

**RESEARCH AND CAREER
DEVELOPMENT WORKSHOP**

20-22 NOVEMBER 2019, UNIVERSITY OF SYDNEY
A THEO MURPHY INITIATIVE

Genomes and biodiversity



Program

We acknowledge and pay respect to the traditional owners of the land on which we meet (the Gadigal people of the Eora Nation). It is upon their ancestral lands that the University of Sydney is built.

As we share our own knowledge, teaching, learning and research practices within this university, may we also pay respect to the knowledge embedded forever within the Aboriginal Custodianship of Country.

The Australian Academy of Science events support and promote diversity, participation and intellectual freedom and excellence. As a condition of participating in this event all delegates, speakers and committee members must abide by the Australian Academy of Science Participants Conduct Policy:

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Information

Overview

The Genomes and Biodiversity: Research and Career Development Workshop is a three-day event for early- and mid-career researchers (EMCRs) and PhD students in the life sciences. The workshop will create a space for EMCRs and research leaders from a range of disciplines to meet and share their latest research.

Location

The workshop will be held at the University of Sydney.

Activities for Day 1 will begin in the Charles Perkins Centre and will end with a networking function at the Courtyard Café. Days 2 and 3 will take place in the Administration Building. Please refer to the map at the end of this booklet for the locations of the different workshop sessions.

Public transport

Opal cards can be used for all forms of public transport in Sydney: buses, ferries, light rail and trains (including to and from the airport). Opal cards can be purchased and topped up at railway stations and ferry wharves. If you are travelling to Sydney for the workshop, we recommend purchasing an Opal card upon arrival (at the airport station).

Food and drink

The workshop will be fully catered. Tea and coffee will be available from 30 minutes prior to the start of each day of the workshop. Attendees will be served morning tea, lunch and afternoon tea on each day. The exception is on Day 1, when afternoon tea will be replaced by canapés and drinks at the Courtyard Café

networking function. Some recommendations for nearby food and drink venues are provided in the map at the end of this booklet.

Wi-Fi access

Free, high-speed Wi-Fi access will be available at the University of Sydney throughout the workshop. Attendees from within the university can log in using their UniKey account. External attendees can log in through eduroam or by using the university's guest network with the following log-in details (valid only for the duration of the event):

Username: gab2019

Password: 48825189

Organising committee

Dr David Duchene
Australian National University

Dr Jemma Geoghegan
Macquarie University

Professor Simon Ho
University of Sydney

Dr Xia Hua
Australian National University

Dr Jackie Mahar
University of Sydney

Dr Jacqueline Nguyen
Australian Museum

Dr Dan Rosauer
Australian National University

Dr Mang Shi
University of Sydney

Ms Cara Van Der Wal
University of Sydney
and Australian Museum

Program

Day 1: Wednesday 20 November

Lecture Theatre, Charles Perkins Centre,
University of Sydney

9.00 am	Registration
9.30 am	Welcome from the Academy Professor Steve Simpson AC FAA FRS, University of Sydney
	Welcome to Country Uncle Chicka Madden, Gadigal Elder
10.00 am	Keynote presentation: Metagenomics, evolution and virus emergence Professor Edward Holmes FAA FRS, University of Sydney
10.30 am	MORNING TEA
11.00 am	Tree Lab: portable genomics for early detection of plant viruses and pests in Sub-Saharan Africa Dr Laura Boykin, University of Western Australia
11.30 am	Ancient genomes shed light on the evolutionary history of sled dogs Associate Professor Shyam Gopalakrishnan, University of Copenhagen
12.00 pm	Reading the story of the genomes: why more data is not enough Professor Lindell Bromham, Australian National University
12.30 pm	LUNCH
1.30 pm	Integrating fossil flowers in angiosperm macroevolutionary analyses Dr Hervé Sauquet, Royal Botanic Garden Sydney
2.00 pm	PRESENTATIONS BY ATTENDEES
	Agriculture, industry and conservation
2.00 pm	Investigating the transcriptomic response of chickpea roots to infection by the oomycete pathogen <i>Phytophthora medicaginis</i> Mr Donovin Coles, Western Sydney University
2.10 pm	A marsupial puzzle using phylogenetics, biogeography and conservation Dr Margarita Medina, University of Canberra
2.20 pm	Back to the future with genetics: the role of genetics in forest conservation Dr Peter Harrison, University of Tasmania

