A message from A/Professor Matt Piper, Honours Coordinator

Welcome to Biological Sciences Honours.

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.

For all projects hosted outside of Monash, students must also have an internal supervisor from the School of Biological Sciences. If you need any help finding an internal supervisor, please contact Matt Piper or Kate Elliott, at: sci-biohonours.coordinator@monash.edu.

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. Students should ensure they are available to attend this two week training period.

Overwhelmed or confused? To get advice on finding a project for honours, or for more information or assistance, please contact:

A/Professor Matt Piper                    Ms Kate Elliott
Honours Coordinator                      Education Program Manager
Email: sci-biohonours.coordinator@monash.edu
# HONOURS PROJECTS

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SCHOOL OF BIOLOGICAL SCIENCES

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

- Ecology and Conservation;
- Evolution in a Changing World; 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.
Professor Sureshkumar Balasubramanian - Phenotypes to Genes and Mechanisms Research Group

<table>
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<tr>
<th>Project Title</th>
<th>Epigenetic regulation of thermal responses in plants</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Prof Sureshkumar Balasubramanian <a href="mailto:mb.suresh@monash.edu">mb.suresh@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Clayton Campus</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus</td>
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</tbody>
</table>

**Background:** When you eat spicy food, you feel the heat and sweat! When the autumn is a bit hot, plants flower and announce an early spring arrival. Have you wondered how do the plants know it is spring to flower? How do they sense temperature and respond? Our work in recent years suggest a key role for epigenetic gene regulation in thermal responses. Students who are interested in this project are encouraged to look at Casal and Balasubramanian, Ann. Rev. Plant Biol, 2019 and Tasset et al, PLoS Genetics, 2018 for background on the proposed project.

**Project Aims:** To characterise the gene regulatory networks involving the gene POWERDRESS, which encodes a component of the Nuclear Co-Repressor (N-CoR) complex using genetic and molecular techniques. The specifics of the project will be decided upon mutual 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.

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<table>
<thead>
<tr>
<th>Project Title</th>
<th>Epigenetic gene silencing in Friedreich ataxia, a triplet expansion disease</th>
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<tr>
<td>Supervisors</td>
<td>Prof Sureshkumar Balasubramanian <a href="mailto:mb.suresh@monash.edu">mb.suresh@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Rucha Sarwade <a href="mailto:rucha.sarwade@monash.edu">rucha.sarwade@monash.edu</a></td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus</td>
</tr>
</tbody>
</table>

**Background:** Trinucleotide repeat expansions underlie several neurogenetic diseases such as Huntington disease, Friedreich ataxia and Fragile X syndrome. Friedreich ataxia occurs due to an intronic repeat expansion associated with epigenetic silencing. This project will investigate the potential molecular mechanisms that lead to epigenetic gene silencing caused by expanded repeats taking advantage of the findings in other systems. Students who are interested in this project 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 and protein work (western blots, immunoprecipitation etc). This project would require you to have strong skills/interest in genetics and molecular biology.
Project Title: Deciphering the splicing code through Genome Wide Association Studies (GWAS)

Supervisors: Prof Sureshkumar Balasubramanian mb.suresh@monash.edu

Other Supervisors: Clayton Campus

Outline of Project

Background: RNA splicing is a key molecular process that plays a vital role in gene regulation. Changes in splicing mediate growth and development of eukaryotic organisms. Differential selection of splice sites in an RNA molecule leads to differential splicing. How is this process decided? What are the genetic determinants of this process? How does this vary and lead to human genetic diseases? This project will investigate some of these key questions. Students who are interested in this project are encouraged to look at Dent et al, NAR-Genomics and Bioinformatics, 2021 and 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 as cloning, sequencing etc. This project would require you have strong skills/interest in computational genetics and molecular biology. Research Methods is not a prerequisite for this project.

Project Title: Genome editing of splicing-associated SNPs using CRISPR

Supervisors: Prof Sureshkumar Balasubramanian mb.suresh@monash.edu

Other Supervisors: A/Prof Sefi Rosenbluh Monash Biomedicine Discovery Institute

Location: Clayton Campus

Outline of Project

Background: RNA splicing is a primary link between genetic variation and human disease. However, linking specific genetic variation with specific splice-sites is a huge challenge. We have recently developed a method to quantify splice-site usage and use this quantification as a phenotype to identify associated SNPs by GWAS (Dent et al, NAR-Genomics and Bioinformatics, 2021).

Project Aim/s: This project aims to apply this method on publicly available human RNA-seq data, identify interesting SNPs and then edit them using CRISPR-based genome editors and then analyse their impact on splicing decisions.

Techniques: This project will use computational analysis of splicing, CRISPR-genome editing methods and other standard molecular biology techniques. A student with strong interest or prior computational programming skills would find it an optimal project.
Project Title | Various projects
Supervisors | Dr Jeremy Barr, jeremy.barr@monash.edu
Other Supervisors | 
Location | Clayton Campus
Outline of Project

**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**: Evolution and development of land plants

**Supervisors**
- Professor John Bowman  
  john.bowman@monash.edu
- Dr Eduardo Flores-Sandoval  
  eduardo.flores@monash.edu
- Dr John Alvarez  
  john.alvarez@monash.edu
- Dr Tom Dierschke  
  tom.dierschke@monash.edu

**Location**: Clayton Campus

**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.

---

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

**Supervisors**
- Professor John Bowman  
  john.bowman@monash.edu
- Dr Eduardo Flores-Sandoval  
  eduardo.flores@monash.edu
- Dr John Alvarez  
  john.alvarez@monash.edu
- Dr Tom Dierschke  
  tom.dierschke@monash.edu

**Location**: Clayton Campus

**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.
<table>
<thead>
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<th>Project Title</th>
<th>Characterisation of the capacity of chelators to promote nutrient bioavailability in hydroponic plant growth systems</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Professor John Bowman  <a href="mailto:john.bowman@monash.edu">john.bowman@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Jamie Selby-Pham  <a href="mailto:Jamies@nutrifield.com.au">Jamies@nutrifield.com.au</a></td>
</tr>
<tr>
<td>Location</td>
<td>Nutrifield, 52 Technology drive, Sunshine West, R&amp;D laboratory and plant growth rooms</td>
</tr>
</tbody>
</table>

**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: 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-sporing 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 only 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 Richard Burke - Ion Transport and Metabolism Research Group**

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Chloride transport in the function of intracellular organelles and human disease</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Richard Burke <a href="mailto:richard.burke@monash.edu">richard.burke@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Clayton Campus</td>
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<tr>
<td>Outline of Project</td>
<td>Background: Members of the ClC 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.</td>
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<td>Project Aims: 1) To determine the cellular defects that arise due to mutation of the Drosophila intracellular chloride transport proteins ClC-b and ClC-c; 2) To screen for genetic modifiers of ClC-b and ClC-c function. 3) To model the effect of human ClC pathogenic mutations in Drosophila</td>
</tr>
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<td>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.</td>
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<tr>
<th>Project Title</th>
<th>Male germline development and infertility in Drosophila</th>
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<tr>
<td>Supervisors</td>
<td>Dr Richard Burke <a href="mailto:richard.burke@monash.edu">richard.burke@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Professor Moira O’Bryan</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus,</td>
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<tr>
<td>Outline of Project</td>
<td>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.</td>
</tr>
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<td></td>
<td>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.</td>
</tr>
<tr>
<td></td>
<td>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.</td>
</tr>
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</table>
**Project Title**: Regulation of copper transport and homeostasis  
**Supervisors**: Dr Richard Burke (richard.burke@monash.edu)  
**Location**: Clayton Campus

