups at position 6 (m6A). Thus, they ‘read’ the m6A marks and target the mRNAs for an as yet unknown fate.

**Techniques**: Our approach is genetic, with loss- and gain-of-function alleles created via CRISPR-Cas9 genome editing and transgenic molecular biological approaches. Gene expression patterns are monitored by in vivo expressed fluorescent proteins and as well as genomic approaches. These skills are broadly applicable to any biological system.
**Project Title**: Characterisation of the capacity of chelators to promote nutrient bioavailability in hydroponic plant growth systems

**Supervisors**
- Professor John Bowman  
  john.bowman@monash.edu  
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- Dr Jamie Selby-Pham  
  Jamies@nutrifield.com.au  
  +61 3 93155815

**Other Supervisors**
- Other Supervisors

**Location**
- Nutrifield, 52 Technology drive, Sunshine West, R&D laboratory and plant growth rooms

**Background**: Chelators form soluble (bioavailable) complexes when bound to metals, including the nutrients calcium (Ca), iron (Fe) and zinc (Zn). Chelators are important to include in hydroponic systems, as these nutrients precipitate out of solution and become nonbioavailable when the hydroponic nutrient solutions increases to sub-optimal pH. A wide range of synthetic and organic chelators are currently used within hydroponics systems.

**Project Aims**: To characterise the chelating efficiency of currently used chelators and chelator-containing products, to identify their capacities to 1) chelate nutrients based on chromophore dissociation efficiency, 2) prevent precipitation and/or solubilise precipitate during sub-optimal pH conditions, and 3) prevent the onset of nutrient deficiency symptoms in plants grown in sub-optimal pH conditions. This project could be adapted to suit either an honours student or masters student.

**Techniques**: This project will utilise techniques including: hydroponic plant growth, ion quantification, and UV/VIS spectrometry. This project would suited to a student with a good grounding in chemistry and plant biology.
Background: Marsupials are the largest radiation of mammals in Australia, but significant amounts of fundamental knowledge of their biology is understudied. Marsupials differ from placental mammals in the way in which they replace their teeth, but the patterns and mechanisms behind this difference are unclear. This project will look at tooth development and replacement in the small dasyurid Sminthopsis to achieve fine-scale developmental mapping of teeth from birth to adult.

Project Aims: 1. Map in 4D the development of teeth in Sminthopsis. 2. Compare tooth development with the tammar wallaby Macropus eugenii. 3. Compare tooth development with other marsupials and placental mammals.

Techniques: 3D scanning, image analysis, 3D quantification, developmental biology.

Image: 3D digitisation of teeth in the tammar wallaby by PhD student Qamariya Nasrullah.

Background: Moving from feeding on land, to hunting underwater, is one of the most dramatic transitions a species can undergo during its evolution. Yet, among mammals, this transition has occurred independently in a number of clades. In order to move and feed in water, species must adapt both their anatomy and behaviour, resulting in startling examples of convergent evolution. Yet, while some clades have become obligate aquatic (e.g. whales and sea cows), other species still maintain important links with the land, coming ashore to breed and rest between hunting trips (e.g. seals and river otters). These semi-aquatic or amphibious species are interesting, because they help us to understand what it is like to be halfway between habitats and habits. Semi-aquatic habits have also evolved independently in a number of clades of Australasian rodent. In addition to the Australian water rat or Rakali (Hydromys chrysogaster), semi-aquatic habits have also evolved in the earless water rat (Crossomys moncktoni) and waterside rat (Parahydromys asper) of New Guinea. Recently, another new species of semi-aquatic rodent was discovered in Sulawesi (Waiomys mamasae). The repeated evolution of aquatic habits among rodents presents an excellent system within which we can explore the ways in which species must adapt to effectively function when moving between both terrestrial and aquatic environments.

Project Aims: 1. Determine whether semi-aquatic Australasian rodents share adaptations that allow them to more efficiently function in aquatic environments. In particular, whether there are adaptations in the structure of the limbs that allow more efficient swimming. 2. Examine these species within a phylogenetic context to assess whether these adaptations are examples of convergent evolution of similar structures.

Techniques: MicroCT scanning, 3D modelling, geometric morphometrics, measurement of museum specimens, phylogenetics.

Image: New species of semi-aquatic rodent Waiomys mamasae.
Project Title: Using phylogenomics to solve a hundred year old fish mystery
Supervisors: Dr Matt McGee
Other Supervisors: matt.mcgee@monash.edu
Location: Clayton Campus, 19 Rainforest Walk
Outline of Project:

Background: Southern Australia contains a high proportion of species found nowhere else in the world. In many cases, we still do not know the close relatives of many species discovered over a hundred years ago.