Ecology, evolution and genetics

2.30 pm **Approaching previously intractable acalyprate fly phylogeny with transcriptome-based phylogenomics**
Dr Keith Bayless,
Australian National Insect Collection, CSIRO

2.40 pm **Ancient DNA and Near Oceania: evaluating genetic methods in the study of zooarchaeological remains across Papua New Guinea**
Ms Sindy Luu,
University of Otago

2.50 pm **Hackflex: low-cost Illumina sequencing library construction for large-scale sequencing**
Dr Kay Anantanawat,
University of Technology Sydney

Microbes, pathogens and health

3.00 pm **Comparative genomics of *E. coli* isolated from adult and paediatric patients with inflammatory bowel disease and controls**
Mrs Mukta Das Gupta,
Australian National University

3.10 pm **Hunting the parasites of our parasites: a 'deliberate' exploration of viruses infecting human malaria protozoan parasites using meta-transcriptomic approaches**
Dr Justine Charon,
University of Sydney

3.20 pm **Transmission at the human-wildlife interface: hospital patients share bacterial pathogens but not resistance genes with local silver gulls**
Dr Bethany Hoye,
University of Wollongong

3.30 pm **Highlights from genetic studies of the Greenlandic population**
Dr Ida Moltke,
University of Copenhagen

4.00 pm **END OF DAY 1**

4.15–6.30 pm **Networking function**

Day 2: Thursday 21 November

Auditoriums 1 and 2, Administration Building (F23),
University of Sydney

8.30 am	WELCOME TEA AND COFFEE
9.00 am	Workshop 1: Workflows for big data Dr Angela McGaughran, Australian National University
10.30 am	MORNING TEA
11.00 am	Workshop 2: Models in genomics and biodiversity analysis Dr Xia Hua, Australian National University
12.30 pm	LUNCH
1.30 pm	Workshop 3a: Spatial analysis of biodiversity Dr Dan Rosauer, Australian National University

	Workshop 3b: Phylogenomics Dr David Duchêne, Australian National University Professor Simon Ho, University of Sydney
3.00 pm	AFTERNOON TEA
3.30 pm	Workshop 4a: Metagenomics and pathogen discovery Dr Jackie Mahar, University of Sydney Dr Mang Shi, University of Sydney

	Workshop 4b: Genome-wide association studies Associate Professor Shyam Gopalakrishnan, University of Copenhagen Assistant Professor Ida Moltke, University of Copenhagen
5.00 pm	END OF DAY 2

Day 3: Friday 22 November

Auditoriums 1 and 2, Administration Building (F23),
University of Sydney

8.30 am	ARRIVAL TEA AND COFFEE
9.00 am	Career development workshop: Harnessing the power of mentoring in progressing your career Ms Bianca Havas, Serendis Leadership
10.30 am	MORNING TEA
11.00 am	Career development workshop: Understanding your signature strengths to develop your proposition Ms Bianca Havas, Serendis Leadership
1.00 pm	LUNCH
2.00 pm	Public talk: Wildlife detectives: the story of genome research, discovery and exploration at Australia's first museum Dr Rebecca Johnson, Australian Museum
3.00 pm	AFTERNOON TEA
3.30 pm	END OF EVENT

Day 1: Presentations

Metagenomics, evolution and virus emergence

Professor Edward Holmes FAA FRS

University of Sydney

[@edwardholmes](#)



Virology is entering a new discovery phase. Bulk RNA shotgun sequencing—meta-transcriptomics—provides a uniquely powerful means to rapidly reveal the microbial composition of any sample without bias, with major implications for the diagnostic sciences and understanding

the drivers of disease emergence. Metagenomic techniques also provide important new information on the composition of the virosphere and the fundamental patterns and mechanisms of virus evolution, and are able to determine disease agents on clinically actionable timescales. Herein, I will demonstrate the utility of meta-transcriptomics for pathogen discovery and disease emergence using a variety of clinical syndromes, both bacterial and viral, from humans and other animals, and for revealing key aspects of the diversity and evolution of the virosphere.