### 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.
### Professor David Chapple - Evolutionary Ecology of Environmental Change Laboratory

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Impact of feral cats on Australian lizards</th>
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<tr>
<td>Supervisors</td>
<td>Prof. David Chapple</td>
</tr>
<tr>
<td></td>
<td><a href="mailto:David.Chapple@monash.edu">David.Chapple@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Alexandra Carthey (Macquarie Uni)</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus</td>
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**Background:** Feral cats consume ~650 million reptiles per year in Australia, and are considered to be a major threatening process for many lizard species. This honours project will investigate the ability for Australian lizard species to recognise feral cats as predators, and whether they exhibit relevant antipredator responses in the presence of chemical cues from feral cats. The project will require fieldwork and laboratory-based studies at Arid Recovery ([https://aridrecovery.org.au/](https://aridrecovery.org.au/)) in South Australia. Available for a Feb 2023 start.

**Project Aims:** Investigate the ability for Australian lizard species to recognise feral cats as predators, and display appropriate antipredator responses.

**Techniques:** The project will involve fieldwork, and laboratory-based behavioural experiments to examine the antipredator responses of several Australian lizard species.

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Conservation and ecology of threatened or Data Deficient Australian skinks</th>
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<td>Supervisors</td>
<td>Prof. David Chapple</td>
</tr>
<tr>
<td></td>
<td><a href="mailto:David.Chapple@monash.edu">David.Chapple@monash.edu</a></td>
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**Background:** Skinks (Scincidae) are the dominant lizard group in Australia, comprising ~460+ 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 involve fieldwork in Western Australia, Northern Territory, or Queensland. Available for either a Feb 2023 or July 2023 start.

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

**Techniques:** The project will involve field-based studies of threatened or Data Deficient Australian skink species.
**Project Title**: The role of structural variation in the evolution of sex-specifically selected genes

**Supervisors**
- Dr Tim Connallon
- Dr Filip Ruzicka

**Location**: Clayton Campus

**Outline of Project**

**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.

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**Project Title**: Topics in theoretical biology

**Supervisors**
- Dr Tim Connallon

**Location**: Clayton Campus

**Outline of Project**

**Background**: Most biological disciplines make use of simple mathematical models to gain insight into the processes that have shaped patterns observed in data. For example, genome sequences provide massive amounts of information about genetic differences between species and genetic variability within species. This information provides clues about processes that have shaped the evolution of genome sequences. We can use mathematical models to explain how different evolutionary processes are likely to have influenced patterns of genetic diversity and divergence across genomes.

**Project Aims**: A mathematical modelling project will be developed in consultation between the honours student and supervisor. The project will address a biological problem of mutual interest to student and supervisor. Examples of recent honours projects include:

- Maintenance of genetic variation in the mitochondrial genome
- Population and evolutionary dynamics of species with separate sexes
- Evolution in species with complex life cycles
- Evolution of chromosomal inversions
- Population genetic models of adaptation and extinction

**Techniques**: The project involves:

- Mathematical modelling of dynamical systems, including the development of recursion or differential equations describing change, analysis of equilibria, and evaluation of the dynamical behaviour of each model.
- Computer simulations to complement and test limiting assumptions of mathematical analyses of the models.
- Using results of the models to explain existing empirical observations, or make new predictions that can be tested by analysing existing data or carrying out new experiments.
<table>
<thead>
<tr>
<th>Project Title</th>
<th>Testing faster-X theory in mosquitoes</th>
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<tr>
<td>Supervisors</td>
<td>Dr Filip Ruzicka <a href="mailto:filip.ruzicka@monash.edu">filip.ruzicka@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Tim Connallon <a href="mailto:tim.connallon@monash.edu">tim.connallon@monash.edu</a></td>
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<td>Location</td>
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Part time by negotiation

**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.
Using artificial intelligence to make evidence-based conservation more efficient

Bioinformatics and Computer Science

Dr Carly Cook

Conservation Management Research Group

Background: Environmental managers must make decisions about the most effective management actions to protect biodiversity. However, managers often do not have access to the best available scientific evidence that could help support their decisions. One way to support managers in making evidence-based decisions is to synthesize the available evidence and provide it to them in a format they can use. However, this requires exhaustive searches of the available literature, filtering this evidence by relevance and quality and then synthesizing the findings into overall lessons. This approach can be extremely time consuming, taking over a year in many cases. This has created significant interest in the ways in which artificial intelligence (AI) might be used to streamline and automate this process. While there has been some progress in developing tools to support evidence synthesis in medicine, the conservation literature poses a unique challenge because of the broad range of species and interventions, and the lack of standardised terminology. As such, there is a need to determine whether the AI advances made in evidence-based medicine and other sectors can be used to support evidence-based conservation.

Project Aims: This project will explore state-of-the-art tools from data science and artificial intelligence, such as natural language processing, and assess their suitability to form part of a tool-kit for streamlining systematic reviews of the conservation literature.

Techniques: This project is ideally suited to a student with a double degree in Computer Science and Biology. The student will require basic training in data science and artificial intelligence approaches, and an interest in environment management. The student will need to develop a detailed understanding of the procedures for evidence synthesis. They will also need to conduct a detailed review of the ways in which artificial intelligence can support each step of the synthesis process. This review will need to identify the available tools used in other fields and evaluate their suitability using a case study. The topic for the case study can be determined in consultation with the student based on their interests.
SCHOOL OF BIOLOGICAL SCIENCES

Professor Damian Dowling - The Experimental Evolutionary Biology Research Group

<table>
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<tr>
<th>Project Title</th>
<th>Does mitochondrial evolution “curse” males to shorter lifespans?</th>
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<tr>
<td>Supervisors</td>
<td>Professor Damian Dowling, <a href="mailto:damian.dowling@monash.edu">damian.dowling@monash.edu</a></td>
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<td>Other Supervisors</td>
<td>Clayton Campus</td>
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Outline of Project

Full time

Background: Evolutionary theory predicts that maternal inheritance of the mitochondria will lead to the build up of mutations in the mitochondrial genome that are sexually antagonistic – harming males, but benefitting females (this idea has been called the “mother’s curse” hypothesis). This is because maternal inheritance of this genome means that all mutations in the mitochondrial DNA are screened for their function only through females (i.e. males never pass their mtDNA onto their children – they are evolutionary dead-ends). Mutations that work well in females are then favoured by natural selection, even when these same mutations are detrimental to male health. Consequently, we predict that mitochondrial genomes will carry numerous “male harming” but “female friendly” alleles, and act as genetic hubs of sexual conflict – that’s a fascinating idea when you consider just how important the mitochondrial genome is in regulating energy production in animals!