Project Aims: The student will sequence DNA from one of these mystery fish, then add the fish into the worldwide evolutionary tree of fishes.

Techniques: Computer skills, including: Basic Linux/UNIX shell commands, Statistics and phylogenetics in R

Project Title: Understanding mass extinction dynamics in fishes
Supervisors: Dr Matt McGee
Other Supervisors: matt.mcgee@monash.edu
Location: Clayton Campus, 19 Rainforest Walk
Outline of Project:

Background: Isolated lakes and islands often contain unique species found nowhere else in the world. Unfortunately, these habitats have experienced some of the highest rates of extinction in the world due to invasive species.

Project Aims: We will extract data on several large lake radiations of fishes, including functional traits and ecology, as well as their extinction patterns, then use statistical models to test what patterns best explain which species go extinct.

Techniques: Image analysis, Statistics in R
Dr Keyne Monro - Evolutionary Ecology Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Local adaptation to arid environment in native and invasive populations of capeweed</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Akane Uesugi <a href="mailto:akane.uesugi@monash.edu">akane.uesugi@monash.edu</a> +61 3 9905 4237</td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Keyne Monro <a href="mailto:keyne.monro@monash.edu">keyne.monro@monash.edu</a> +61 3 9905 5608</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk</td>
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Outline of Project

Background: How do invasive weeds spread? What ecological and evolutionary factors determine their distributions? Adaptation to local climate, particularly at the edge of species distributions, is thought to drive rapid range expansion in invasive species. Whether patterns of local adaptation are repeatable within invasive ranges, and how they differ from patterns in native ranges, is rarely tested.

Project Aims: This project will test for local adaptation in multiple transects along aridity gradients in invasive capeweed (Arctotheca calendula) populations in Australia, as well as in native South African populations. A student will conduct a common garden experiment in the greenhouse to estimate genetic divergence in traits associated with drought tolerance and avoidance.

Techniques: Greenhouse experiment, secondary metabolite analyses using HPLC, measurements of photosynthetic capacity.
### Project Title

**TADPOAL: Thermal and Developmental Physiology of Anuran Larvae**

**Supervisors**

Dr Reid Tingley  
reid.tingley@monash.edu

**Other Supervisors**

**Location**

Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background**: Predictions of species range shifts in changing environments commonly rely on correlative statistical models relating species distributions to climate. Correlative models can be useful tools for understanding contemporary biodiversity patterns, but are often unsuitable for extrapolation to novel climates. In response, there is now a focus on mechanistic approaches that incorporate physiology and behaviour, but these models tend not to include the potential for geographic variation in range-limiting traits, such as rates of growth, development, and metabolism. The TADPOAL project aims to solve this problem by developing generalisable methods for predicting geographic variation in developmental strategies, using frog tadpoles as a test case. This information will, in turn, enable ecologists and conservation managers to better predict and manage the effects of environmental change on biodiversity. Projects on the ecophysiology of adult frogs that are part of the TADPOAL project are also available (e.g., brown tree frogs *Litoria ewingii*).

**Project Aims**: The TADPOAL project aims to characterise and explain geographic variation in developmental strategies of frog tadpoles along environmental gradients, and provide the needed tools to account for that variation in forecasts of species distributions in changing environments.

**Techniques**: TADPOAL projects offer small bouts of field work, detailed lab experiments, and the option to integrate lab experiments with mechanistic niche modelling. Students will gain expertise in ecophysiology, and skills in tadpole husbandry and high-throughput phenotyping (e.g., metabolic rate estimation, digital photography).

Images: Common garden setup for raising tadpoles from different populations; Growling Grass Frog *Litoria raniformis* (Photo by Geoff Heard)

### Project Title

**Understanding the impact and spread of exotic newts in suburban Melbourne**

**Supervisors**

Dr Reid Tingley  
reid.tingley@monash.edu

**Other Supervisors**

**Location**

Clayton Campus, 25 Rainforest Walk

**Outline of Project**

**Background**: European smooth newts have recently settled in on Melbourne’s suburban fringe, but we still know very little about the species’ potential impact, its current distribution, or how best to contain its spread.

**Project Aims**: This project aims to investigate the potential ecological impacts of smooth newts on Australian fauna; map the species’ distribution with environmental DNA sampling and/or detector dogs; and explore new methods to improve trapping success.