Tree Lab: portable genomics for early detection of plant viruses and pests in Sub-Saharan Africa

Dr Laura Boykin

University of Western Australia

[@laura_boykin](#)



Portable DNA sequencing technology has great potential to reduce the risk of community crop failure and help improve livelihoods of millions of people, especially in low-resourced communities. Crop losses due to viral diseases and pests are major constraints on food security and

income for millions of households in sub-Saharan Africa. This case study presented conditions of working in-field with limited or no access to mains power, laboratory infrastructure and internet connectivity, and with highly variable ambient temperatures. An additional challenge is that, generally, plant material contains inhibitors of downstream molecular processes, making effective DNA purification critical. We successfully undertook real-time on-farm genome sequencing of samples collected from cassava plants on three farms, one in each country. Cassava mosaic begomoviruses were detected by sequencing leaf, stem, tuber and insect samples. The entire process, from arrival on farm to diagnosis, including sample collection, processing and provisional sequencing of results, was complete in under three hours.

Ancient genomes shed light on the evolutionary history of sled dogs

Associate Professor Shyam Gopalakrishnan

University of Copenhagen



Although perhaps our closest domestic companion, considerable controversy still surrounds our understanding of dog (*Canis lupus familiaris*) domestication. While it is widely accepted that it was the first animal to be domesticated, exactly where, how many times and even when remains

heavily debated. While modern genomes have limited use for these questions, ancient canid genomes have allowed exploration of lost diversity and thus helped better address these questions. Using more than 100 resequenced modern wolf, dog and ancient canid genomes, we investigated the evolutionary history of sled dogs. We identified an ancient canid that is ancestral to the modern sled dog lineages and further identified that Greenlandic sled dogs are probably the closest modern relative of the original sled dog lineage. Further, we show that selection on key genes that led to adaptation of the dog as a draft animal in the cold arctic began more than 10 000 years ago.

Reading the story in the genome: why more data is not enough

Professor Lindell Bromham

Australian National University

[@macroevocoe](#)

We are fortunate to be working in a time when the amount and breadth of data is exploding and our computer power keeps increasing. Now our greatest limitation to getting meaning from analysing these data is our understanding of the evolutionary processes that generated the data. Our assumptions about evolutionary processes have a huge effect on the answers we get, yet these assumptions are rarely reality checked. How can we use what we know about evolution to improve bioinformatic analyses and to identify cases where we might be led astray?

Integrating fossil flowers in angiosperm macroevolutionary analyses

Dr Hervé Sauquet

Royal Botanic Garden Sydney

[@hsauquet_rbg Syd](#)



The rise of angiosperms was a major revolution in Earth's history, yet many aspects of their diversification remain unresolved. Extant and fossil data are both critical to understand angiosperm macroevolution and intersect, particularly in calibration of molecular dating analyses and in phylogenetic

assessments of fossil taxa, but this integration often remains limited, and both sources of data are typically underutilised. Here, I present results emerging from two collaborative efforts to improve this integration. First, I will outline a new molecular dating study of angiosperms as a whole, calibrated with the most comprehensive set of fossil age constraints to date (238 calibrations). I will then introduce the first results from a second study aiming at including 100 fossil flowers as tips in angiosperm phylogenetic analyses by recording their traits in our expanding eFLOWER dataset. These two studies demonstrate the importance of macroevolutionary research that is firmly grounded in morphological trait and fossil integration.

Highlights from genetic studies of the Greenlandic population

Assistant Professor Ida Moltke

University of Copenhagen

[@idamoltke](#)



Almost all genetic studies of disease are performed in European and Asian populations and such studies have led to interesting findings. But for common diseases, such as type 2 diabetes, the genetic variants these studies have identified have limited impact at population level because

they are rare or have small effects on disease risk.