Project Aims: We are offering 2 projects, whereby the students will test the idea that mitochondrial genomes carry “male-harming” mutations that affect sex differences in life-history. One student will focus on lifespan, the other on reproductive success. The students will explore the idea that maternal inheritance of mitochondria plays a role in driving the evolution of sex differences in these traits (when it comes to lifespan, for example, in Australia females live on average 5 years longer than males). They will also test whether there are “counteradaptations” hidden in the nuclear genome that try to restore the balance of this genetic conflict by offsetting the negative effects of the mitochondrial mutations. The Dowling lab has prepared for this project by developing the tools and resources the student will need to test this hypothesis. This includes a set of unique genetic strains of fruit flies, each of which carry a different genotype, and which enables the student to explore the effects of mitochondrial genotype, nuclear genotype, and their combination on sex differences in lifespan and reproductive performance of the flies.

Why study evolutionary and behavioural ecology in fruit flies? Fruit flies are great animals to study processes of sexual conflict, concepts of evolutionary ecology related to life-history, and animal behaviour. For example, males are very coercive, and compete with each other, and with females, for access to reproductive opportunities. This includes participating in complex mating behaviours that include “fencing” – essentially swordplay with their forelegs. The ejaculate of these males also contains toxic proteins that have evolved to manipulate the reproductive physiology and lifespan of the females. The flies might be small, but this is actually a massive advantage when it comes to doing scientific research on them, since it means we never have a problem with sample sizes, and we can breed them up quickly and study them with relative ease.

Techniques: The student will learn cutting edge techniques in experimental design relevant to the fields of evolutionary biology and ecology. They will learn to work quickly with 1000s of live animals, and set up, and implement experiments that are able to separate “causation” from “correlation”, with the power to disentangle genetic vs non-genetic effects on lifespan, and to hone in on the contribution of the mitochondria to determining traits like lifespan. This involves working extensively with stereomicroscopes, collecting, sexing, and crossing fly populations, and using equipment developed for behavioural and physiological phenotyping. The student will learn to synthesise and appraise key research and concepts in evolutionary ecology, to position their research at the forefront of the scientific discipline, and to lead and manage a major research project, within a dynamic and collaborative team setting. They will become proficient with the quantitative analysis of data, using statistical approaches such as linear mixed modelling.
Dr Maria Ermakova

Project Title: Genetic engineering of sorghum for improved biomass and grain yield

Supervisors: Dr Maria Ermakova, maria.ermakova@monash.edu
Other Supervisors: Professor Ros Gleadow
Location: Clayton Campus

Outline of Project:

Background: In the next 50 years we will have to produce more food than we have produced since the beginning of civilization. Creating and testing new approaches to make plants more productive is essential to provide desired increases in crop yield. Our approach is to improve photosynthesis, the process that plants use to convert sun energy, carbon dioxide and water into sugars and that forms a basis of plant productivity.

Project Aims: The project will include characterisation of new transgenic sorghum lines with improved photosynthesis and developing a method for high-throughput testing of new gene-editing targets in sorghum tissue culture.

Techniques: Golden Gate cloning, sorghum tissue culture and transformation, CRISPR-Cas9, RT-PCR, Western blotting, leaf gas-exchange and chlorophyll fluorescence.

Project Title: Evolution of photosynthetic ATP production in land plants

Supervisors: Dr Maria Ermakova, maria.ermakova@monash.edu
Other Supervisors: Professor John Bowman
Location: Clayton Campus

Outline of Project:

Background: ATP, produced using solar energy captured through photosynthesis, acts as the universal cellular energy cofactor fuelling all life processes. To combat drought, heat and other environmental stresses, plants need to spend ATP that would otherwise be used for growth and seed production. Discovering different strategies that land plants can use to generate more ATP will help to create crops that are better suited for future climate scenarios.

Project Aims: The project will use a basal land plant Marchantia and the higher plant Arabidopsis genetically engineered to require high ATP production rate in order to survive. These plants will be characterised for their photosynthetic properties and gene-edited to identify specific reactions that contribute to production of extra ATP.

Techniques: Cloning, CRISPR Cas9 and plant transformation, RT-PCR, Western blotting, leaf gas-exchange, chlorophyll fluorescence and leaf absorbance.

Photo credits: Dr Florian Busch and Dr Julia Walter.
### Power Cascade Law of Growth in Animals and Plants

**Project Title:** Power Cascade Law of Growth in Animals and Plants

**Supervisors:**
- A/Professor Alistair Evans
- alistair.evans@monash.edu

**Other Supervisors:**
- Clayton Campus

**Outline of Project**

**Background:** The Evans EvoMorph lab has recently discovered a new law of growth that controls the shapes of teeth, horns, claws and thorns in plants and animals. This new law is called the ‘power cascade’ and it determines the shapes that are most commonly made for these structures according to a simple power law. The power cascade is present in vertebrates (from fish and amphibians to dinosaurs and mammals), invertebrates (including insects, spiders and squid) and plants (such as lemon tree and rose bush). When the power cascade controls the default shape for structures, this significantly influences the shapes that evolve in animals. We have shown that it can estimate the age of elephants from the growth of their tusks, and predict the shapes of Tyrannosaurus teeth. Computer simulation of growth following the power cascade can replicate the final shape of these structures.

**Project Aims:**
- This project will examine how the power cascade affects the growth and evolution of structures in a range of organisms, from insects to plants, depending on the interests of the student. This may include the shapes of leaves, insect bodies or whale teeth. Computer simulations of growth can be used to further discover how growth influences the evolution of shape.

**Techniques:**
- This project will use a variety of 3D and 2D imaging and analysis techniques to measure the shapes of structures. For 3D data, we use microCT and medical CT imaging and laser 3D surface scanning, and then process data in 3D software (Avizo, Geomagic, Blender). For 2D data, we use ImageJ for processing and measurement. Computer simulation of growth can use Mathematica or custom-built developmental simulation software.

### Tooth Development in the Marsupial Sminthopsis

**Project Title:** Tooth Development in the Marsupial Sminthopsis

**Supervisors:**
- A/Professor Alistair Evans
- alistair.evans@monash.edu

**Other Supervisors:**
- Clayton Campus

**Outline of Project**

**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.
**Project Title**: Macaranga secondary metabolite trade-offs in ant-plant symbioses

**Supervisors**
- Dr Chris Lee  
  chris.lee@monash.edu
- Dr Zoe Yek Sze Huei  
  yek.szehuei@monash.edu
- Professor Ros Gleadow  
  ros.gleadow@monash.edu

**Other Supervisors**
- Professor Ros Gleadow  
  ros.gleadow@monash.edu

**Location**
Mulu National Park, Borneo, Malaysia;  Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background**: Ant-plant symbioses are complex interspecific interactions found only in tropical environments. Typically, in such symbioses, plants provide housing structures (e.g. domatia) and food rewards to their ant symbionts. In return, the ants protect their plant host against herbivore attack and encroaching climbing plants, as well as provide nutrients that promote host plant growth.

