School of BioSciences

Research Prospectus
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The School of BioSciences aims to be a leading international research centre in the Biological Sciences. At present, the School leads more than 240 research projects supported by competitive funding of about $100m. Each research area is filled with world-class experts addressing topics such as conservation and climate change, evolution and behaviour, genetics and development, marine biology or plant biodiversity.

The School is home to a vibrant community of over 200 students studying a PhD, masters or honours degree in these fields.

The School of BioSciences is a leader and participant in various collaborative centres, including the Australian government’s Cooperative Research Centres (CRC) program which encourages collaboration between research institutions and industry, and Australian Research Council (ARC) Centres of Excellence. These are hubs of expertise developed to allow high-quality researchers to collaborate with other universities within Australia and overseas to maintain and develop Australia’s international standing in research areas of national priority.
Our research aims to enhance crop productivity to feed the growing world population while reducing the negative impact of agriculture on the environment.

My research group investigates how environmental conditions impact the beneficial interactions of plant roots with soil microbes and how beneficial microbes may improve abiotic stress tolerance in plants with a focus on agronomically-important crops such as wheat and barley. We are also interested in enhancing our understanding of novel super crops such as chia and quinoa and how these new crops are impacted by new environmental conditions during domestication in Australia. The focus of this research is to understand how to maintain the nutritional benefit of the seeds of these new super crops when exposed to suboptimal conditions.

We are also involved in a larger research initiative aiming to develop novel fertiliser technologies to enhance nitrogen uptake in crops while reducing the negative impact of nitrogen leaching into the atmosphere and groundwater. I am particularly interested in monitoring plant health when exposed to these newly developed fertiliser technologies.
My research is focused on understanding fundamental molecular mechanisms of how genes are controlled and applying that understanding to controlling and combatting fungal diseases, as well as developing new or improved applications for the use of fungi in biotechnology.

Fungi are everywhere. They are the major recyclers of waste — from the backyard composite bin to the forest floor — are in the air and are both on and in our bodies. They are important for food, chemical and pharmaceutical production and are being developed as building products. However, some fungi are also pathogens that infect and kill many plants and animals, including humans. Infectious diseases are a major health burden in society leading to morbidity, mortality and immense health care costs. Amongst all the infectious diseases, fungi are the hidden killers. Fungal infections affect about 25% of the world’s population, with mortality rates often higher than 50% and death rates over 1.5 million people a year. The increasing incidence of invasive fungal infections over the last few decades has followed the increasing population of immunocompromised individuals due to AIDS, immunosuppressive drug treatments for transplant recipients, anti-cancer chemotherapy treatments, prolonged antibiotic therapy, and other factors such as steroid use in COVID-19 recovery. The high mortality rate is a consequence of many factors, including our poor understanding of these pathogens, the lack of rapid and reliable diagnostics and a very limited arsenal of effective antifungal drugs. Using an array of genetic and genomic approaches, the research in the lab aims to understand how fungi infect humans, get around the immune defence systems and cause disease.

Both pathogenic and non-pathogenic fungi, like all organisms, respond to their environment. These responses can be transient, allowing for rapid adaptation to changing conditions, or permanent, as in the case of development. Responding to external and internal signals, which is fundamental to all life, involves detecting these signals and responding with changes in gene expression. Understanding how cells and organisms control their responses to these signals is another key area of research in the lab. Using fungi as the model organism, the work is focused on how genes control these responses and how these controlling genes are themselves controlled. The research is of basic biological importance but also has implications in understanding and treating disease, and improving biotechnological processes that use fungi that are important in industry and have direct economic impacts as pathogens.
I aim to develop sustainable solutions for pest management using genetic approaches.

Controlling invasive fruit fly in Australia

Releasing sterile male insects into the environment on a massive scale can reduce and eradicate insect pests through an approach called the sterile insect technique (SIT). Sterile males seek out and mate with wild females, who can’t lay fertile eggs, causing the population to rapidly decline. We’re actively working with research partners (University of Adelaide, Macquarie University) to develop improved SIT factory strains of Queensland Fruit Fly, which is an oppressive and persistent burden to the horticultural industry. Separating males from females in the factories is an ongoing challenge we’re trying to solve by making genetic sexing strains that enable males to be mechanically sorted from females based on pupae colour, or through heat sensitivity genes that conditionally kill females. We’re also introducing visible markers to flies in the laboratory to make it simple to distinguish our sterile flies from wild ones.

Insecticide resistance

Insecticides are the frontline defence many farmers use to control crop pests, yet the way in which they kill is often poorly understood. We’re working with natural bacterial toxins produced by Bacillus bacteria (Bt) that target and kill specific pests (including the diamondback moth), to understand how they work and why they are harmless to so many beneficial insects. This work has led us to focus on insect ion transporters, aquaporin water channels, and cellular pathways involving cell death. Sometimes mutations can arise in the insect genomes, causing insects to become resistant to toxins or chemicals. Genetic and genomic approaches have enabled us to understand how resistance to Bt toxins and diamide insecticides in particular can evolve in the field, and we’re trying to develop kits for early detection of resistance.

Gene drives and genomics

Gene drives are selfish genetic elements passed on to offspring at rates much higher than expected by chance. We’re collaborating with other research groups to overcome some major challenges associated with developing synthetic gene drives. This laboratory-based research has the potential to impose a fitness cost or benefit to a population and therefore may have applied outcomes in the future.

Plutella xylostella, the diamondback moth, is the most destructive pest of brassica crops (cabbage, canola) worldwide.
My mission is to improve understanding of the diversity of the Australasian flora so that this knowledge can underpin its conservation, management and utilisation.

I work on the diversity, evolution, classification and biogeography of Australasian flora, with particular emphasis on flowering plants and ferns. This research relies heavily on genetic markers and generally involves field work, molecular lab work, comparisons of plant morphology and use of herbarium specimens. It provides fundamental data on genetic variation in native plants to test and refine their naming and classification.

This knowledge of plant taxonomy and relationships underpins the management and conservation of biodiversity because it defines the units (species, subspecies, areas of genetic diversity) that are the objects of management.

Flowers of *Eucalyptus sepulcralis*.

Flowers of *Philotheca pungens*. 
In the Plant Systematics Research Group we aim to describe and understand large scale patterns of evolution within the Australasian flora (plants) and fauna (fungi). Our research investigates possible explanations for patterns in the distributions of diversity. Our research informs descriptions and distribution mapping of the plants and fungi for the flora of Australia.

**Plant evolution**

We reconstruct the tree of life for native Australasian lineages using genetic and genomic data, estimating the timing of plant diversifications using molecular dating techniques. We use morphological and genetic data to distinguish species so that they can be accurately identified in the field.

**Plant biogeography**

Our research investigates how distributions of extant taxa have been shaped by evolutionary processes over time, particularly focusing on lineages with distributions in the Southern Hemisphere. We are interested in identifying traits that have enabled Australian taxa to adapt to changing climatic conditions and habitat availability during the Tertiary Period.
I study anything microbiological. I am fascinated by microbes since they rule Earth and have done so for 3.5 billion years. Microbes control all biogeochemical cycles and facilitate the persistence of all of life on Earth.

I am a microbiologist who has pioneered and championed procedures that reveal microbes and their functions in many natural and engineered systems. I have been instrumental in discovering microbial contributions to practical aspects of water (eg algal blooms on the Darling River), wastewater and solid-waste treatment, which have led to improvements in treatment and energy savings. My work with host-associated microbes has substantially explained animal conditions, including equine and ruminant gut upsets and microbes involved in coral larval settlement and bleaching.

I have extensively trained non-microbial professionals in new microbial procedures to facilitate industry upskilling and founded collaborations with arts-science experts to disseminate microbial knowledge via children’s books.

A respirometer for measuring oxygen production or utilisation. Photosynthetically generated oxygen by animals (eg corals, anemones) containing photosynthetic algae is measured under light conditions (see lots of lights).

Sampling for cyanobacterial bloom material following the fish kills in 2019 in the Darling River at Menindee, NSW.
I identify problems that the rapidly expanding aquaculture industry has within production or creates with its environmental impacts. I create solutions to these problems with new techniques and technologies to improve production, secure the welfare of animals in farming systems and reduce the industry’s environmental footprint.

Our laboratory works on all aspects of aquaculture production, the welfare of animals under production and the environmental footprint of aquaculture. Projects span the great diversity of modern aquaculture species produced in the millions of tons, including algae, shellfish, crustaceans and fish.

We first look for key problems that the industry is experiencing or creates through its activities; many of these problems are difficult and require fresh thinking. We apply our knowledge across many aspects of aquaculture to develop solutions that work in the real world, not just the laboratory, and conduct experiments at proof-of-concept scale to test new ideas. We then partner with aquaculture producers to run experiments at industry scale, often using settings where tons or millions of animals are under production.