Based on population genetics arguments, we chose to study the historically isolated and small Greenlandic population, and I will present some of our results. This includes identification of a variant that has substantial impact on the population, because it both has a large effect on disease risk and is common in Greenland. In fact, it explains 10–15% of all type 2 diabetes cases in Greenland. Interestingly, this variant is basically only present among Inuit, so would likely never have been found through studies of Europeans and Asians, highlighting one of several reasons why genetic studies of other populations are important.

Presentations by attendees

Agriculture, industry and conservation

Investigating the transcriptomic response of chickpea roots to infection by the oomycete pathogen *Phytophthora medicaginis*

Mr Donovan Coles

Western Sydney University

[@ColesDonovin](#)

In Australia, the chickpea industry is threatened by the root pathogen *Phytophthora medicaginis*, which causes yield-reducing root rot disease during wet seasons. *P. medicaginis* is thought to be a hemibiotrophic pathogen that initially colonises its host asymptotically like biotrophic pathogens and then later, once it has become established, begins to kill host tissue like necrotrophic pathogens. To date, how chickpea roots respond to this kind of infection strategy putatively observed for *P. medicaginis* has not been investigated. We employed an RNA-sequencing approach to investigate the root transcriptomic response of a susceptible chickpea host during infection by *P. medicaginis*. I will discuss how gene ontology enrichment has shed new light on our understanding of disease progression in a susceptible host.

A marsupial puzzle using phylogenetics, biogeography and conservation

Dr Margarita Medina

University of Canberra

[@maggie_medrom](#)

We determined the possible ancestral distribution of marsupials, identified evolutionary hotspots across biomes and determined conservation priorities per country. The results showed that the area reconstruction for Australasian marsupials goes back to South America and involves different dispersal and vicariant events. We found areas of ancient evolutionary refugia in temperate and montane biomes and areas of neo-endemism in tropical forests. Conservation prioritisation and ranking analysis showed that Queensland and Tasmania have the highest scores. We conclude that a combination of vicariance and dispersal events shaped the extant Australasian marsupial distribution and that more geographic data is needed for the Americas to provide a better assessment on conservation prioritisation.

Back to the future with genetics: the role of genetics in forest conservation

Dr Peter Harrison

University of Tasmania

@PAHarrison

Using quantitative and molecular genetic studies on eucalypts, I show how putatively neutral markers can provide a window in time to disentangle the role of past events in shaping a species' evolutionary history, and how quantitative variation in early age traits and reduced representations of a species' genome can inform the role of climate in shaping adaptation. I present these case studies considering how genetics is informing conservation strategies, as well as provenancing strategies for ecological restoration. I then give a brief overview of how we are embracing the genomics era through pooled sequencing to identify genomic signatures of evolutionary change in forest ecosystems.

Ecology, evolution and genetics

Approaching previously intractable acalyptrate fly phylogeny with transcriptome-based phylogenomics

Dr Keith Bayless

Australian National Insect Collection, CSIRO

@thekeithing

Prior attempts to decipher the evolutionary relationships between major lineages of Schizophora, including fruit flies, bush flies and *Drosophila*, have been obstructed by high species diversity and diversification rates. Our approach, analysing thousands of genes from combinations of transcriptomic and exome capture data, offers a robustly supported evolutionary tree in which the primary branching framework of Schizophora is clarified for the first time. Revisionary syntheses integrating our phylogenomic results on flies with morphology and ecology are underway. A robust understanding of the evolution of the entire group was necessary to form testable hypotheses and discover evolutionary patterns in previously obscure critical lineages.

Ancient DNA and Near Oceania: evaluating genetic methods in the study of zooarchaeological remains across Papua New Guinea

Ms Sindy Luu

University of Otago

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The genetic study of archaeological materials has profoundly enriched our understanding of past human societies. My research, using DNA metabarcoding of zooarchaeological material, allows us to describe the changes in human subsistence strategies and resource use by genetically identifying species of morphologically undiagnostic bones.