Macaranga is a genus of tropical trees found in Africa, Australasia and Asia that includes many species that demonstrate ant-plant symbioses. It is also part of the Euphorbiaceae, a plant family notorious for its plethora of toxic secondary metabolites such as the cyanogenic glycosides in cassava, an important food crop. In Macaranga, a combination of ant-plant symbioses and secondary metabolites are utilized to protect the plant; however, the nature of the symbiosis varies at different developmental stages. During the sapling stage, leaves are new and few and ant protection appears to be a more significant contributor to successful tree growth. As host trees grow in size and age, the symbiotic ants' interactions are restricted to the young shoots and new leaves. We hypothesized that as host plants grow, the metabolic cost will switch from producing mostly food rewards to attract ants at the sapling stage, to producing defence compounds (e.g. flavonoids) in mature trees. We expected that there should be a detectable trade-off in the food rewards and chemical defence compounds produced as the host tree grow.

**Project Aims**: This project aims to examine the food reward and defense chemical production quantity and composition at two developmental stages of Macaranga host tree that engage in obligate ant-plant symbiose. We would like to examine if there is an age-dependent trade off in production of these compounds.

**Techniques**: Field site: Mulu National Park where Macaranga triloba (an obligate ant-plant) occurs at high density. Sampling design: Trees less than 1 m high will be sampled as an approximate to sapling stages. Trees more than 3 m high will be sampled as an approximate to mature trees. Student will identify the tree species and sample individuals from both tree age categories at multiple field sites. Food rewards (i.e. food bodies) will be collected from three domatia from each tree for quantification. Three leaves without herbivory damage will be collected from young and old parts (for mature trees) of the tree for chemical defence analyses in the lab.

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**Project Title**: Impact of climate change on tropical crops

**Supervisors**
- Professor Ros Gleadow  
  ros.gleadow@monash.edu

**Other Supervisors**
- Professor Ros Gleadow  
  ros.gleadow@monash.edu

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

**Background**: The Plant Ecophysiology Group research the impact of the climate on the nutritional quality of plants and food security. The focus is on the form and function of tropical crops that make cyanide and other toxins. Current projects include effect of drought and temperature on cassava, taro and sorghum, and their wild relatives.

**Aim/s**: Taro is a staple food for about 2 million people living in the Pacific. It is a good source of carbohydrate but contains sharp crystals of calcium oxalate that irritate the throat and can cause serious illnesses. This project funded by the Australian Centre of International Agricultural Research examines the effect of rising global temperature on the growth and nutritional value of Fijian taro varieties in collaboration with Fijian researchers. Alternative projects are available on other crops.

**Techniques**: Students will be taught any techniques required. This project will focus on physiology and use established methods in photosynthesis, growth and crop yield. Other techniques include chemical analysis of plant tissues (pipetting and spectroscopy) and distribution modelling. Projects can be tailored for GEN students to focus on the molecular regulation of pathways of interest.

Street market in Fiji with taro corms tied in bunches in front (Photo: R.Gleadow)
Sex differences and the evolution of infectious disease (various projects)

Supervisors: A/Prof. Matt Hall
A/Prof. Matt Hall matthew.hall@monash.edu

Other Supervisors: Clayton Campus

Outline of Project:

Background: Sex differences in the prevalence and severity of infection are universal. Across the animal kingdom, one sex is often described as the “sicker sex”, with females typically more susceptible to infection in invertebrates, whereas males suffer more in mammals and birds. Yet the science that guides our understanding of infectious disease routinely overlooks the pervading impact of sex. This gap begins at the very initial stages of research and discovery, when females are typically excluded from animal studies, or the sex of the subject is not explicitly modelled or controlled for in the published results. Using the model system of the water flea Daphnia magna, a variety of projects are available that explore how male-female differences can dampen or accelerate the spread and evolution of a pathogen.

Project Aims: Possible aims include: i) Can males or female limit the spread of a pathogen by reducing a pathogen’s basic reproductive number (R0); ii) Does competition between pathogens occur differently in each sex and shape the maintenance of genetic variation in a pathogen population; and, iii) How does habitat quality influence the spread of disease and is a high quality habitat the same for each sex.

Techniques: This project will utilise techniques including: epidemiological modelling, cross-infection experiments, animal handling and culturing, evolutionary genetics, and dietary manipulations. Students will learn how to wrangle, visualise, and analyse data using R. This project would suit to a student with an interest in ecology, animal behaviour and evolutionary biology, as well as health and disease.

Global change and host-pathogen interactions (various projects)

Supervisors: A/Prof. Matt Hall
A/Prof. Matt Hall matthew.hall@monash.edu

Other Supervisors: Clayton Campus and Jock Marshall Reserve

Outline of Project:

Background: Global change is predicted to result in a dramatic shift in the transmission and distributions of infectious disease. The combination of increasing temperatures and more prevalent outbreaks of disease has the potential to place species closer to the brink of extinction than previously thought. Key to predicting winners and losers under the nexus of infection and global change is any mismatch between hosts and pathogens in their thermal tolerances. Infection risk, for example, may well decrease if a host can thrive in conditions that are detrimental to the pathogen. Yet rarely are the thermal limits of hosts and pathogens considered in unison, hampering our ability to accurately forecast population declines under global change.

Project Aims: Possible aims include: i) What host-pathogen traits are most susceptible to thermal stress and how does this influence the possible invasion of a pathogen as captured but its basic reproductive number (R0); ii) How does temperature influence the maintenance of genetic variation in a pathogen population; and, iii) Who is most susceptible to the combination of infection and thermal stress in a population – the old, young, male or female or other demographics.

Techniques: This project will utilise techniques including: epidemiological modelling, cross-infection experiments, animal handling and culturing, evolutionary genetics, and thermal phenotyping assays. Students will learn how to wrangle, visualise, and analyse data using R. This project would suit to a student with an interest in ecology and evolutionary biology.
**Project Title** | Adaptation to contemporary climate change  
**Supervisors** | Dr Kay Hodgins, kathryn.hodgins@monash.edu  
**Other Supervisors** | Dr Paul Battlay  
**Location** | Clayton Campus  

**Outline of Project**

*Background:* Some invasive species have the remarkable ability to rapidly adapt to the local climatic conditions that they encounter as they expand their range. One such species is common ragweed, which has rapidly adapted to local climates in Australia and Europe over the past 100 years since its introduction to these regions. However, we know that native North American populations have already experienced a shift in season length over this same period because of contemporary climate change and we expect that this change in the environment has driven adaptive shifts in multiple traits. We have re-sequenced whole genome samples from hundreds of historic and contemporary samples of this invader in the native range of North America.

*Project Aims:* By comparing the genome sequences of the historic and contemporary populations the student will track the signals of climate change adaptation over the past 100 years to identify regions of the genome potentially responsible for contemporary climate change adaptation.

*Techniques:* This project would involve bioinformatic and statistical analysis. Specifically, we have already identified candidate genes important for climate adaptation in contemporary populations such as those involved in flowering time. The student would determine if these loci have changed in their allele frequencies over time by comparing historic and contemporary sequences at the same geographic location.

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**Project Title** | When is hybridisation helpful or harmful to invasive species?  
**Supervisors** | Dr Kay Hodgins, kathryn.hodgins@monash.edu  
**Other Supervisors** | Dr Paul Battlay, Dr Akane Uesugi  
**Location** | Clayton Campus  

**Outline of Project**

*Background:* 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 new environments encountered during invasion. We have identified a remarkable and repeated pattern of invasion and hybridisation between two species of sea rocket introduced to multiple areas of the globe. Using common garden analysis and a 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 these species. Traits involved in defense against herbivores often evolve during invasion because the introduced range typically has a very different set of enemies compared to the native range. One theory even predicts the evolution of reduce investment in defense during invasion and that this should allow populations to invest more in growth and reproduction and become more aggressive invaders.