A seaweed culturing experiment to determine species that can grow in wastewater and turn a problem into an opportunity to create new, valuable products.

The salmon louse is the worst parasite of farmed salmon, costing over a billion dollars each year to control in aquaculture. Our work has created new farming technologies that prevent infections by 80%.
My research contributes to understanding how the evolution of biological adaptations are shaped by natural and sexual selection.

Chemical communication

My research aims to understand how biotic and abiotic factors influence chemical communication and thus shape receptor (antennae) morphology in insects. We address these questions in diverse systems, including reproductive behaviour; social systems; and inter-specific associations, typically of insects and spiders. Our methods include inter-specific comparative analyses; field and laboratory experiments; chemical analyses; and various modelling techniques. Pheromones, like other organic compounds, are degraded by ozone, UV light, and radicals.

While we know that pheromone plumes attenuate through the dispersal of molecules, the additional impact of pheromone degradation is poorly understood. Thus, one focus of our research is to highlight the significance of odour survival for insect chemical communication by examining how atmospheric conditions, including air pollution, affects signal integrity, antennal morphology and signal perception.
Natural ecosystems are degrading at a dramatic pace, and this is primarily due to the consequence of anthropogenic climate change and widespread land degradation. Our research focuses on finding the DNA markers of ecosystems’ vulnerability or resilience across multiple plant species.

We combine experimental and computational approaches to study the effect of environmental variation and stress on natural population. We use a range experimental models (Arabidopsis, Drosophila, ryegrass) to test hypotheses related to climate change and pesticide exposure.

**Climate change-proof population management**

Active population management will be increasingly indispensable to mitigate the effect of human perturbation. However, the perfect management scheme, either to restore or suppress a species, is yet to be designed. In particular, we are interested in using genomics tools to make sure the restoration will be successful, retains a maximum of genetic diversity and is climate change-proof.

**Controlling pests and weeds**

The emergence of pesticide resistance is evolution in action. Weed populations in Australia have been particularly good at emerging resistance to all the chemical they have been exposed to, providing a fascinating model for the study of evolution to a well-defined selective agent.

**Genomics of native Australian fruits**

Australia is a megadiverse country and hosts a large amount of plants with immense potential benefits for medicine and agriculture. Unfortunately, native fruits have rarely been considered crops and their potential remains largely untapped. With emerging genome technology, we aim to fill the gap so that native fruits can represent a sustainable alternative to conventional crops.
Australia is famous for its marsupials, which display many fascinating and distinctive features that reflect their early phylogenetic separation from most other mammals. Sadly, many species have progressively declined or become extinct due to various impacts of European settlement, including the introduction of invasive vertebrate pests. My laboratory aims to understand many aspects of marsupial reproduction and development, partly in appreciation of their position in mammalian evolution and partly to develop technologies that will enhance their future conservation. Additionally, we are developing synthetic biology strategies for both marsupial conservation and for eliminating invasive vertebrate pest populations that threaten much of Australia’s native fauna.

Early development, reproduction and stem cell biology of the fat-tailed dunnart (in collaboration with Professor Andrew Pask’s laboratory)

Early development of marsupials contrasts markedly from that of eutherian (‘placental’) mammals in many fundamental aspects that reflect their early branching within the mammalian evolutionary tree. For example, whereas the blastocysts of mice and humans comprise an outer trophoblast surrounding a cavity and an inner cell mass (which gives rise to the fetus), marsupial blastocysts comprise only a unilaminar epithelium with no inner cell mass — instead, the fetus arises from a sub-population of cells (‘pluriblast’) within the unilaminar epithelium.

Our research uses methods such as gene expression analysis and cell culture to examine the regulation of pluripotency and development of the germline in marsupials. We use a small dasyurid marsupial — the fat-tailed dunnart — as a model, since it offers similar advantages to the laboratory mouse by being small and easy to breed in captivity. While our research aims to develop the dunnart as a genetically manipulable marsupial model, it also has the potential for applications in conservation of threatened marsupial species, such as by restoring genetic diversity from cryopreserved cell lines.

The potential for gene editing to protect the northern quoll from cane toad toxin (in collaboration with Professor Andrew Pask’s laboratory)

Northern quolls populations have declined markedly due to predation on the introduced cane toad. Outside Australia, natural predators of bufonid toads (including cane toads) are resistant to their toxin due to known sequence differences in genes encoding certain isoforms of the alpha subunit of Na/K-ATPase. We are investigating whether introducing these sequence changes (using CRISPR) will confer bufotoxin resistance in our marsupial model, the fat-tailed dunnart, and thus whether a similar edit will protect northern quolls from further population declines (and loss of genetic diversity) due to cane toad predation.

Genetic biocontrol (in collaboration with Dr Patricia Jusuf’s laboratory)

Numerous introduced pest species in Australia threaten native species and reduce agricultural productivity. Recently developed gene drive technology could allow humane, targeted elimination of almost any vertebrate pest population. Our research aims to use the zebrafish as a model for optimising the design of gene drives in any vertebrate, including mammals, fishes and cane toads. We are also optimising gene editing methods in two target species — cane toads and European carp — to facilitate future production of suppression gene drives for these two species.
Our research aims to increase the success of human IVF by increasing pregnancy rates and decreasing time to pregnancy. We aim to ensure the development and selection of embryos that will establish a viable pregnancy and the birth of a healthy singleton child.

**Human infertility**

Infertility affects 1 in 6 couples worldwide and, for many, in vitro fertilization (IVF) is their only means of conceiving a child. Although 4% of all children born in Australia are conceived through IVF, there is an urgent need to increase the current success rates. Understanding the fundamentals of embryonic development and how the embryo interacts with the endometrium of the uterus to facilitate implantation remain key biological challenges.

**Embryo culture**

For the past 40 years my research has focused on understanding the physiology and metabolism of the preimplantation embryo, and how we can use such information to improve assisted human reproduction. My group has developed several successful culture systems used in human IVF today, and we are currently working on a new antioxidant system to reduce oxidative stress for sperm, eggs and embryos. These works will ultimately increase the overall success rates of IVF.

**Embryo viability**

It is important that, following IVF, only a single embryo is replaced in the mother-to-be. Transferring more than one embryo gives rise to the possibility of conceiving twins if two embryos are replaced, and triplets if three embryos are replaced, etc. Therefore, it is essential to be able to identify the most viable embryo for transfer. Our team has worked on the development of methods to assess viability before transfer. Improving embryo selection will decrease the time it takes to establish a pregnancy and ensure only one embryo is replaced.

**Developmental Origins of Health and Disease (DOHaD)**

This looks at understanding the relationship between diet and culture conditions on embryo programming through the newly discovered axis of metaboloepigenetics (how metabolism affects embryonic gene expression and fetal programming). These works are essential to understand how embryo culture conditions (or maternal diet for natural conception) impact and regulate development, and have consequences for the life-long health of the children conceived.
Seeds are a major source of food for a large portion of the planet’s inhabitants — hence understanding how seeds develop, particularly the factors that influence the size and shape of seeds, is of fundamental importance. My research addresses a fundamental question in seed biology: how does an embryo within the seed develop and what are the genetic factors that govern final seed size? We aim to use knowledge gained from our studies to improve crop yields by altering the size and shape of seeds.

Embryo formation during seed development

The formation of specific cell types during plant embryogenesis depends on the generation of precise spatial patterns of gene expression. How these gene expression patterns are established remains poorly understood and hence is of major biological interest. My research group aims to identify new pathways involved in gene regulation and show how these are involved in establishing cell identity during the early stages of embryogenesis. Our work involves using a range of genetic, genomic, molecular and cell biological approaches.

Seed size control

Seed size is a major driver of plant yield, and yet the genetic pathways regulating seed size are poorly described. In partnership with international colleagues, my group is investigating the mechanisms that control seed size by focusing on the role played by the seed coat in regulating seed growth. Achieving a better understanding of seed size control will enable us to use this knowledge to potentially improve crop yields.

Plant transformation technologies

In collaboration with colleagues in the School of BioSciences, my research group is looking at developing or improving genetic transformation technologies for crops such as canola and chia. Being able to quickly and cheaply generate transgenic plants will enable the agricultural industry to use gene-editing technologies to develop crops that have superior nutritional qualities, as well as be better able to withstand changing climate and the emergence of new pathogens.
My research interest has shifted over the years from purely scientific research to a combination of biosciences and tertiary education. My research focuses on evaluating ways to assist student progression, retention, academic success, and completion rates in the field of tertiary science, specifically in biosciences. I try to motivate my students to learn by getting them involved in what I teach and research — I believe that many students find it easier to learn and become involved if they enjoy what they are learning and if they see it as relevant. To this effect I am passionate about researching higher education and biosciences in general so that I can encourage the same passion and interest in our students.