The results additionally assess the preservation potential for ancient DNA in the tropics, where degradation is accelerated. However, DNA preservation is also site and context specific, and my results demonstrate this phenomenon across Papua New Guinea. Overall, I provide a positive outlook for further genetic studies of prehistoric remains in the Western Pacific for archaeological investigations.

Hackflex: low-cost Illumina sequencing library construction for large-scale sequencing

Dr Kay Anantanawat

University of Technology Sydney

@kanantanawat

One of the limitations of large-scale high-throughput sequencing is the cost of library preparation. We developed a low-cost protocol for the production of Illumina-compatible sequencing libraries called Hackflex. The protocol is based on the standard Illumina Nextera Flex Kit. Each reaction can be generated at a cost of A\$6.50 using diluted bead-link transposase and reagents created from basic chemicals in a laboratory. We have successfully tested the protocol on three different bacterial genomes that contain different levels of GC contents: *Escherichia coli* MG1655, *Staphylococcus aureus* ATCC25923 and *Pseudomonas aeruginosa* PAO1. The assessment of the quality of the libraries generated using Hackflex shows that the quality of the libraries is compatible with the standard Flex protocols. The protocol will greatly benefit the project with large-scale DNA sequencing.

Microbes, pathogens and health

Comparative genomics of *E. coli* isolated from adult and paediatric patients with inflammatory bowel disease and controls

Mrs Mukta Das Gupta

Australian National University

Several studies implicate bacteria in the pathogenesis of inflammatory bowel disease (IBD), and *Escherichia coli* is one of the leading candidate triggers. Our aim was to identify genes of *E. coli* associated with IBD. This study involved whole genome comparisons of 179 *E. coli* strains, isolated from Crohn's disease patients, ulcerative colitis patients and controls. Our findings suggest that different bacterial properties and genes of *E. coli* are associated with paediatric and adult Crohn's disease patients, and lymph nodes isolates. These may allow *E. coli* to evade the host immune system and play a role in the aetiopathogenesis of IBD.

Hunting the parasites of our parasites: a 'deliberate' exploration of viruses infecting human malaria protozoan parasites using meta-transcriptomic approaches

Dr Justine Charon
University of Sydney

Eukaryotes of the genus *Plasmodium* cause malaria, a parasitic disease responsible for substantial morbidity and mortality in humans. However, the nature and abundance of any viruses carried by these divergent eukaryotic parasites is unknown. We investigated several *Plasmodium* species' viromes by performing a meta-transcriptomic study of blood samples taken from patients suffering from malaria and infected with *P. vivax*, *P. falciparum* or *P. knowlesi*. This resulted in the identification of a novel RNA virus that we termed Matryoshka RNA virus 1 (MaRNAV-1), encoding an RNA polymerase and restricted to *P. vivax*, as well as an associated hypothetical viral segment of unknown function. Additional screening revealed that MaRNAV-1 was abundant in geographically diverse *P. vivax* derived from humans and mosquitoes. A related bi-segmented narnavirus-like sequence (MaRNAV-2) was also retrieved from Australian birds infected with a *Leucocytozoon*—a genus of eukaryotic parasites that group with *Plasmodium* in the Apicomplexa subclass hematozoa.

Together, these data support the establishment of two new phylogenetically divergent and genomically distinct viral species of protists, including the first virus-infecting

Plasmodium parasites. As well as broadening our understanding of the diversity and evolutionary history of the eukaryotic virosphere, the restriction of infection to *P. vivax* may be of importance in understanding *P. vivax*-specific biology in humans and mosquitoes, and how viral co-infection might alter host responses at each stage of the *P. vivax* life cycle.