*Project Aims:* The student will help determine if particular regions of the genome have moved from one sea rocket species to the other through hybridisation during invasion. The student will then determine if these genomic regions are associated with defense traits in common gardens of invasive hybrids as predicted by theory.

*Techniques:* This project would involve bioinformatic analysis and lab work. Specifically the student would quantify chemical defense traits followed by a genome wide association analysis using a SNP set already identified. The sequencing and greenhouse work is complete.
Dr Scarlett Howard - Integrative Cognition, Ecology and Bio-Inspiration (ICEB) Research Group

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<th>Project Title</th>
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<tr>
<td>One, two, bee: Numerical abilities in foraging honeybees</td>
<td>Dr Scarlett Howard <a href="mailto:Scarlett.Howard@monash.edu">Scarlett.Howard@monash.edu</a></td>
<td>Clayton Campus</td>
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**Background:** Despite having a miniature brain, honeybees show impressive learning, memory, and cognitive abilities, such as maze navigation, concept acquisition, human face discrimination, and categorisation of visual stimuli. In recent years, honeybees have been shown to have impressive numerical capability. They can perform tasks such as quantity discrimination, addition and subtraction, odd vs. even categorisation, learn the rule of greater vs. lesser, match numbers to symbols, and more. We aim to understand more about the numerical abilities they have and how we can push the cognitive limits of a miniature brain.

**Project Aims:** The objective of this project is to determine whether honeybees prefer to use ratio or absolute number to solve a numerical task. We will then determine how well honeybees can discriminate between different ratios. The student will train free-flying honeybees to perform these numerical tasks and then test the bees on their performance during challenging ratio comparisons.

**Techniques:** Animal handling, experimental design, data analysis using R, conducting animal behaviour experiments.

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<th>Location</th>
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<tr>
<td>Pollinating the urban jungle: Does urbanisation impact the personality of native bees</td>
<td>Dr Scarlett Howard <a href="mailto:Scarlett.Howard@monash.edu">Scarlett.Howard@monash.edu</a></td>
<td>A/Prof. Matthew Symonds (Deakin University)</td>
<td>Clayton Campus</td>
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**Background:** Over half of the world’s human population currently resides in cities and towns. The UN reports that by 2050, this will rise to 70%. Animal personality, also referred to as behavioural syndromes, coping styles, and temperament, is defined as behavioural differences in individuals which are consistent across time and/or situations. Some personality traits are more suited to an animal living in urbanised habitats, such as high exploratory behaviour, high boldness, and high aggressiveness. Much research on animal personality in urban environments has focused on vertebrates such as birds, mammals and reptiles, but the impacts of urbanisation on insect behaviour are largely unknown.
Project Aims: This project will involve visiting sites of low, moderate, and high urbanisation and collecting native bees. The bees will be tested for personality traits such as boldness and exploration at two different time points to determine if personality changes across urban gradients and if it is consistent across time.

Techniques: Animal handling, experimental design, data analysis using R, conducting animal behaviour experiments, fieldwork.

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<tr>
<th>Project Title</th>
<th>Flower preferences of native Australian bees</th>
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<td>Supervisors</td>
<td>Dr Scarlett Howard</td>
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<td><a href="mailto:Scarlett.Howard@monash.edu">Scarlett.Howard@monash.edu</a></td>
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<td>Professor Bob Wong</td>
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<td><a href="mailto:Bob.Wong@monash.edu">Bob.Wong@monash.edu</a></td>
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<td>Location</td>
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Background: Bees are considered one of the most important insect pollinators. Therefore, understanding how they choose which flowers to visit and then pollinate is essential for crop production and native plant reproduction. Angiosperms (flowering plants) use flower colour, scent, size, shape, and other signals to attract or deter potential animal visitors. Pollinators, such as bees, use these flower traits to detect flowers in the environment and select which flower to land on. Bees have preferences for certain colours, patterns, shapes, and sizes. Past work has focused on the preferences of introduced species, such as honeybees and bumblebees, meaning we know little about the foraging strategies and decision-making processes of native Australian bees.

Project Aims: This project will examine the preferences of native Australian bees for flower colour, pattern, shape, or size, or a combination of these traits. The project will explore how pollinator choices shape pollination, flower evolution, and plant-pollinator interactions.

Techniques: Animal handling, experimental design, data analysis using R, conducting animal behaviour experiments.
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.
## Project Title
The role of the gut microbiota in the regulation of blood pressure

### Supervisors
A/Professor Francine Marques  
francine.marques@monash.edu

### Other Supervisors

### Location
Clayton Campus

### 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.

![Diagram A](image1)

![Diagram B](image2)

![Diagram C](image3)
Project Title: Do eggs compete for sperm
Supervisors:
- Professor Dustin Marshall
dustin.marshall@monash.edu
- Dr. Hayley Cameron
hayley.cameron@monash.edu
Other Supervisors: Clayton Campus

Outline of Project:

**Background:** Most marine organisms reproduce by shedding eggs and sperm into the water column, whereupon they meet and fertilisation occurs. Competition among sperm for access to eggs is well recognised in this system, with important implications for the evolution of gamete size. In contrast, the degree to which eggs compete for sperm is far less understood - but has the potential to drive the evolution of female reproductive strategies (e.g. egg size), and may have even contributed to the evolutionary transition from external to internal fertilisation.

**Project Aims:** The aim of the project is to examine whether egg size mediates competition among eggs for sperm in marine broadcast spawners.

**Techniques:** This project will have both a field and laboratory component. It will combine in vitro fertilisation techniques, field collections (and potential out-planting experiments) and various laboratory assays. The project would suit a student with an interest in ecology or evolution.

Note: alternative projects within the field of marine evolutionary ecology are open for discussion.
Dr Michael McDonald - Experimental Evolution Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Using evolution to combat multidrug resistance in H. pylori</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Michael McDonald <a href="mailto:mike.mcdonald@monash.edu">mike.mcdonald@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Terry Kwok</td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus</td>
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<tr>
<td>Outline of Project</td>
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**Background:** The evolution of antibiotic resistance is a major global challenge. No matter how many new antibiotics are invented, evolution renders frontline antibiotics useless one by one, until now multidrug resistant (MDR) strains of most pathogens are common. It is essential that we learn from previous mistakes and employ evolutionary stable strategies that incorporate an understanding of the genetic changes that cause resistance.

**Project Aims:** The goal of this project is to characterise the core network of antibiotic resistance and compensatory mutations in a range of species. This will be achieved using MDR clinical strains, genomics and a novel experimental evolution approach that exploits some pathogen’s (H. pylori, A. baumanii and S. pneumoniae) natural capacity for recombination. In our first few years of study with H. pylori, we have discovered new genes involved in resistance evolution and potential susceptibilities.

**Techniques:** Short and long-read genome sequencing, bioinformatic genome assembly, experimental evolution and molecular biology.