I am currently a bioscience lecturer at the University of Melbourne. Previously, I was a Senior Lecturer in Science at Australian Catholic University. Involved in the teaching and preparation of the Bachelor of Biomedical Science and Bachelor of Nutrition Science degrees, I also performed the duties of the National Professional Practice Lead (Science) and the Honours course coordinator for the Science discipline. Prior to this, I worked as a lecturer in biotechnology at Swinburne University of Technology, where I taught into many subjects across the biotechnology degree.

I hold both a Bachelor of Science (Honours) and PhD titled ‘Design and development of synthetic vaccine constructs and delivery systems’ from the University of Melbourne. My research interests include enterovirus vaccine design and antiviral discovery; dengue fever virus vaccine design and antiviral discovery; and influenza virus antiviral discovery. I have recently completed a masters degree in education and am pursuing research in tertiary education within the field of science, technology, engineering and maths (STEM). I am now a Senior Fellow of the Higher Education Academy.
Plants rely on circadian clocks to integrate daily and seasonal environmental cues to coordinate growth, physiology and metabolism. A mismatch between the circadian clock and the local environment is detrimental to growth and fitness. Optimisation of circadian clocks in crops for new environments can contribute to enhanced food production.

**Plant circadian rhythms**

The circadian system is a biological time-keeper comprised of inputs (light, temperature, stress), an oscillator (a gene regulatory network) and outputs (physiology, metabolism, development). It influences almost all aspects of the plant and allows them to anticipate daily changes in the environment and adapt to seasonal conditions. Our main interest is to define the roles of metabolism and nutrition within the plant circadian system. We consider mechanisms of gene transcription, translation and post-translational control that influence circadian rhythms. Our research aims to make advances to understand fundamental aspects of plant cell biology, and also generate opportunities to develop crops or agricultural practices that match specific growth environments.

**Metabolic signals in the circadian system**

Sugars, which are the major product of photosynthesis, adjust circadian rhythms by modifying clock gene expression and protein levels. We use the regulation of the circadian system by sugars to define mechanisms of dynamic metabolic signalling in plant cells, and transcriptomics and chemical biology to reveal these metabolic signals. We are currently investigating how sugars generate these signals, and how they control gene expression.

**Circadian control of leaf senescence and seed nutrition**

Leaf senescence is a controlled developmental process which drives nutrient remobilisation in ageing leaves according to seasonal cues. Ethylene is a plant hormone that controls plant development, promotes leaf senescence and can adjust circadian rhythms in plants. We are investigating the mechanism by which ethylene affects circadian rhythms and the impact on leaf senescence and seed nutrition.

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**Dr Mike Haydon**

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Metabolism
Nutrition
Signalling
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Plants have actively shaped our planet through photosynthesis, and enabled the formation of stable modern human societies through their utilisation in agriculture. As a result, understanding fundamental aspects of how plants grow, develop and reproduce is essential if we intend to maintain ecosystems, agriculture and ultimately, human civilisation. My research adds to fundamental knowledge in the area of plant growth and development for future generations to enhance and improve our interactions with the planet.

Plant glycomics

My group is focused on understanding metabolic partitioning between the endomembrane and how it relates to plant cell wall biosynthesis. Plant cell walls are mainly comprised of complex sugars and provide structural support as well as being a plant’s primary interface with the environment. Cell walls are also important commodities (eg biomass for animal feed and biofuels) and can have major impacts on human health (eg through dietary fiber). Many of the precursors involved in cell wall biosynthesis are produced in the cytosol and thus require active transport into the endomembrane for assembly into cell wall polymers. My group has been instrumental in characterizing these transport processes in plants and fungi. The group also examines glycan modifications and glycan-binding proteins and their roles in endomembrane sorting.

Our main focus is the model plant Arabidopsis thaliana, as extensive genetic resources are available in this species to enable us to decipher which genes are involved in plant cell wall biosynthesis. Importantly, work undertaken on Arabidopsis can be readily extrapolated to important agricultural species. The lab applies and develops biochemistry, molecular and bioinformatic approaches and employs mass spectrometry to explore aspects of plant cell biosynthesis, with a focus on protein biochemistry.
Our aims in the applied pest area are to develop novel non-chemical approaches to reduce the impact of mosquito disease vectors on disease transmission, and to decrease the damage done by agricultural pests to food production. We also aim in the ecological genetics area to develop new thinking based on evolutionary theory to help conserve biodiversity, and to ensure that threatened species can adapt to climate change and other stresses into the future. We apply genomic tools in achieving these overall aims and in understanding biological processes.

Pest and disease control

My focus is on pest control in invertebrates, and in the diseases they spread. We develop novel approaches for suppressing disease-carrying mosquito vectors based on the manipulation of bacteria that live inside mosquito cells, and use microinjection to generate new strains of pests and disease vectors that are less harmful due to the bacteria they carry. We develop integrated pest control options for the grains industries, and we investigate how landscape changes can be harnessed to provide pest control services.

Applied ecological genetics

My group focuses on adaptation to rapid environmental changes in a range of species, including adaptation to climate change. We develop ways of incorporating evolutionary approaches when making predictions about adaptive capacity and when predicting species distribution shifts under climate change. We have expertise in genetics, genomics and physiological ecology. We work on threatened species and in threatened ecosystems.
We are doing research to provide a more secure planet for all people and the environment. A better understanding of how organisms can attack other organisms should provide new strategies for protection, which has wide implications for the deleterious impacts that fungi can have in plant disease, human health and degradation of products.

Our research focuses on the biology of fungi and aims to discover the genes found in these diverse organisms that enable them to cause diseases in plants and animals. The fungi are one of the most diverse groups of organisms on the planet, and while our focus is primarily on those that cause problems, other fungi are highly beneficial to humans as sources of food or pharmaceuticals. Research in the Parkville campus laboratory uses a full spectrum of approaches, from classical genetics and mapping through to genomics, gene editing and other molecular biology approaches.

Our strong partnerships with others, particularly at Grains Innovation Park in Horsham, complement the plant pathology aspects with field studies. Specific aspects of the research in cases are orientated around specific fungi or problems (e.g., blackleg disease of canola, cryptococcosis in humans) but often intersect through comparative approaches to explore fundamental aspects or emerging concepts in biology.

Blackleg lesions on canola caused by *Leptosphaeria maculans*.

Neopseudocercosporella capsellae, agent of white leaf spot of canola, expressing green fluorescent protein.
My mission is to undertake novel research that advances our understanding of aquatic environments. The aim of this research is to support the rational and ecologically sustainable use of marine resources. I aim to make a substantial contribution to research that can help resolve issues in the marine environment that are significant to broader society.

Fish ecology and the relationship between fish and the environment

I conduct research on a wide variety of topics related to the ecology of fish in marine, estuarine and freshwater systems. These topics include larval dispersal, recruitment of young, movement and migration, feeding and growth, and relationships with habitat (eg seagrass, mangrove, algae, reefs). Studies are focused mainly on important fishery species in marine and estuarine waters and the factors that influence fluctuations in the populations.

A variety of tools are used to conduct this research, in particular the chemistry and structure of fish otoliths (ear bones) that can provide information on age, growth, recruitment, movement and migration. Other tools include various methods of tagging to study movement and migration. Computer modelling is used to study the patterns of larval dispersal of fish.

Detailed studies are also conducted on the environment that influences fish. These include food chain impacts such as the input of nutrients to the marine environment and subsequent plankton productivity through the food chain to fish. This research involves the application of ecosystem modelling, supported by field studies on phytoplankton and zooplankton. Detailed studies are also conducted on key habitats for fish, in particular the biology of seagrass and factors that influence growth and cover.
Plant nutrition and biofortification

My research group investigates nutrient metabolism in plants with the aim of producing ‘biofortified’ crops that improve human nutrition. We are particularly interested in iron and zinc because many of the world’s most important food crops contain low amounts of these essential micronutrients, and more than two billion people suffer from iron and zinc deficiencies. Our research focuses on how plants absorb nutrients as well as the myriad of factors affecting nutrient bioavailability in edible parts of plants. We are also interested in understanding the nutrient decreases that occur in cereal crops under elevated atmospheric carbon dioxide and determining if certain biofortification strategies can counteract these decreases.
My work is cross-disciplinary and will aid our understanding of the long-term evolutionary impact of artificial light at night. The data will be of significance and provide much-needed data for a wide range of stakeholders involved in the areas of urban planning and biodiversity monitoring, including government agencies, the lighting industry and the wider public. It will increase the profile of Australia in the burgeoning field of ecological light pollution and create an outstanding international networking and research platform for at least three early career scientists.