Transmission at the human-wildlife interface: hospital patients share bacterial pathogens but not resistance genes with local silver gulls

Dr Bethany Hoye
University of Wollongong
[@bethanyhoye](#)

Multi-drug-resistant Enterobacteriaceae are increasingly detected in wildlife, however it is unclear whether these infections result from microbial evolution within wildlife hosts or spillback from anthropogenic infections. Understanding transmission pathways is critical to managing anti-microbial resistance and public health. Using *Salmonella* in the Illawarra region as a model system, we employed WGS to investigate exchange between populations (human: hospital patients; wildlife: silver gulls breeding on nearby islands) and long-term persistence within populations of these pathogens, the antimicrobial resistance genes they harbour and the mobile genetic elements on which the resistance genes are carried.

Day 2: Research development workshops

Workflows for big data

Dr Angela McGaughran
Australian National University
[@ang_mcgauhran](#)

This workshop will take participants through common workflows for big data. We will start with experimental design and move through genomic library preparation to common bioinformatic problems. We will finish with a worked example of population genomics in action, where we use code in R to understand the effects of translocation and founder events on the genetic diversity of Australian populations. For those who want to follow along with the demonstration, the package `PopGenome` will need to be installed in R.

Models in genomics and biodiversity analysis

Dr Xia Hua
Australian National University

This workshop will introduce some basic mathematical models in population genomics, phylogenomics, and phylodynamics. Some of these models are relevant to the afternoon workshops, including species distribution models in biodiversity and spatial analysis, multi-species coalescence process and birth-death process in phylogenomics, and regression models in genome-wide association studies. The workshop will focus on the mathematical foundations of these models so that participants will have a rough idea on how to develop a mathematical model for their own studies. No software is required for this workshop. Participants are assumed to have a basic understanding of calculus, probability and statistics.

Biodiversity and spatial analysis

Dr Dan Rosauer

Australian National University

This workshop will introduce concepts and methods for mapping spatial patterns of biological diversity. It will consider the meaning, measurement and use of diversity metrics such as phylogenetic diversity and endemism. Through prepared examples, participants will learn how to link spatial and phylogenetic data for a group of species to both visualise and measure the spatial component of evolution, for example to identify areas with distinct or unique biota. The software [Biodiverse](#) will be used for this workshop. Participants are assumed to be familiar with interpreting phylogenetic trees but do not need prior experience with spatial information.

Phylogenomics

Dr David Duchêne

Australian National University

Professor Simon Ho

University of Sydney

This workshop will present an introduction to the challenges associated with phylogenetic analyses of genome-scale data. Participants will learn about data filtering, gene tree incongruence and inferring species trees. A hands-on session will involve the analysis of a multigene dataset to resolve the phylogenetic relationships among marsupial families. The software required for this workshop are [MEGA](#) and [ASTRAL](#). Participants are assumed to be familiar with interpreting phylogenetic trees and some of the basic principles of molecular evolution.

Metagenomics and pathogen discovery

Dr Jackie Mahar

University of Sydney

Dr Mang Shi

University of Sydney

This workshop will provide training on how to find potential pathogens in meta-transcriptomic data. This will include guidelines for (i) *de novo* assembly of meta-transcriptomic data, (ii) taxonomic assignment and annotation of assembled transcripts/genomes and (iii) comprehensive

characterisation of potential pathogens, including identification of false positives. Participants will be guided through a bioinformatics pipeline using a reduced dataset on a high-performance computer with the required software and databases already installed. The software required for this workshop are [PuTTY](#) (if working from a Windows machine) and an FTP client such as [FileZilla](#). Participants are assumed to have a basic understanding of command line.

Genome-wide association studies

Associate Professor Shyam Gopalakrishnan

University of Copenhagen

Assistant Professor Ida Moltke

University of Copenhagen

This workshop will give a brief, basic introduction to genome-wide association studies (GWAS). This will include hands-on experience with running a GWAS and plotting the results, and will cover some of the potential caveats and related important quality control and data filtering steps.

We will be working on a server with all necessary programs installed. The only software required for this workshop is a program that allows you to log in into this server using SSH and open figure files remotely. For Windows users, this requires that you install [MobaXterm](#). Mac users can use Terminal, but please make sure you also have [XQuartz](#) installed (default on some Macs, but not all, and it makes viewing of figure files via SSH a lot easier). Linux users should not need to install anything.