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Experimental evolution of an artificial microbiome</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Michael McDonald <a href="mailto:mike.mcdonald@monash.edu">mike.mcdonald@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td></td>
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<tr>
<td>Location</td>
<td>Clayton Campus</td>
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<td>Outline of Project</td>
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</table>

**Background:** Microbial communities comprised of many interacting species sustain all ecosystems. Anticipating the disruptive effects of microbial adaptation in response to shifts in the environment, such as climate change and the use of new antibiotics, is an important goal. Experimental studies of evolution have provided insights into the speed of adaptive change, and its genetic causes, but have not considered the unique conditions experienced by microbes cohabiting with other species. Since the members of a microbial community are themselves part of the environment, the presence of one species will alter the selective pressures faced by their co-habiting species. This interaction between ecology and evolution, or eco-evolutionary feedback, means that adaptation to a given antibiotic, nutrient source or temperature will be quite different for a species evolving in isolation than for a species embedded within a microbial community.

**Project Aims:** The objective of this study is to determine the rates and genetic mechanisms of adaptation for microbes co-evolving with other species within a community. This will be achieved by evolving replicate populations of yeast and bacteria - either mixed together or in isolation. Large scale measurements of phenotypes and whole-genome DNA sequence data for all populations will be analysed to determine the plausibility of anticipating adaptive change, as well as to unravel the molecular details of specific instances of co-evolution.

**Techniques:** Short and long-read genome sequencing, bioinformatic genome assembly, experimental evolution and molecular biology.
Background: Machine learning techniques offer great promise for dramatically increasing the size and speed of data collection in the biological sciences, including automated counting and identification from images.

Project Aims: The student will train a machine learning algorithm to quantify the type and number of vertebral elements across a dataset of thousands of images, then examine this data in an evolutionary context using phylogenetics.

Techniques: Computer skills, including: Python, Phylogenetics in R

Background: Animal coloration has prompted intensive study by biologists over the last several hundred years, but large datasets and evolutionary trees are required to accurately understand what factors promote colour pattern biodiversity.

Project Aims: The student will compile photographs of marine fishes, then train a machine learning algorithm to quantify colour pattern diversity. They will then analyse colour pattern diversity in a phylogenetic context across a large evolutionary tree of fishes.

Techniques: Computer skills, including: Python, Phylogenetics in R

Background: Molecular phylogenetics has dramatically improved our ability to understand evolutionary relationships between groups of organisms, but it is necessary to combine this information with fossil data to accurately estimate divergence times.

Project Aims: The student will build a phylogeny based on whole genomes, then combine this information with fossil data to accurately infer divergence times across vertebrates.

Techniques: Computer skills, including: R, Phylogenetics software, including RAxML, IQ-TREE, BEAST, and RevBayes
<table>
<thead>
<tr>
<th>Project Title</th>
<th>Using computer vision to understand animal movement</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Matt McGee</td>
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<tr>
<td>Other Supervisors</td>
<td><a href="mailto:matt.mcgee@monash.edu">matt.mcgee@monash.edu</a></td>
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<tr>
<td>Location</td>
<td>Clayton Campus</td>
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<td>Outline of Project</td>
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<td>Full time or Part time</td>
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**Background:** Quantifying animal movement and behaviour with video data is often challenging and slow with conventional methods, but new advances in computer vision can dramatically speed up the process.

**Project Aims:** The student will utilize a database containing thousands of videos of fish feeding behaviour and develop a means to accurately quantify behaviour with supervised machine learning techniques.

**Techniques:** Computer skills, including: R, Python

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Using computer vision to quantify 3D skull data</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Matt McGee</td>
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<tr>
<td>Other Supervisors</td>
<td><a href="mailto:matt.mcgee@monash.edu">matt.mcgee@monash.edu</a></td>
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<tr>
<td>Location</td>
<td>Clayton Campus</td>
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<tr>
<td>Outline of Project</td>
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<td>Full time or Part time</td>
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**Background:** Three-dimensional imaging techniques allow for detailed measurements of biological structures, but analysing such data is time-consuming. New computer vision techniques offer ways to dramatically speed up data collection.

**Project Aims:** The student will use pre-existing CT scan data for a range of vertebrates in conjunction with newly available supervised machine learning techniques to automatically measure various skull traits.

**Techniques:** Computer skills, including: Python, R

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Identifying invasive species using large biodiversity datasets</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Matt McGee</td>
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<tr>
<td>Other Supervisors</td>
<td><a href="mailto:matt.mcgee@monash.edu">matt.mcgee@monash.edu</a></td>
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<tr>
<td>Location</td>
<td>Clayton Campus</td>
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<tr>
<td>Outline of Project</td>
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<td>Full time or Part time</td>
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</table>

**Background:** Invasive species drive extinction events, habitat destruction, and economic damage worldwide, but there is still much debate on mechanism.

**Project Aims:** The student will integrate a large evolutionary tree of fishes with information from biodiversity databases with information on invasive species to create large statistical models predicting invasion risk and potential damages in Australia and worldwide.

**Techniques:** Computer skills, including: Statistics and phylogenetics in R
**Project Title**  
*Impacts of Quaternary climate change on shaping past reptile and frog communities along a 3000km latitudinal gradient, from the Australian tropics to the temperate south*

**Supervisors**  
Dr Jane Melville  
jane.melville@monash.edu  
jmelv@museum.vic.gov.au

Dr Scott Hocknull  
scott.hocknull@qm.qld.gov.au

**Other Supervisors**

**Location**  
Clayton Campus and Melbourne Museum

**Outline of Project**

**Background:** The honours project/s will contribute to a larger study funded by an ARC Discovery grant, focusing on using existing palaeontology collections, 3D imaging, ancient-DNA, proteomics, and new machine-learning analytical approaches to investigating the impacts of Quaternary climate change on shaping past reptile and frog communities along a 3000km latitudinal gradient in Australia.

**Project Aims:** The broad project aims are to: 1. Quantify how reptile and frog community composition has changed over the past 500,000 years at multiple fossil sites spanning four climatic regions across the full latitudinal gradient of (mainland) Australia. 2. Determine how these faunal changes correlate with climate and vegetation shifts past and present, with predictions into the future.

**Techniques:** Honours project/s may involve field work, 3D imaging of fossils through CT scanning, molecular biology techniques, proteomics, and new machine-learning analytical approaches.
Project Title: Developmental responses to environmental change
Supervisors: Dr Christen Mirth
Other Supervisors: Clayton Campus

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.

Project Title: Adapting feeding responses to environmental stress
Supervisors: Dr Christen Mirth, Professor Carla Sgro, Dr Lesley Alton
Other Supervisors: Clayton Campus

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 behavioural assays and spectrophotometer analysis to quantify food intake. Students will also gain expertise in fly husbandry, some basic molecular biology, and statistical analysis.
**Project Title**: Growing up in a changing world: how does adaptation to novel environments affect larval tolerance to thermal and nutritional stress?