My main area of research is in the field of behavioural ecology, with a particular focus on the impact of artificial night lighting on individual fitness and community structure. Since the introduction of electrical street lighting, many species live in environments with no period of ‘true darkness’. Scattered light from urban areas may extend beyond city boundaries, resulting in regions that have no street lighting but that are still exposed to unnaturally long periods of light. Accumulating evidence suggests that such ‘urban light pollution’ has catastrophic health implications for all species (including humans) and puts ecosystem function at risk. To date, the mechanism underlying this remains unconfirmed.

One of our current aims is to investigate whether artificial light at night drives evolutionary change using a combination of field observations, laboratory experiments and advanced genetic techniques. This is a multi-disciplinary study involving several masters and PhD students that will provide a significant advancement in the understanding of the impact of light at night for animals and will enhance our capacity to predict the outcome of future urban expansions for all species. The outcomes will have broad implications for estimating the future biodiversity and health of our urban areas and will benefit both globally and within Australia by providing much-needed data regarding the likely resilience of species currently residing in our major cities.
The brain is one of the most complex organs in the human body, composed of over 80 billion nerve cells that need to be made, specialised and connected correctly for the brain and associated central nervous system organs to function properly. Environmental (e.g., trauma) and genetic (neurodevelopmental and neurodegenerative) risk factors can lead to devastating disorders that cannot be cured. In the Neural Development and Regeneration lab, we study how the nerve cells in the central nervous system are normally correctly generated, what exactly goes wrong when specific genes are not functioning correctly, and what we can learn from related, highly regenerative animals that might help us to allow missing, damaged or lost human nerve cells to regenerate.

Development of the central nervous system

As an extension of the central nervous system, the retinal nerve cell sheet in the eye of all vertebrates contains the same types of nerve cells as, for example, the brain and spinal cord. By taking advantage of the rapid development of the genetic zebrafish vertebrate animal model, we can easily combine functional gene manipulation with phenotypic analysis using live imaging and fixed tissue to understand how individual genes affect the development of nerve cells: their gene expression; their anatomical connections; and ultimately their function. By combining gene function with live imaging of the temporal sequence of genes expressed within each of the distinct nerve cells, we can start building a network map that explains how the development and proper specialisation of vastly different types of nerve cells is coordinated.

Regenerating adult nerve cells

Humans have very limited capacity to repair damaged nerve cells caused by trauma (e.g., in diving or car accidents) or neurodegenerative disease. In our lab, we aim to decipher how highly regenerative related animals are able to regenerate damaged nerve cells.

The zebrafish vertebrate shares most of the same genes as humans, yet zebrafish are able to activate a distinct set of genes to coordinate highly efficient regeneration of nerve cells from stem cell types that also exist in humans. If we can understand and re-activate these genes in humans, we may be able to teach the brain and related organs to self-regenerate.

Visual disease modelling and treatment screening

The zebrafish animal model shares over 82% of human disease-causing genes and has unique advantages that allow it to be used for high throughput studies. To our knowledge, we have developed the only interdisciplinary visual zebrafish phenotyping pipeline that allows us to assess anatomical, electrophysiological and behavioral phenotypes of hundreds of zebrafish larvae each week. We are using our pipeline to screen through the hundreds of novel human genes implicated (by genome-wide association studies) in childhood myopia to identify the few important causative gene candidates that will need to be targeted for focused prevention and treatment strategies. We are also using established zebrafish glaucoma models to screen for the potential of novel Australian plant-derived antioxidants in preventing or treating the visual nerve cell loss that ultimately leads to blindness in glaucoma patients. We work with clinicians and neuroscientists using established mammalian animal models to take forward our findings towards clinical translation.
My research aims to develop and apply mechanistic models of how species respond to environmental change based on how individuals experience and respond to their environments across their whole life cycles. Compared to the more traditional descriptive/statistical modelling methods, mechanistic models can make reliable and robust predictions under complex and novel environmental settings. They can also reveal ‘management levers’ that can be used to improve (for conservation) or hamper (for pests and invasive species) species of applied interest.

**Ecological forecasting**

I have pioneered the field of ‘mechanistic niche modelling’ for forecasting species responses to environmental change. This involves the development of modelling tools that apply first-principles models of energy and mass exchange between organisms and their environments to predict their behaviour, life cycles, life histories and, ultimately, distribution and abundance. My research in this area involves laboratory work to measure functional traits required by the models and field work to test the models. A large part of this work has involved the development and testing of microclimate models. The approach is highly general, and we apply it to animals (including humans) and plants in both terrestrial and aquatic environments. It is powerful because it can infer species’ responses to novel environmental change as occurs during species invasions and under climate change.

**Metabolic ecology**

One of the most fundamental characteristics of living things is the way they take up resources from their environment and use them to grow, maintain and develop their bodies and ultimately reproduce. Metabolic theory aims to characterise this process from first principles, and I work with one particular theory, the Dynamic Energy Budget theory, to study the life cycles and life histories of organisms.

**Conservation biology**

Australia has a rich and diverse biota, but many species are threatened by human actions. Most of the focus on threatened species is on vertebrates, but most of our animal diversity lies within the invertebrates. Our research on ecological forecasting is applied to conservation in many organisms to predict suitable habitat (western swamp turtle, greater glider, koalas, great desert skink) or forecast stress events (flying foxes). But we also have a research program to recover native grasshoppers, including the nationally listed Key’s matchstick grasshopper. We integrate field ecology with genetic approaches and captive studies to develop conservation strategies for these species.
We value marine ecosystems for many reasons, but they are challenged by many of our everyday activities. If we want to keep enjoying our bays and coasts, we need to manage these activities well. Effective management needs strong science, but the diversity of Australia’s seas and the range of challenges mean that we can’t study every situation in detail, so we need research that builds a general understanding that we can then apply to new situations.

**Disturbance and resilience**

Many natural phenomena, such storms, heat waves and diseases, can disturb coastal ecosystems. We need to understand how animals and plants respond to these forces of change, particularly whether they are resilient or whether long-term changes occur. Along urban coastlines, human activities also create change. Human activities may be novel with no natural counterpart, or they may represent changes in rates or intensities of existing natural disturbances. Managing coastal environments sustainably depends on understanding how these human activities affect coastal ecosystems.

**Environmental monitoring and assessment**

An important part of making the right decisions about environmental impacts is making sure that we are precise about the questions that we are asking, that we collect data that can give us a clear, unambiguous answer to particular questions and that we apply appropriate statistical models that match the structure of the data that we collect. Helping biologists do this effectively is an important task, and I write and teach about these issues, including authoring two books.
I do research designed to have impact, to change government policy on various biosecurity measures, such as effective border quarantine and post-border surveillance measures, as well as policy responses to climate change.

My research specialises in biosecurity, large-scale computational modelling, climate change, and natural resource and environmental economics. I work on estimates of the potential economic damages from climate change across different temperature settings for over 120 different countries and over 50 commodity sectors, as well as emissions reductions pathways. I also do work on the economics of biosecurity for plant, animal and human health. This involves work on optimal post-border surveillance for the early and cost-effective detection of pests and diseases to protect agriculture and the environment.

Left: Along with ‘flattening the curve’ for COVID-19, there’s an urgent need to address potential damages from climate change.
Plants are an essential pillar for all life on earth. The shape and chemical composition of individual plant cells have significant implications for the food we consume and many of the everyday materials we use, as well as our health. Our research is focused on two areas. First, we are dissecting the pathways and mechanisms mediating plant cell wall biosynthesis. Second, we are applying our understanding of plant biology and development to better forecast the levels of airborne pollen in Victoria.

Melbourne Pollen Count

Every spring, Victorians in their thousands are affected by grass pollen allergies that trigger their hay fever and asthma, serious conditions that reduce quality of life by disrupting day-to-day activities such as work and school. Not surprisingly, spring is a bad season for asthmatics, because this difficulty with breathing caused by a narrowing of the airways in the lungs and hay fever are strongly associated conditions. People with hay fever are more likely to have asthma, and most asthmatics also have hay fever.

In Victoria, when the weather conditions are right these seasonal grass pollen allergies can turn into something far more serious: thunderstorm asthma. Thunderstorm asthma is a sudden increase in asthma in the community after a thunderstorm to the point where an epidemic takes place that places health services under extreme stress. We use innovative and cutting-edge interdisciplinary research, digital technologies and citizen science to deliver a valued service that helps Victorians better manage their allergies by counting and forecasting pollen levels around Victoria. We are also working towards identifying factors that contribute to epidemic thunderstorm asthma events.