**Techniques**: This project could involve behavioural experiments, genetic analyses, field surveys, and/or statistical modelling.

Image: A male smooth newt (Photo by Adam Elliot).
The School of Psychological Sciences is at the forefront of brain function research in Australia with roots in the basic discovery sciences, cognitive, clinical and brain neurosciences and the social sciences. Formalised within our research intensive institute, the Monash Institute of Cognitive and Clinical Neuroscience, our research current themes range from addiction to sleep with the goal of translating scientific discoveries to directly improving diagnosis and treatment of acquired, developmental and degenerative brain pathologies.
**Project Title:** Cellular Modelling of Attention Deficit Hyperactivity Disorder (ADHD) Risk Genes

**Supervisors**
- Dr Ziarih Hawi  
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- Dr Janette Tong  
  janette.tong@monash.edu
- Professor Mark Bellgrove  
  mark.bellgrove@monash.edu
- A/Professor Robert Bryson-Richardson  
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**Other Supervisors**
- Dr Janette Tong  
  janette.tong@monash.edu
- Professor Mark Bellgrove  
  mark.bellgrove@monash.edu
- A/Professor Robert Bryson-Richardson  
  robert.bryson-richardson@monash.edu

**Location**
Clayton Campus, School of Psychological Sciences, 18 Innovation Walk, Level 5

**Outline of Project**

**Background:** ADHD is the most prevalent psychiatric condition affecting 7.4% of Australian children and adolescents. Its features include extreme levels of motor activity, impulsivity and inattention that persist into adult life in 30-60% of cases. Genetic influences are recognised as a major predisposing factor, with heritability for ADHD estimated between 75-90%. Recent meta-analysis of data arising from genome wide association studies (GWAS) of 20,183 ADHD cases and 35,191 controls identified 12 single nucleotide polymorphisms (SNPs) that meet the stringent statistical standards for genome wide association (P≤5×10^{-8}) with ADHD.

**Project Aims:** To elucidate the effect of the most significantly ADHD-GWAS variant and SNPs in linkage disequilibrium (non-random correlation between alleles) with it by genetically engineering the ADHD associated and non-associated variants into human neuronal cell line. This project could be adapted to suit either an honours student of a PhD student.

**Techniques:** This project will utilise techniques including but not limited to polymerase chain reaction (PCR), cDNA syntheses, quantitative PCR, DNA cloning, and editing using the CRISPR-Cas9 technology, cell culture and Western blot.

This project would suited to a student with a good grounding in genetics and cell biology.
The Hudson Institute is a leading Australian medical research institute located in the heart of the Monash Health Translation Precinct in Clayton, Victoria.

We bring together 450 brilliant scientific minds to unlock the mysteries of the human body and enhance human health.

Our 51 research laboratories are clustered into five specialist centres undertaking basic and clinical research across cancer, innate immunity and infectious diseases, and women’s and baby health.

We embrace an open structure encouraging collaboration between disciplines, empowering our scientists to examine problems from a wide range of perspectives and sparking out-of-the-box approaches to discovery.
### Project Title

**Identifying novel sex determination genes responsible for DSD**

**Supervisors**
- Professor Vincent Harley  vincent.harley@hudson.org.au  +61 3 8572 2527
- Dr Alejandra Reyes  alejandra.reyes@hudson.org.au

**Other Supervisors**
- Hudson Institute of Medical Research, Monash Medical Centre

**Location**
- Hudson Institute of Medical Research, Monash Medical Centre

**Outline of Project**

**Background:** Disorders of sex development (DSDs), formerly intersex, are congenital conditions where gonadal or anatomical sex is atypical. DSDs encompass a wide range of abnormalities, including hypospadias (abnormal urinary opening in males), gonadal dysgenesis (underdeveloped or imperfectly formed gonads), and ambiguous genitalia and sex reversal (i.e., XX males and XY females).

**Project Aims:** Our aim is to identify genes causing DSDs, and the molecular mechanisms underlying testis and ovary formation in the mammalian embryo.

**Techniques:** This proposal will provide new insights into the molecular control of testis development, and thus offer the potential to improve diagnosis and clinical management of DSD. Approaches include human genetics, as well as molecular, cell and developmental biology.

**References:**

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### Project Title

**The biological basis of gender identity**

**Supervisors**
- Professor Vincent Harley  vincent.harley@hudson.org.au  +61 3 8572 2527
- Dr Jaco Erasmus, Monash Gender Clinic
- Professor Melissa Southey

**Location**
- Hudson Institute of Medical Research, Monash Medical Centre

**Outline of Project**

**Background:** Gender identity is the gender with which a person identifies. Studies suggest that gender identity is affected by genetic, prenatal hormonal or postnatal social determinants.