We assume very little prior knowledge except for a basic understanding of what it means to test for association between a specific genetic variant and a given phenotype. It will be helpful but not essential to have some knowledge about what statistical tests can be used to test for such an association.

Day 3: Career development

Harnessing the power of mentoring in progressing your career

Ms Bianca Havas

Serendis Leadership



Mentoring is a unique opportunity for an individual to receive advice, support and a more senior perspective on their personal objectives and challenges. This workshop session will focus on how to develop successful and impactful mentoring relationships

to assist your career development and leadership.

Participants will explore what mentoring is (as distinct from coaching or sponsorship), the value and impact of mentoring to their career, what makes a successful mentoring relationship, how to define objectives and drive the agenda, and how to approach challenging conversations. This workshop session will also provide insights and case studies.

Understanding your signature strengths to develop your value proposition

Ms Bianca Havas

Serendis Leadership

To enhance their career, individuals traditionally tend to focus on what they need to improve, fix or develop. This session will take participants on a different journey: what drives their performance? What particular strengths do they bring to their role or research? What should be their development plan? How can they enhance their own profile and network within and outside their role, organisation or field?

Participants will explore the concept of strengths and start articulating their key unique strengths. They will then reflect on how to drive their career according to those strengths, and how to develop their profile and be recognised for potential roles that match their signature strengths.

Public lecture: Wildlife detectives: the story of genome research, discovery and exploration at Australia's first museum

Professor Rebecca Johnson

Australian Museum

[@DrRebeccaJ](#)



Professor Rebecca Johnson is the director of the Australian Museum Research Institute (AMRI), a wildlife forensic scientist, conservation geneticist and chief investigator of the Koala Genome Consortium. As the first female director of science at the Australian Museum in its 192-year

history, Rebecca's career has encompassed all of the challenges associated with being a senior executive woman in STEM. Her passion for conservation and collaboration, and a knack for challenging the scientific status quo, has led her to a non-traditional path in science. From climbing remote mountains in the Solomon Islands to meet village chiefs in traditional dress (aka semi-nude) to giving expert wildlife forensic evidence to Australian and New Zealand courts, to sequencing the koala genome, Rebecca will share tales from her fascinating life in science.

Rebecca will describe the breadth of AMRI research and how the museum utilises their natural science collections. These collections are some of Australia's oldest and most valuable research infrastructure, collected through the Museum's journey of discovery, exploration and education. Rebecca will demonstrate this through case studies from her work in policing the illegal wildlife trade, protecting Australia's borders from invasive species and leading the koala genome consortium, one of the first Australian-led genome sequencing projects. Her goal is to show how important museum research is to engage and educate the next generation of researchers, and inspire custodianship of our natural world in the next generation.

Workshop Venues

- ★ Charles Perkins Centre
University of Sydney
- ★ Courtyard Cafe (Holme Building)
University of Sydney
- ★ Administration Building
University of Sydney