Understanding how plant cell walls are made

Plant cells are surrounded by a polysaccharide-rich cell wall that has a similar role to an animal’s skeleton in determining the overall form, growth and development of the plant. The properties of the plant cell wall also have significant implications for the food we consume and many of the everyday materials we use including paper, textiles and wood. Yet despite the importance of the plant cell wall, relatively little is known about the functions of many of the polysaccharides it is composed of and the molecular components involved in its synthesis. In part this is because most studies have focused on higher-order plants such as *Arabidopsis thaliana* which have significant levels of genetic redundancy making it difficult to assign a function to a specific gene. To address this, we have been developing a simpler model plant system to study cell wall biosynthesis. The basal land plant *Marchantia polymorpha* is in one of the earliest diverging land plant lineages still alive today. Its genome contains little or no genetic redundancy making it ideal to study complex molecular and cellular processes. We use these two genetic model systems from opposite ends of the evolutionary spectrum of land plants — the flowering plant *Arabidopsis* and the liverwort *Marchantia* — to better understand how plants make their cell walls to further our knowledge of polysaccharide synthesis not only in plants, but all eukaryotes.
My mission is to cure the world of malaria and to save the Great Barrier Reef.

Our group is interested in malaria and symbiosis, two topics that seem somewhat far apart but are in fact strangely interconnected. Our research has led to a paradigm shift in understanding the malaria parasite. We had a central role in discovering that the malaria parasite is a kind of microscopic plant. We found the remnants of a plant-like chloroplast in the parasite, which is now providing novel ways to tackle this serious disease and revealed that the large group of parasites to which malaria belongs arose from symbiotic algae that converted to parasitism probably as much as 500 million years ago.

Healthy and malaria infected red blood cells.

Coral symbionts like these dinoflagellates feed their animal host and are essential for survival. Coral bleaching due to warming is caused by loss of the symbionts, which eventually leads to dead coral.
I am passionate about understanding our natural world, in particular how animals interact with their environment and with other species. Knowing our world and having a deep understanding of how and why it is the way it is can help us connect better to our surroundings and ultimately promote the importance of protecting our wildlife and ecosystems.

My research interests combine the worlds of behavioural ecology and macroevolution. I am curious about the evolution of animal behaviours and the adaptations that these have to their habitat. Why have these strategies evolved? How do they affect the evolutionary destiny of the species? For most of my research, I combine work in the field, laboratory or museum with broad-scale comparative analyses. This integrative approach allows us to understand in-depth the evolutionary drivers of the diversity of forms and colours we see in nature.

The two main research areas in my group are the ecology and evolution of bird nests and the evolution of colours in animals, mainly birds and insects. By looking at the evolutionary history of traits like nests or colour we can understand the diversity in our world. Nests are fundamental for the reproduction of birds and they can vary significantly from species to species, adapting to the particular lifestyle of each species. We explore which environmental pressures have driven the evolution of particular nest features, such as the size or shape of the nest.

Colour is used by animals for defence, mate attraction and to control their temperature. As such, it is a critical trait for survival. In my group we also use museum collections and information from the field and laboratory to reveal why the incredible colours we observe in nature have evolved.

The Cotton Harlequin Bug (Tectocoris diophthalmus) is an Australian insect that presents warning colourations to advertise its repellent odour to potential predators. It is one of our research model systems.

Grey fantail (Rhipidura albiscada) sitting on its nest.
I am a quantitative ecologist working in marine and freshwater systems, investigating how animals respond to environmental change on contemporary and evolutionary time scales. I am keenly interested in the impacts of, and adaptations to, fishery activity, natural and human-induced flow variability, and environmental change. I ask questions at different levels of biological organisation, ranging from individuals to assemblages, using field-based and experimental techniques.

Climate change and fishing impacts in aquatic environments

My research primarily focuses on understanding the evolutionary causes of within-species phenotypic diversity and its ecological consequences in individual fitness, species persistence and assemblage composition. Understanding these fundamentals allows me to explore more applied questions.

An important part of my work has focussed on quantifying the impacts of climate change on fishes and predicting likely impacts of this on fishery productivity. I have used otolith-based data to recreate global-scale oceanographic dynamics, and I am currently investigating the role of fishery activity in inducing trait selectivity and density-dependent processes (additive and synergistic effects of fishing and warming).

Statistical modelling

I have developed novel models to analyse individual-level thermal reaction norms and species-wide thermal responses in fish, and the environmental drivers of life-history trait variation, in particular growth, recruitment and movement. I use sophisticated analytical techniques to provide inference at different levels of biological organisation (often concurrently), ranging from within individual variation to among-population, regional and species-wide trends. My research is often directly implemented by end users.
My dual aims are to improve our understanding of the natural world and take an evidence-based approach to understanding what makes for impactful learning in the University.

I am fascinated by the causes and consequences of variability in mating systems, particularly the relative importance of sexual and natural selection, the role of visual and acoustic signals and the way in which cooperation and conflict interact in complex social groups. Much of my work combines field studies of behaviour with the use of molecular markers to assign parentage, to better understand the fitness outcomes of different individual strategies.

Why birds?

They exhibit remarkable variation in their life histories, their reproductive success is neatly contained in a nest and they can be readily marked for individual identification. And of course, they are endlessly engaging and surprising in their natural history and behaviour.
I use the biomedical model organism, the fruit fly Drosophila melanogaster, to discover and understand the role of genes that control the behaviour of epithelial cells. These genes typically play conserved roles in humans, and so the lessons learned in flies can provide crucial understanding of their role in human embryonic development, cancer and wound-healing.

Netrins and wound healing

Netrins are versatile proteins best known as secreted axonal chemoattractants, but more recently shown to be potent regulators of epithelial plasticity during development, cancer and wound healing. We have found that Netrins can stimulate epithelial cells to undergo a transition to a mesenchymal, migratory state (undergo EMT), but also can polarise migrating cells to help them reform epithelia. Recently we’ve also found that Netrin expression is rapidly upregulated at the edge of epithelial wounds in humans, zebrafish and flies, and is required for fly thorax closure, a developmental model for wound healing. We are currently exploring the signalling pathways that activate Netrin expression in response to epithelial damage and those that act downstream to effect Netrin-dependent closure.

Epithelial homeostasis in the adult midgut

Maintenance of an adult gut involves the constant replacement of cells that die or are damaged. New cells are provided by intestinal stem cells, which divide to produce progenitor cells called enteroblasts. We are studying how enteroblasts detect and respond to damage and subsequently differentiate into the absorptive enterocytes that line the gut. Our focus is on the morphogenetic mechanisms by which enteroblasts maintain their spatial distribution, how they collaborate to seal wounds and how they incorporate into the epithelium.
Approximately four per cent of young Australian men are infertile. For the majority, no cause can be identified. Similarly, numerous epidemiological studies have revealed that infertile men have a higher morbidity and die younger than their fertile counterparts. The reasons for this burden are unknown. Within the Male Infertility and Germ Cell Biology lab, we aim to define how sperm are produced, the causes of infertility and the implications of infertility for health more broadly. Insights obtained from this research will inform human and animal health, evolutionary processes, contraceptive development and cell biology.

**Male infertility and germ cell biology**

My research group aims to identify key mechanisms required for male germ cell development, the aetiology of human male infertility and the interplay between fertility and health. This is achieved using a range of genomic, biochemical and cell biological methods, including the development of unique model systems and state-of-the-art imaging methods.

**Building a functional sperm**

Sperm are a triumph of design. While their development is complex, the final sperm cell is elegant in its simplicity. The shape of the sperm is dictated by a range of cytoskeletal elements and their regulatory pathways and is a key determinant of function and ultimately evolutionary processes. Within our lab, we aim to identify these processes and ultimately harness this knowledge to identify causes of infertility, contraceptive targets and to understand fundamental mechanisms of cell biology more broadly.

**The genetic causes of human male infertility**

In partnership with the ‘International Male Infertility Genomics Consortium’ we are identifying genetic mutations that lead to human male infertility. In order to validate causality, we are modelling these genetic variants in animal models. In doing so, we are providing diagnostic certainty and identifying novel pathways required for fertility.

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**Moira O’Bryan**

Male infertility
Germ cell biology

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Australia has one of the world’s worst track records in mammalian extinctions. We are working to develop much needed genetic and assisted reproductive technologies to help save our threatened and endangered wildlife and maybe even think about bringing them back after extinction. Human fertility is also dropping at an alarming rate, with an unprecedented increase in reproductive disorders attributed to exposure to chemicals in the environment that interfere with our natural hormones. My lab examines how these chemicals impact our development and cause both short and long-term impacts on our reproductive health.