**Supervisors**
- Professor Carla Sgro  
  carla.sgro@monash.edu
- Dr Christen Mirth  
  christen.mirth@monash.edu

**Location**
Clayton Campus, 25 Rainforest Walk

### Outline of Project

**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.
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>
</tr>
</thead>
<tbody>
<tr>
<td>Supervisors</td>
<td>Dr Akane Uesugi <a href="mailto:akane.uesugi@monash.edu">akane.uesugi@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td>Dr Keyne Monro <a href="mailto:keyne.monro@monash.edu">keyne.monro@monash.edu</a></td>
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<tr>
<td>Location</td>
<td>Clayton Campus, 18 Innovation Walk</td>
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</table>

**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: Climatic effects on colours of Australian birds

Supervisors:
- Professor Anne Peters
  - anne.peters@monash.edu

Location:
- Clayton Campus, Museum Victoria, potentially other musea

Outline of Project

Full time or Part time.

**Background:** Animal size, shape and appearance often vary geographically along climatic gradients and—when consistent and general—these patterns have been formalised as ecogeographical rules. Interest in these rules has experienced a recent revival, since they can reveal how animals have adapted to climatic variation in the past, and how they may react to future changes. Animal coloration is one of the traits that varies predictably with climate as described by Gloger’s rule (darker coloration in wet and warm regions, presumably for camouflage), and Bogert’s rule (darker coloration in colder regions, for thermoregulation). Recent comparative analyses indicate that birds may follow aspects of both rules, since species that live in wet and cold regions are darker coloured than those in dry and warm areas. However, these effects do vary between regions and taxonomic groups, and sometimes temperature effects prevail over precipitation or vice versa. Whether this heterogeneity indicates that the rules are not generally valid and/or that they apply depending on the specific ecological/environmental circumstances, can only be determined by comprehensive large-scale analyses.

**Project Aims:** This project will quantify how climatic effects shape intra-specific geographic variation in plumage coloration in a large sample of bird species. Specifically, the aim is: (1) establishing the generality of climatic effects on bird coloration, and (2) determining whether intrinsic (phylogeny, body mass, life history, etc) or extrinsic factors (strength and type of climatic gradient, habitat) explain why some species follow the rules more closely than others. This will be the first large-scale quantitative assessment of climatic effects on intra-specific colour variation in any group of animals and its outcomes will have implications for our understanding of patterns of diversification, climatic adaptation and potential climate change impacts.

**Techniques:** The project will involve measuring plumage coloration of museum specimens across 50-100 species of Australian birds using reflectance spectrometry. These specimens will be sourced from the ornithological collections at Melbourne Museum and possibly ANWC (Canberra) and/or Australian Museum (Sydney). The project will involve complex statistical analyses. This project will be advised by Dr Kaspar Delhey (Max Planck Institute for Ornithology).

**Most relevant publications**

From our previous Honours student, Audrey:


<table>
<thead>
<tr>
<th>Project Title</th>
<th>By negotiation</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Professor Anne Peters, <a href="mailto:anne.peters@monash.edu">anne.peters@monash.edu</a></td>
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<tr>
<td>Location</td>
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<td>Outline of Project</td>
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**Background:** I will consider projects suggested by students in the areas of behavioural ecology, conservation ecology, climate change ecology and adaptation, telomere ecology. I prefer studies on birds, but other organisms will be considered. Check my webpage: https://petersresearchgroup.org

**Project Aims:** dependent of project

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

Supervisors: A/Professor Matt Piper matthew.piper@monash.edu

Other Supervisors: A/Professor Matt Piper matthew.piper@monash.edu

Location: Clayton Campus

Outline of Project

Available Part-Time

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.
**Reproduction and foraging of penguins**

**Professor Richard Reina - Ecophysiology and Conservation Research Group**

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

**Mid-year start only**

**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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**Project by negotiation**

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<tr>
<th>Project Title</th>
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<tbody>
<tr>
<td>Supervisors</td>
<td>Professor Richard Reina</td>
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<tr>
<td></td>
<td><a href="mailto:richard.reina@monash.edu">richard.reina@monash.edu</a></td>
</tr>
<tr>
<td>Other Supervisors</td>
<td></td>
</tr>
<tr>
<td>Location</td>
<td>Clayton Campus, 19 Rainforest Walk and possible field sites</td>
</tr>
</tbody>
</table>

**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.

**Project Aims:** Dependent on project.

**Techniques:** Will vary with project.
Professor Carla Sgro - Genetics, Evolution, Biodiversity & Climate Change Research Group

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

**Supervisors**
Professor Carla Sgro  
[carla.sgro@monash.edu](mailto:carla.sgro@monash.edu)

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

**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.

**Project Title**: Feeding ecology of Drosophila and its impacts on climatic adaptation

**Supervisors**
Professor Carla Sgro  
[carla.sgro@monash.edu](mailto:carla.sgro@monash.edu)

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation Walk

**Outline of Project**

**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.

**Project Title**: The potential for transgenerational effects to increase or reduce climate change risk

**Supervisors**
Professor Carla Sgro  
[carla.sgro@monash.edu](mailto:carla.sgro@monash.edu)

**Other Supervisors**

**Location**
Clayton Campus, 18 Innovation Walk, Level 4

**Outline of Project**

**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 reproductve 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.

**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.

**Techniques**: Drosophila husbandry, experimental design, data analysis.
**Dr Sridevi Sureshkumar - Genetics At The Core Research Group**

**Project Title:** Mechanisms of triplet repeat expansions

**Supervisors:**
- Dr Sridevi Sureshkumar
- Sridevi.sureshkumar@monash.edu

**Other Supervisors:**
- Clayton Campus, 18 Innovation Walk

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**Full time**

**Background:** We have recently shown that intronic triplet repeat expansions trigger small RNA-mediated pathways causing gene silencing in model plant Arabidopsis thaliana. We have identified more than twelve components involved in gene silencing. Among the twelve components, six of them share the homology to human genes. More than 40 plus neuronal genetic disorders are known to cause by triplet repeat expansions. However, the underlying mechanisms are not known due to a lack of a model. Here we propose, Arabidopsis is a facile model to study intrinsic triplet repeat expansion mediated gene silencing. Technically amiable to manipulate the genes and feasible to perform large scale phenotypic screens within short periods. In this study, we will explore genetic screens to identify additional components involved in repeat mediated gene silencing. The identified potential genetic components will be tested in FRDA (Human triplet repeat genetic disorder) cell lines in the space of translation biology.

**Project Aims:**
1) Mapping the mutants using innovative sequencing methodologies.
2) Genetic complementation analysis.
3) Molecular characterization of potential components.
4) Test the identified components in the Human FRDA Cell lines

**Techniques:** For this project we will use, SHORE map, Next gen sequencing, genetic crosses (complementation analysis), phenotypic analysis, PCR, RT PCR and qPCR. For pull down assays we will use CHIP and CHIP seq. To Measure the RNA and Protein levels we will use blot western and Northern blot to quantify the RNA (in addition to qPCR).