**Project Aims:** We are investigating the role of genes in patients with gender identity disorders.

**Techniques:** This project involves undertaking genetic association studies in the world’s largest cohort of male-to-female transsexuals. In one project it focuses upon genes involved in sex hormone synthesis and signalling. In another it focuses upon epigenetic changes potentially induced during transitioning.

**Reference:** Foreman et al. (2019) JCEM 104:390-396
### Project Title
Mouse modelling of clinical sex reversing mutations affecting FGF signalling

### Supervisors
- **Dr Daniel Bird**
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- **Professor Vincent Harley**
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### Other Supervisors
- **Ms Zhenhua Ming**
  - vincent.harley@hudson.org.au

### Location
Hudson Institute of Medical Research, Monash Medical Centre

### Outline of Project

**Background:** We have identified the first FGFR2 mutations in XY female sex reversed DSD patients. One case, a heterozygous FGFR2c-C342S mutation in a patient with both 46,XY gonadal dysgenesis and Crouzon syndrome is unusual since gonadal defects have not yet been reported in Crouzon patients. We turn our focus to the ligand the binds the FGFR2 receptor, called FGF9.

**Project Aims:** We have identified several missense FGF9 mutations affecting testis development in DSD. We will use our 'knockin' and 'knockout' mouse models to understand the role of signalling and FGF9 in particular in testis determination and disease and to identify FGF9-regulated genes and signalling pathways which might be defective in DSD patients.

**Techniques:** Analyses of male and female markers will be carried out, as well as markers of FGF signalling. Training includes basic cell and molecular biology as well as: embryonic microdissection, whole mount/section in situ hybridisation and immunofluorescence.


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### Project Title
Characterisation of novel gonadal targets of Sox9

### Supervisors
- **Professor Vincent Harley**
  - vincent.harley@hudson.org.au
- **Ms Zhenhua Ming**
  - vincent.harley@hudson.org.au
  - +61 3 8572 2527

### Location
Hudson Institute of Medical Research, Monash Medical Centre

### Outline of Project

**Background:** For the majority of DSD cases the underlying genetic aetiology is unknown. In males the Sry gene (testis determining factor) located on the Y chromosome upregulates the expression of Sox9, a critical 'hub' gene involved in male sexual development. However little is known about its downstream targets. By extensive data mining of gonadal microarrays, RNAseq, ATACseq and SOX9 ChIPseq we have identified genes directly regulated by SOX9. These candidate genes are up regulated in XY mouse testis compared to XX ovaries during development. See for example the expression of Bex2), and down regulated in sex reversed XY ovaries ablated for Sox9.

**Project Aims:** We will examine the expression profile of these genes during the critical sex determining period in a wildtype setting.

**Techniques:** We will perform detailed expression profiling in XX and XY embryonic gonad of wild type mice during the critical sex determination period E11.5-E13.5, postnatally and at adult stages. We will also perform SOX9 ChIPseq on gonads and promoter/enhancer analyses.

### Project Title: Transcriptional regulators as cancer targets: new models and therapeutic approaches

**Supervisors:**
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  - +61 3 8572 2774

**Other Supervisors:**

**Location:**
- Hudson Institute of Medical Research, Monash Medical Centre

**Outline of Project:**

**Project description:**
Transcriptional regulators play a key role in activating oncogenic pathways that impinge on tumour growth, invasion and metastasis. We have recently used CRISPR to generate cancer cell lines with fluorescent and luminescent reporters of key transcriptional pathways in colorectal cancer. In this project, the student will utilise cell biology and molecular biology techniques to dissect the components of the transcriptional machinery in cancer and identify new therapeutic targets.

### Project Title: Understanding cancer resistance to chemotherapy

**Supervisors:**
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  - +61 3 8572 2774

**Other Supervisors:**

**Location:**
- Hudson Institute of Medical Research, Monash Medical Centre

**Outline of Project:**

**Project description:**
The majority of cancers initially respond very well to standard of care chemotherapeutics but invariably become resistant leading to cancer relapse and patient mortality. This project seeks to identify novel therapeutic targets that will synergise resensitize tumours to chemotherapies in the resistant setting.

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**Genetically engineered transcriptional reporter cancer cells are used to identify regulators of oncogene expression.**
NOTES