I head the Evo-Devo-Repro group. My research uses comparative mammalian genetics to identify critical and conserved genes driving development, particularly of the craniofacial region and reproductive tract. My work in reproduction has uncovered novel roles for estrogen in male development and helped define the impacts of environmental contaminants on male reproductive health.

My comparative genetics work has led to the sequencing of several marsupial genomes, including that of the extinct Tasmanian Tiger. I use genome-wide, cross-species comparisons to define regions of the genome targeted by evolution to drive diversity and adaptation.
The goals of my research are to improve the sustainability of pest insect control strategies through a greater understanding of the biology of insect pests and how insecticides work on them. Knowledge from studies on how insecticides work can help guide their appropriate use and allow the prediction of resistance mechanisms that might arise, informing resistance monitoring and management strategies. I am also looking at alternative pest control strategies, including area-wide population suppression and novel therapeutics such as vaccines which will help meet the growing desire of both producers and consumers to reduce the reliance on the use of chemical insecticides in agricultural systems.

Population genetics and parasitic biology of *Lucilia cuprina* (Australian Sheep Blowfly)

Blowflies can be a significant problem for Australian sheep meat and wool producers. They are ectoparasites that target live sheep, laying their eggs on the wool which after hatching then proceed to feed on the sheep. In addition to the impact of blowflies on sheep health and welfare, the prevention and damage to production from flystrike cost the industry 100s of millions of dollars annually.

We are using genomics, particularly looking at the way the DNA varies in blowfly populations across the country, to understand the population structure. This can then be used to understand how resistance to insecticides that control them might spread, and also to help assess whether alternative area-wide control strategies could be successful. Other aspects of the research examine the early parasitic stages of the blowfly to identify potential proteins that are critical for their survival and that could be targeted with novel therapeutics such as a vaccine to help protect sheep from flystrike.

Characterising how insecticides work and ways insects can become resistant to them

Insecticides are classified by their mode of action, or how they work, on a target protein in an insect. Improving our understanding of the target can allow us to better predict the potential of a pest to develop resistance to the insecticide and allow diagnostic tests to monitor field pest insect populations to be developed. There are also significant concerns about the impact of insecticides on non-targeted insects, and we are looking at how insecticides could also affect insect behaviours such as sleep patterns, courtship and mating as well as other aspects of insect fitness such as development, fertility and even movement. We are doing this by both studying impacts of exposure to high and low doses of insecticide, and also by studying the importance of the insecticide-targeted protein for a wide variety of fitness and behavioural measures. As many insecticide targets are receptors found the brains of insects, we are also using available methods including gene-editing techniques, confocal microscopy and proteomics to study areas of receptor biology, including how they are assembled correctly and traffic to the membrane, what interactions they have with other proteins and how mutations that lead to resistance can impact the function of the receptor.
I work towards a better future for my children’s generation.

I try to bring evolutionary perspectives into applied problems across conservation, agriculture, and health. There are real wins to be had, and creative new management possibilities if we take an evolutionary perspective. I have a background in ecology and evolution and have strengths in data analysis and modelling.

I have worked on a wide range of systems and have made important contributions in two main areas:

1. Evolution on invasion fronts
2. Rapid evolution in conservation.

My work on invasion fronts showed that the process of invasion selects for high rates of dispersal and population growth. As a consequence, evolution causes invasions to accelerate. These evolutionary forces are near-universal, applying to all sorts of invasions, from pathogens to cane toads to tumours. In the process, I unearthed a new evolutionary process — spatial sorting — that is a spatial analogue to natural selection; natural selection operating through space rather than time.

My work on evolution in conservation showed that threatening processes (eg climate change, invasive species, habitat destruction) typically impose selection on impacted populations. Resultantly, these populations will often adapt in response to threats. Seen this way, one of the primary challenges of conservation is to help populations to adapt to a changing world. This perspective brings a suite of creative new management ideas to the table; ideas that, because they aid adaptation, can be very efficient and cost-effective.

Understanding the evolutionary forces on invasive cane toads can help us to plan and implement more effective control strategies.
Globally, pollution is widespread and a substantial problem that compromises human and environmental health as well as the ecosystem services we rely on for clean air and water, agriculture and recreation. While we have achieved substantial global economic growth over the past few decades it has often been associated with large amounts of pollution. In Australia, it is estimated we have over 160,000 contaminated sites containing about 75,000 different chemicals and with clean-up costs of approximately $160 billion. Our pollution problem is substantial and we need safe, effective and evidence-based approaches to assess and sustainably manage it.

**Effects of contaminants in the terrestrial environment**

My research group aims to reduce the risk of contaminated land to humans and the environment, focusing on the effects of contaminants in the terrestrial environment such as in soil, plants, invertebrates and human health. We use ecotoxicology and soil chemistry principles to solve knowledge gaps in the environmental risk assessment and remediation of contaminated land. My research group covers traditional pollutants (eg metals and hydrocarbons) as well as emerging chemicals such as per and poly-fluoroalkyl substances (PFAS) and microplastics. Currently, we have a focus on urban pollution and Antarctica.

The outcomes from my research group have been incorporated into government guidance and policy used by industry to make more accurate risk assessments of contaminated land and by the community to garden more safely.

Some of my areas of research include:

- Environmental risk assessment relating to potentially contaminated land
- Ecotoxicological testing of plants and invertebrates (eg earthworms, springtails, tardigrades, rotifers and nematodes)
- Bioavailability processes in soil systems
- Heavy metal and trace element biogeochemistry
- Phytoremediation and phytomining; biosolids and land application of wastes; mining remediation.

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**Associate Professor Suzie Reichman**

Pollution  
Ecotoxicology  
Soil chemistry  
Environmental risk assessment

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Australia has led the way in the field of reproduction for decades, initially from the breeding of sheep and cattle and more recently with its exceptional IVF and assisted reproduction techniques. However, while we have the highest extinction rates of our wildlife in any developed country, few resources have gone into understanding how reproduction is controlled and the disastrous effects that environmental toxins and land clearing have had. Additionally, because they are mammals, understanding their reproduction has led to some aspects being translated into human medicine. We have an amazing resource in this country, yet relatively few study these unique and iconic animals.

Our research focuses on understanding reproduction and development in mammals (including humans), primarily using marsupials as biomedical models. Australian mammals are especially interesting and provide a unique opportunity for the study of the development of the embryo, foetus and young because they are born after a very short pregnancy and do most of their development after birth, usually in the pouch supported by a long and sophisticated lactation.

Our studies are wide-ranging and cover a number of related but distinct topics. Our team investigates sex determination, sexual differentiation, epigenetics and genomic imprinting, the molecular and hormonal regulation of testis, ovary and phallus development (including sex reversal and hypospadias), as well as the effects of environmental toxins (environmental endocrine disruptors) on reproduction, the control of embryonic diapause and gene expression during early embryonic development and placentation, post-natal growth and lactation. We also research reproduction and development of monotremes in collaboration with the University of Queensland and Currumbin Wildlife Sanctuary. We have been involved in the genomes of several Australian mammals, namely the tammar wallaby, koala, platypus and echidna. Our work is supported by the National Health and Medical Research Council, the Australian Research Council and ARC Linkage grants.

The newborn tammar wallaby pouch young. It weighs only 400mg and will stay in the pouch for 9-10 months to complete its development.

Tammar wallaby with young.
My research is motivated by two general questions:

1. What is the genetic basis of the adaptation that shapes the wonderous biodiversity observed on planet earth?

2. How can we control pest insects without damaging that biodiversity?

More specifically, my lab group focuses on the microevolutionary processes of adaptation, the molecular evolution of gene families, especially those involved with detoxification processes in insects, and genetic methods of pest control such as RNAi and gene drives. The approaches we take are typically genetic (linkage mapping, association studies, transgenic manipulations, and allele frequency change in lab populations) and are explicitly couched in an evolutionary context where we often examine within and between species variation in genomic datasets to identify the genetic targets of natural selection. The lab also deploys population simulation analyses (eg for gene drive modelling), has contributed to some theory (eg to account for recombination among paralogs in gene family evolution) and has an interest in the history of invertebrate taxonomy.

Much of our research has focussed on the model insect Drosophila melanogaster but we have also focussed on major insect pests of agriculture, such as the cotton bollworm Helicoverpa armigera and the green peach aphid, Myzus persicae.
Biosecurity is a critically important function of national government but also a shared responsibility with state governments, industry, other stakeholders and every citizen. CEBRA strives to support the national regulators in managing biosecurity risk by identifying or developing new tools and ways of thinking. Since its inception as ACERA in 2006 the Centre has worked closely with DAWE (and MPI, since 2013) to help traverse the maturation as science-based regulators.