Our Recommendations

Cafés

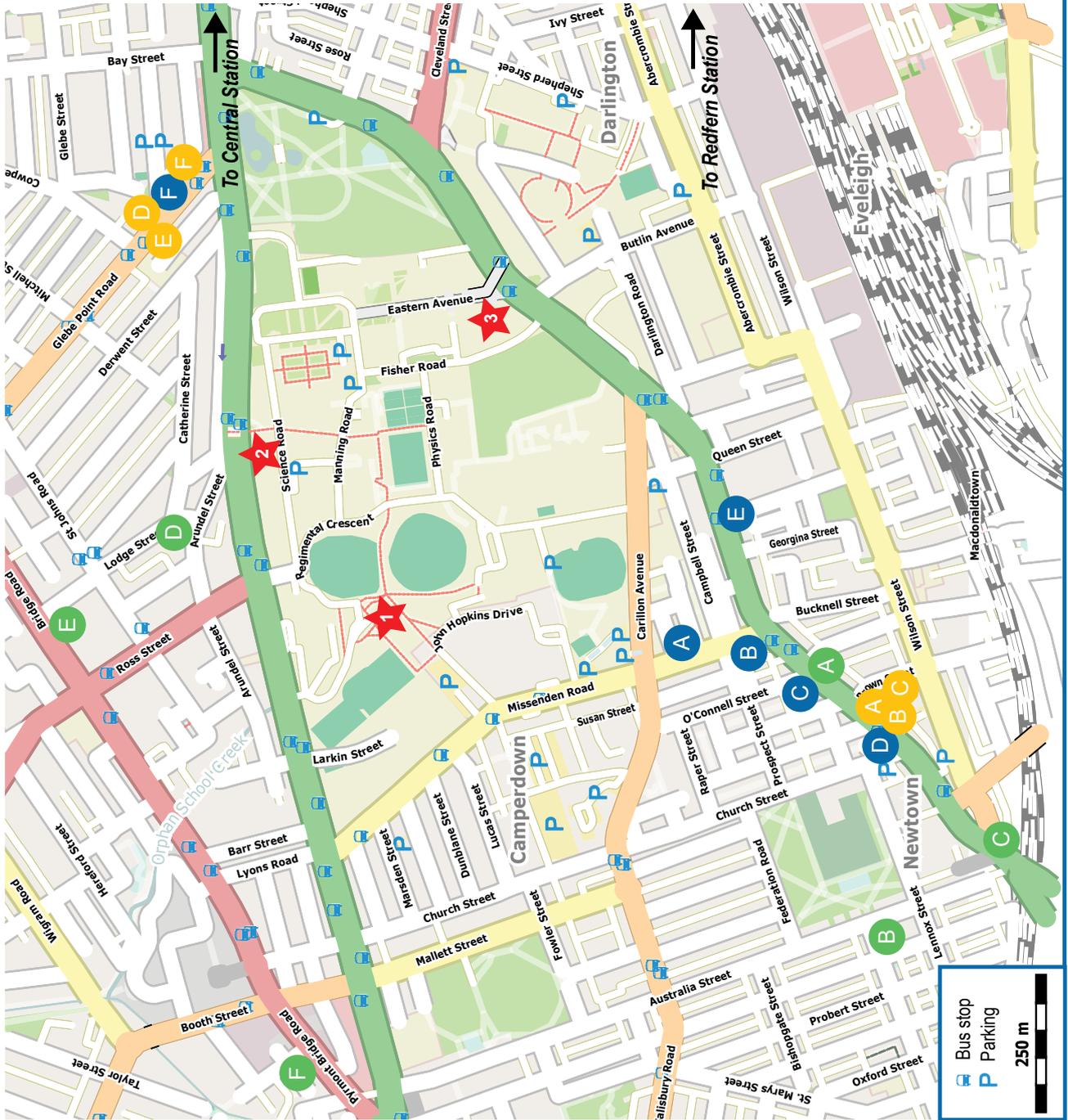
- Hoochie Mamma A Shenkin Espresso Bar D
- Campos Coffee B Urban Bites E
- Brewtown C Baade Manors F

Cheap Eats

- Dumpling King A Burger Ten D
- Newtown B Goku Ramen E
- North Indian Diner C At Home Thai F

Drinks

- Newtown Hotel A Forest Lodge Hotel D
- Courthouse Hotel B The Nag's Head E
- The Bank C Wayward Brewing F



Sponsors

The Genomes and Biodiversity: Research and Career Development Workshop is proudly supported by the Australian Academy of Science through the Theo Murphy Initiative (Australia), the University of Sydney and the University of Copenhagen.

The Theo Murphy (Australia) Fund

The Genomes and Biodiversity: Researcher and Career Development workshop is supported by the Royal Society of London—the national academy of science of the United Kingdom and the Commonwealth—through the Theo Murphy (Australia) Fund.

The Royal Society of London is a self-governing fellowship of many of the world's most distinguished scientists, drawn from all areas of science, engineering and medicine. The society's fundamental purpose, reflected in its founding charters of the 1660s, is to recognise, promote and support excellence in science and to encourage the development and use of science for the benefit of humanity.



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