**Model organism:** Arabidopsis thaliana and Human FRDA cell lines.

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**Project Title:** The association of regulatory RNAs in gene regulation

**Supervisors:**
- Dr Sridevi Sureshkumar
- Sridevi.sureshkumar@monash.edu

**Other Supervisors:**
- Clayton Campus, 18 Innovation Walk

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**Full time**

**Background:** The regulatory RNAs like siRNAs miRNAs, dsRNA, and long noncoding RNA, play a fundamental role in regulating gene expression. Recently we have shown that small interfering RNAs (siRNAs) regulates the triplet repeat mediated genetic loci in wild Arabidopsis wild strain Bur-0, identified in Ireland. More than 40 plus neuronal genetic disorders are affected by triplet repeat expansions associated with gene silencing, or protein toxicity leads to potential pathogenicity. Although the molecular pathogenicity is not well understood due to a lack of models. We mapped the phenotype to IIL1 locus harbored a long GAA triplet repeat expansion in the intron, quite parallels to the human triplet repeat disorder FRDA triplet repeat expansions occurred in the first intron of FXN gene. Subsequently, discoveries from our lab show that RNA polymerase PolIV and POLV regulate the gene silencing through RNA I machinery. At this point, it is ambiguous to know which substrate is for the small RNA formation in triplet repeat loci. The molecular analysis indicates that PolIV and POLV activity are required for gene silencing but by which molecular signals remain elusive? We think unusual structures over the repeat regions may play a role in increasing double-stranded RNA (dsRNA) or antisense RNA at IIL1 Locus. This could result in IIL1 mRNA degradation achieved through siRNAs. To understand the phenomenon, we would screen the activity of dsRNA or antisense RNA in Bur-0 and suppressors at the RNA level. The existing signatures like triplet repeats and downstream signals like change in chromatin marks are reliable indicators to explore R loop formation at IIL1 locus. R loop is a special chromatin structure contains both single-strand DNA and RNA molecule in hybrid form. Thus, we will examine R loop formation at IIL1 locus and the subsequent role in gene regulation.

**Project Aims:**
1) Accessing the dsRNA and antisense RNA in Bur-0 and Genetic suppressor.
2) Investigate the R loop structures formation at IIL1 locus and Genetic suppressor.

**Techniques:** PCR, RT PCR and qPCR,CHIP , CHIP seq and DRIP sequencing. To Measure the RNA and Protein levels we will use blot western, Northern blot, and qPCR. Model organism: Arabidopsis thaliana.
**Project Title**  |  The effect of size and temperature on energy intake and use  
**Supervisors**  |  Professor Craig White  
**Other Supervisors**  |  craig.white@monash.edu  
**Location**  |  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**  |  The genetic architecture of rates of metabolism and water loss  
**Supervisors**  |  Professor Craig White  
**Other Supervisors**  |  craig.white@monash.edu  
**Location**  |  Clayton Campus, 25 Rainforest Walk  
**Outline of Project**  

**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.
Dr Sean Williamson - Ecophysiology and Conservation Research Group

<table>
<thead>
<tr>
<th>Project Title</th>
<th>Improving shark and ray conservation through better fisheries management</th>
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<tr>
<td>Supervisors</td>
<td>Dr Sean Williamson</td>
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<td></td>
<td>Dr Carly Cook</td>
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<td>Other Supervisors</td>
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<td>Location</td>
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**Outline of Project**

**Background:** This project will explore the impact of recreational fishers on the conservation of sharks and rays. These species are often not the target of recreational fishers, but when they are caught, they are generally released or killed. Research suggests that post-release outcomes for these species can be poor, but that simple changes to fishing practices could significantly improve the outcomes for these species. This research project will work to better understand how fishers interact with sharks and rays when caught, and to develop and trial methods to influence the behaviour of fishers to limit their impacts on captured individuals. A key component of this project will be understanding how conservation psychology techniques can be used to achieve positive behaviour change, and the effectiveness of different types of messaging in achieving this change.

The Honours project is available for a Semester 1 start in 2023. We will consider exceptional students who are only available for Semester 2 start in 2023, but preference will be given to students who can still attend the 10th World Recreational Fishing Conference in Melbourne between February 19-22, 2023. The project will form part of a collaboration with Dr Sean Williamson, Dr Carly Cook, Dr Jessica Walsh, and Prof. Richard Reina from Monash University, the Victorian Fisheries Authority, Victorian Recreational Fishers Peak Body and Flinders University.

**Project Aims:**
1. To understand recreational fisher knowledge and practices when capturing and releasing sharks and rays
2. To develop and implement a range of strategies to educate fishers about how to minimise the impacts on vulnerable species
3. Evaluate the effectiveness of education programs on changing attitudes and behaviours of recreational fishers

**Techniques:** This project will involve both qualitative and quantitative methods. The student will design and implement an online survey of recreational fishers. They will also conduct in-person surveys with fishers at piers, jetties, and boat-ramps. The student will need to network with a range of stakeholders, including fishers, fisheries managers, fisheries representatives, researchers and conservationists.
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.
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 ($P \leq 5 \times 10^{-8}$) 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 plot.

This project would suited to a student with a good grounding in genetics and cell biology.
HUDSON INSTITUTE OF MEDICAL RESEARCH

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.
**Background:** Differences of Sex development (DSD) are congenital conditions where gonadal, anatomical or chromosomal sex is atypical. Many people with gender variances are comfortable identifying themselves as intersex. They represent ~1% of live births and encompass a wide clinical spectrum, including hypospadias (atypical urinary opening in XY individuals), gonadal dysgenesis, and atypical external genitalia. In many cases the genetic etiology is not known.

**Project Aims:** To identify genes linked to intersex conditions, and the molecular mechanisms underlying gonad formation in the developing mammalian embryo. This project has the potential to improve understanding of DSD as well as diagnosis and clinical management of other related health outcomes such as cancer risk, infertility and gender dysphoria, and life-threatening conditions such as salt wasting.

**Techniques:** Genomics (exome sequencing), Biochemistry and cell biology, mouse models. Approaches include human genetics, as well as molecular, cell and developmental biology.

**References:**
Lee et al. (2019) PNAS 116:16577

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**Background:** Gender identity is the gender with which a person identifies. Gender identity may be congruent or incongruent with chromosomal or physical sexual characteristics. Transgender individuals are subject to high rates of discrimination. Biological explanations of gender identity have been associated with increased acceptance of transgender individuals. Evidence from brain imaging and genetic association studies with transgender individuals suggests that the gender with which one identifies may have a biological (hormonal) basis.

**Project Aims:** To undertake genome-wide genetic and epigenetic analysis of transwomen. This project is hopes to provide a greater understanding and awareness of transgender individuals, working towards improving outcomes for the transgender community.

**Techniques:** One project involves genetic association studies (GWAS); the other, a methylome analysis before and after transitioning.

**Papers arising from previous Honours students’ projects:**
Foreman et al. (2019) JCEM 104:390-396,
Hare et al. (2009) Biological Psychiatry 65:93-6
**Mouse modelling of clinical sex reversing mutations affecting FGF signalling**

**Project Title:** Mouse modelling of clinical sex reversing mutations affecting FGF signalling

**Supervisors:**
- Professor Vincent Harley
- Dr Yuan Chen

**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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**Characterisation of novel gonadal targets of Sox9**

**Project Title:** Characterisation of novel gonadal targets of Sox9

**Supervisors:**
- Professor Vincent Harley
- Dr Yuan Chen

**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, postnataally and at adult stages. We will also perform SOX9 ChiPseq on gonads and promoter/enhancer analyses.