**Biosecurity risk management**

Biosecurity is the suite of activities undertaken by national and state regulators and other stakeholders to protect Australia’s environment, agriculture, economy, health and social and cultural amenity from invasive pests and diseases — in short, to protect our way of life! Biosecurity risk management demands a delicate balance between enabling travel and trade and all the benefits that these activities bring and protecting the values that we hold dear. Science to support biosecurity risk management calls on a wide range of skills, including statistics, applied mathematics, economics, biology, ecology, sociology and so on.

With our primary stakeholders, namely Australia’s Department of Agriculture, Water and the Environment and New Zealand’s Ministry for Primary Industries, CEBRA works across these areas to co-develop and deliver problem-centred research projects. Our primary motivation is to help our stakeholders deliver more efficient, robust, science-based biosecurity outcomes. These projects range from estimating the market and non-market value of the biosecurity system to Australia (it’s more than $300 billion across a 50-year timespan) or the utility of bulk milk testing for diseases (Yes if there’s already an outbreak! No if there isn’t!) to developing risk-based inspection schemes that reward compliance and can change stakeholder behaviour, and efficient surveillance systems for invasive pests.

An example of a container ship in Port Philip Bay piled high with sea containers. Sea containers are a known pathway for invasive pests and pathogens.

A biosecurity greenhouse. These plants are being grown out to see if they are infected by pathogens. This check can take years.
My mission is to develop knowledge that can be applied to solve or help mitigate against some of the world’s largest disease problems for aquaculture, thereby improving the sustainability of worldwide aquaculture.

Fish and shellfish are healthy sources of protein and nutrients, and aquaculture production is growing around the world. But there are many challenges faced by these industries. Access to reliable, fast growing, disease resistant and stress resilient seedstock is needed to ensure ongoing sustainability. My research concerns the application of genomics to the genetic improvement of fish and shellfish in aquaculture.

White spot syndrome virus disease

White spot syndrome virus (WSSV) is a contagious and lethal disease that causes billions of dollars of losses globally. It can decimate whole prawn farms within a few days of infection and preventative measures have proven ineffective. Our research demonstrated that genomic selection could be used to achieve more than 10% improved resistance within one generation of selection and that there is high potential for future genetic improvement using this technology.

Sea lice infestations affecting Atlantic salmon

Sea lice are a major pest species affecting fish welfare in many countries. Current preventative measures and treatments are not completely effective. We know that Atlantic salmon vary in their ability to resist infection by lice and that some species of salmon are particularly resistant to lice. I am leading two research projects working closely with industry and a team of overseas collaborators to better understand the genes involved in conferring resistance to sea lice and developing strategies for creating a more resistant strain of Atlantic salmon. These projects are using the latest transcriptomics, CRISPR-Cas9 (molecular scissor) and gene-mapping technologies.

Barramundi seedstock

Barramundi is an iconic tasty fish species growing in popularity around the world. I have been working with the main supplier of seedstock to barramundi farmers to implement genomic selection for creating an elite strain of fast-growing resilient stock.
The vivid colours of the natural world are one of the most striking and beautiful aspects of life’s diversity. Our team studies the biology of light and colour. How are these colours produced and perceived in different animal groups, and what is their biological function? We tackle questions at different scales of biological organisation – from optical properties at the nanometre scale to global patterns of colour diversity.

**Biological optics and visual ecology**

We study the mechanisms that produce vivid colours and diverse optical effects, such as iridescence, metallic appearance and highly reflective surfaces. The biological function of these complex optical effects depends on how they are perceived, so we also study visual perception using a combination of visual physiology, behavioural experiments and computational modelling.

**Near-infrared properties and thermal control in animals**

More than half of the energy in direct sunlight falls within near-infrared (NIR) wavelengths, beyond the limit of human and animal vision. Absorption of solar radiation in these wavelengths significantly affects heat gain, yet almost nothing is known of the diversity and mechanisms of near-infrared properties in animals, let alone their adaptive value. We are investigating the relationship between climate and reflectance of both visible and near-infrared light in a range of taxa, from reptiles and birds to butterflies and beetles.

**Bio-informed technologies and design**

Structural colorants are used in a vast array of manufactured goods, from banknotes to plastics and paint, but are produced unsustainably from non-biodegradable materials. Nature produces the most vivid structural colours of all using just a few abundant, biodegradable materials. Natural materials have simultaneously been fine-tuned for other essential properties such as wear resistance, water-repellence and thermal control. We are collaborating with scientists in several other discipline areas to design better, multi-functional and more sustainable coloured materials informed by biology.
My research is focused on developing better predictive and mechanistic models of biological systems. My work is characterised by methodological breadth and development of state-of-the-art statistical and reverse engineering methods that allow biological and biomedical scientists to develop mechanistic models of biological systems. Mechanistic models capture our knowledge, and unlike statistical or machine learning models which can strictly only interpolate available data, they also allow for extrapolation thereby testing our knowledge.

Developing such mechanistic models described by systems of ordinary differential equations, stochastic differential equations, (stochastic) partial differential equations, Markov Jump processes or hybrids thereof is computationally and conceptually demanding. To meet these challenges my group and I have been developing:

1. Stochastic simulation approaches and computationally efficient approximations
2. Statistical and reverse-engineering approaches to learn the structure of models that describe cellular function from data and determine kinetic parameters of such models
3. Model selection approaches that explore potentially large model spaces in order to identify sets of models support by available data and background information
4. Multi-scale modelling methods which allow us to investigate processes ranging from molecular interactions inside cells to processes underlying tissue formation, and
5. Statistical approaches for the analysis of in vivo live cell and tissue imaging data.

I have been applying these methods in a range of systems and synthetic biology applications, including:

1. Inference and analysis of biological networks, such as protein-protein interaction networks, gene regulation networks and metabolic networks and processes
2. Model development and analysis of signal transduction processes and their effects on cell physiology in bacteria as well as in eukaryotic systems (especially mammalian cell lines, but also yeast)
3. Multi-scale modelling of immunological and developmental processes in the fruit fly Drosophila melanogaster and zebrafish Danio rerio as well as murine and human stem cell systems, and
There is an emerging global crisis arising from the increasing concentration of economic and population centres in coastal areas leading to rapidly increasing environmental change and risk. Solutions to the environmental impacts resulting from climate change, habitat loss, pollution, resource extraction and invasive species in marine and coastal ecosystems require solutions-focused science that co-produces knowledge, technologies and practices. This must be done in conjunction with relevant stakeholders to inspire and enable local communities, industry and government to act in ways that support their values and sustainable development goals.

**Nature-based solutions to climate change**

We undertake research into the ecological and socio-economic effectiveness of harnessing nature to combat the causes and impacts of climate change in the coastal zone.

**Maximising the biodiversity benefits of habitat restoration**

We identify the behavioural responses and fitness consequences of habitat restoration projects to improve outcomes for wildlife.

**Improving marine conservation planning and fisheries management**

We combine empirical field studies, biophysical modelling and analytical chemistry to investigate what causes the large fluctuations in replenishment of marine fish stocks.
The overuse of chemicals in agriculture leads to ecosystem degradation, threatens the resilience of our food systems and contributes to the evolution of insecticide resistance in many invasive insect pests. Our mission is to develop sustainable agricultural pest management practices for healthier ecosystems and improved food security.

Our research aims to improve the health and resilience of anthropomorphised and natural ecosystems. In particular, our work supports Australian farmers in managing their production systems, with a view to achieving long-term sustainability and environmentally beneficial outcomes.

**Novel pest management**

Each year insect pests lead to billions of dollars in lost productivity in Australian agricultural industries. Our work is exploring novel approaches to utilise endosymbionts (bacteria, associated with insects, living in host cells) for the management of plant pests. This includes exploring ways to block plant virus transmission, influence host plant utilisation and increase the impact of beneficial organisms in farming systems.

**Resistance modelling and management**

For the first time, we are working to create a national insecticide resistance prediction and diagnostic capacity for the Australian grains industry, which could be extended to other agricultural industries. We are applying risk analysis to determine key resistance risks, including the identification of new threats of resistances entering Australia. Molecular markers underpinning chemical resistance are also being explored in order to support farmers to proactively manage insecticide resistance.

**Beneficial insects**

Chemicals remain the predominant means by which to manage insect pests attacking Australian food crops. But what happens to all the beneficial insects that get sprayed too? Despite being an important part of Integrated Pest Management (IPM), beneficial insects are mostly killed through the routine application of insecticides. Our research aims to build greater capacity for the stewardship of beneficial species and reduce Australia’s reliance on insecticides to control plant pests.
Plants and algae provide the food, clean air and environmental quality on which we depend. Our overarching goal is to improve crop quality and better understand adaptations to environmental change through research that investigates the cell biology processes by which plants and algae form and modify their cell walls, traffic cargo throughout the cell and subsequently adapt to the environment.

Cell biology of plants and algae

My research seeks to identify the processes by which the cell walls of plants and algae are developed, maintained and changed throughout the life cycle and during interactions with the environment. My lab uses state-of-the-art microscopy techniques, including live cell imaging and electron microscopy, to localise sub-cellular components and relevant molecules and structures to understand structure-function relationships. This work is complemented by molecular-genetic, biochemical and biophysical techniques.

Advanced microscopy and imaging

Advanced microscopy techniques and imaging are remarkable tools to understand processes and functions at the cellular level. Utilising imaging techniques ranging from optical to electron microscopy and associated analytical technologies, this research develops insights into the microscale adaptations that occur during the life cycle of organisms and also during adaptations to the environment. My research also contributes to the development of cutting-edge techniques for investigating biological processes at the micro to nanoscale.
Our research focus is to develop sustainable strategies for growers to minimise the impact of crop diseases. Few agricultural diseases can be eradicated, and many are constantly evolving; our research is aimed at staying ahead of blackleg disease to give growers the best yields possible.

Minimising the impact of fungal diseases in agricultural crops

My research focuses on blackleg disease, the most devastating disease of canola worldwide. With industry partners, I use a ‘genome to paddock’ approach to development management strategies for growers to help minimise the impact of this disease. Specifically, this research has led to the development of:

- Molecular and glasshouse tools to characterise the resistance genes in all Australian canola cultivars
- A novel disease management strategy for canola growers — viz. rotation of cultivars with different sources of resistance over time
- Assays that monitor levels of disease in canola paddocks with the findings communicated to farmers who then implement appropriate disease control strategies
- The biannual Blackleg Management Guide (in collaboration with industry leaders) which farmers use to select cultivars to sow each year, and
- Assays to show that blackleg fungal isolates are becoming resistant to fungicides with increased fungicide usage.

Example of the new upper canopy infection symptoms caused by blackleg. Infection of the flowers results in direct yield loss as no pods, and therefore seed, are produced from these infected flowers.
Good intelligence analysis is critical for national security but is difficult, and errors or gaps are inevitable. My goal is to help improve the quality and efficiency of analysis by harnessing academic knowledge and expertise and working in close collaboration with the intelligence community.

My research is focused on how to improve intelligence analysis and analytical or critical thinking more broadly. It is a sub-field of applied epistemology (the study of knowledge). My research group, the Hunt Lab for Intelligence Research, is involved in a variety of projects covering topics like the nature of analytic rigour, how to improve critical thinking in intelligence analysis and how to obtain high-quality analytic reasoning through teamwork or crowdsourcing. Much of our work makes use of the SWARM platform for collaborative analysis, developed with major funding from the US Intelligence Advanced Research Projects Activity. Recent or current projects include delivering the first major report on analytic rigour in intelligence; studying how training in structured argumentation impacts the quality of reports and decision making in large organisations; and studying ways of measuring the quality of reasoning in intelligence reports. We have a particular interest in the potential for generating high-quality open-source intelligence from crowds of citizens, a capability we call the ‘Hunt Arena.’
Can endosymbionts alter climate change resilience in insects?

Heritable endosymbionts — microscopic bacteria living exclusively within host cells — are widespread in insects. A handful of studies indicate that endosymbionts may influence the thermal tolerance of their host, yet whether they alter the upper thermal limits, adaptive potential and climate change risk of insects is unknown. We are currently investigating whether endosymbionts alter climate change vulnerability, and exploring the potential for endosymbionts to be used as a tool to modify climate change resilience in insects.

Male fertility and climate change

Estimates of climate change vulnerability typically use the temperature at which adults stop moving or die (known as critical thermal limits) to forecast climate change risk across species from different habitats. However, my research suggests that male fertility may be more sensitive to warming than critical thermal limits, and is therefore a better predictor of climate change vulnerability. Sadly, many species are already experiencing temperatures precariously close to their upper fertility limits. I am currently interested in further exploring plastic and evolutionary genetic responses in male upper thermal fertility limits.
To enhance coral thermal bleaching tolerance via bioengineering approaches and assist corals in surviving this century while climate warming is brought under control (ie to ‘buy time’ for coral reefs).

Assisted evolution to enhance coral climate resilience

Climate change causes an increase in the frequency, intensity and duration of summer heatwaves which are the main drivers of the rapid decline of coral reefs worldwide. Sustained periods of elevated temperatures cause the loss of microalgal endosymbionts from coral host tissues (coral bleaching), resulting in coral starvation and ultimately death. Climate models predict most reefs in the world will experience summer heatwaves and associated mass coral bleaching every summer before the end of this century. Many researchers and reef managers therefore argue that in addition to strong action to reduce the emission of greenhouse gases, active reef restoration is required to ensure coral reef persistence into the future. My team is using bioengineering methods to enhance thermal bleaching tolerance of corals aimed at producing tolerant coral stock for reef restoration. We use a range of approaches, including the experimental evolution of microalgal endosymbionts outside the host followed by reintroduction of heat-evolved strains into hosts, the development of bacterial probiotics, coral hybridisation and preconditioning.

Deciphering the roles of coral-associated microbes

Corals associate with a wide diversity of microbes, including photosynthetic dinoflagellates, fungi, bacteria, archaea and viruses, many of which are critical for coral health and survival. While we have a reasonable understanding of the identity of some of these microbial organisms, their functions within the coral holobiont are poorly understood. My team applies a diversity of methods ranging from metabarcoding, proteomics, metagenomics, metatranscriptomics and metabolomics to advanced visualisation, phenotyping and experimental manipulation to decipher the roles of coral-associated microbes.
We advance the knowledge in our field of research on a daily basis by doing solid basic research and training undergraduate and postgraduate students. In doing so, the basic science we do can contribute to applications in the seaweed industry, the algal-based biotechnology sector and coral reef conservation. Students gain a thorough understanding of the scientific process and highly desired skillsets in bioinformatics and other fields of biology.

Algal evolution and biodiversity

Eukaryotic algae have a rich evolutionary history. Originating more than a billion years ago through a series of primary and secondary endosymbiosis events, they have diversified in almost all imaginable directions. We reconstruct phylogenetic trees of different algal groups and use those trees to study their diversification and evolution, focusing on a range of topics, including speciation, evolution of traits through geological time, the emergence of important cellular and physiological innovations and plastid endosymbiosis events.

We also conduct taxonomic research asking how molecular and morphometric data can complement one another in algal species delimitation. Morphological species delimitation tends to be problematic, and some algal species boundaries are blurry. We combine morphological and DNA data to accurately pinpoint these boundaries.

Algal biology and genomics

We are interested in how our favourite algae function in their environment, and we work on their physiology and genome biology to understand this better. One species we focus on is Ostreobium, a genus of green algae endolithic (rock-dwelling) in calcium carbonate substrates. Because it lives in a rock, it shows a range of adaptations to the low-light conditions it experiences there. Much of our genome sequencing work is focused on green algae, with the recently completed nuclear genome of Ostreobium and several studies on the structure and evolutionary dynamics of organelle genomes.

We are also interested in how algae associate with bacteria: while it is well known that algae rely on bacteria for certain vitamins and other compounds and that some bacteria deter grazers, there is much more to learn about these interactions.

Coral holobiont biology

Coral reefs are spectacular ecosystems held together by the calcium carbonate skeletons secreted by corals. The functions of the microbiota residing in the skeleton are barely understood, but it is clear that drastic changes happen in the skeletal microbiome during bleaching. Our research aims to develop better insight into this understudied skeletal side of the coral holobiont.
Our mission is to discover and engineer how the root systems of plants grow and function, to sustain healthy life on Earth and in future in space — because plant roots are the foundation of plants, and plants are the foundation of humanity.

My group discovers how the root systems of plants, including their microbiomes, grow and function in natural and agricultural environments. We want to improve root water use and carbon functions for food and environmental societal challenges. Roots are the ‘hidden half’ of plant science because they are below ground and out of sight of the human eye.

My group works with national and international collaborators and the University of Melbourne Imaging Centre to use advanced imaging technologies for our discoveries of roots. These include real-time live imaging, miniature ecosystems that fit under a microscope and 4D visualisation of roots in soil using computed tomography. We study root systems of diverse plants, from plants native to the Australian deserts to advanced breeding lines to plants for space habitation. The outputs of our research are new knowledge that we publish and root system designs for new plant types and growing environments that save water, land and energy.