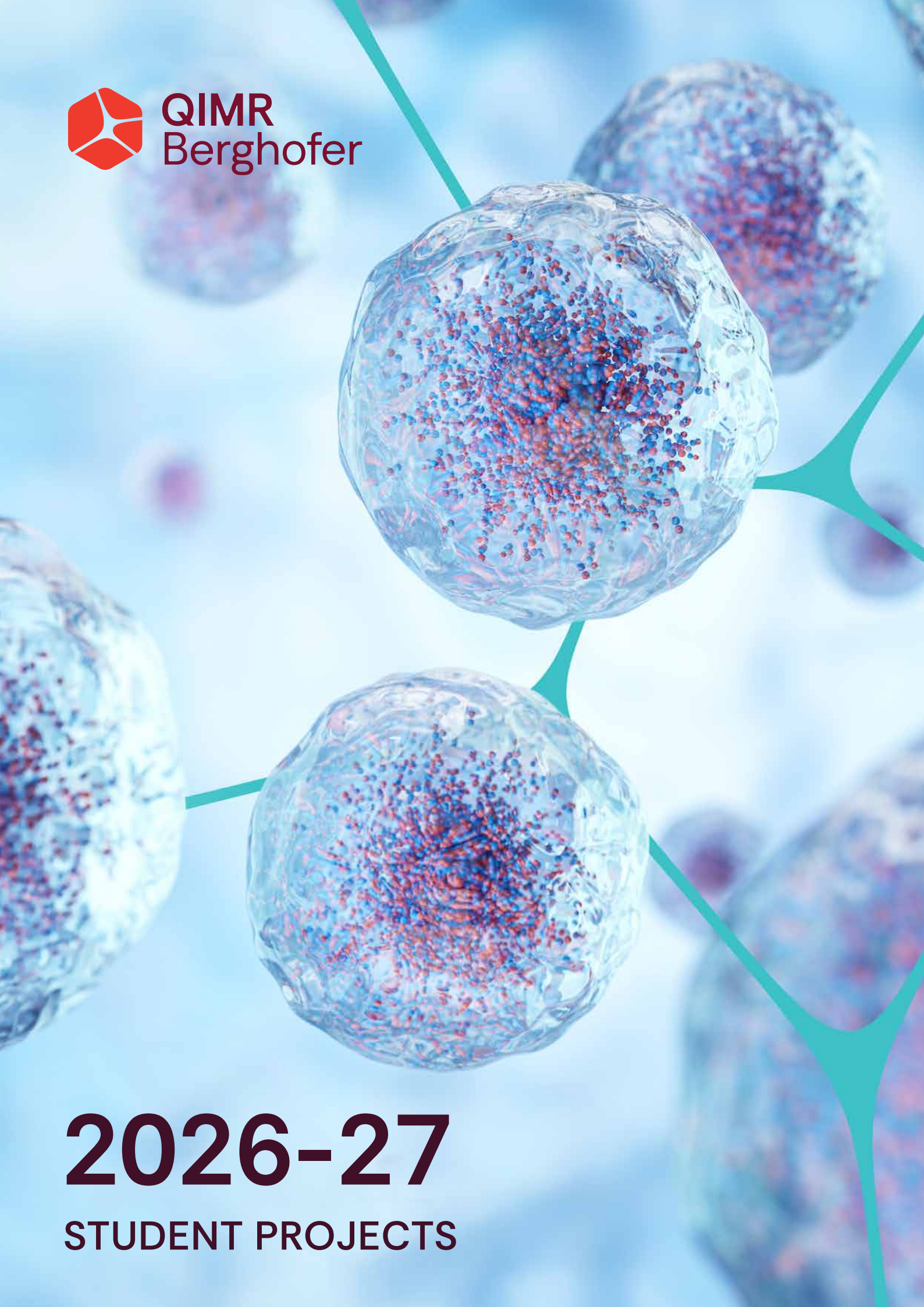
QIMR Berghofer



2026-27

STUDENT PROJECTS

Acknowledgement

QIMR Berghofer acknowledges the Traditional and Cultural custodians of the lands, waters, and seas across Queensland, pay our respects to Elders past and present, and recognise the role of current and emerging leaders in shaping a better health system. We recognise the First Nations peoples in Queensland are both Aboriginal peoples and Torres Strait Islander peoples and support the cultural knowledge, determination, and commitment of First Nations communities in caring for health and wellbeing for millennia.

Director's Welcome

QIMR Berghofer stands among Australia's most distinguished medical research institutes, with a proud legacy dating back to 1945. The Institute is dedicated to improving human health through impactful medical research that tackles the most pressing medical challenges of our time. We pursue this by advancing new diagnostics and developing more effective treatments and strategies to prevent and treat disease. Our work is driven through four major relevant programs: Cancer Research, Infection and Inflammation, Brain and Mental Health, and Population Health (disease causation, prevention and control).

Today, more than 1,000 scientists, professional staff and students call QIMR Berghofer home. Their dedication and expertise have produced an impressive body of work – 588 unique scientific publications in 2024-2025 alone, attracting more than 50,000 citations. Our collaborations with industry and partners generated over $9.1 million in commercial and contract research income.

As a student at the Institute, you become part of an exceptional global community of talented, emerging researchers. Here, you will work alongside world-leading experts in state-of-the-art laboratories and participate in seminars highlighting the newest discoveries in our fields. You will be encouraged to ask bold questions and contribute to solving the world's most pressing medical challenges. While here, you will be well supported by a professional team who will help you to navigate your chosen academic path. Throughout your time with us, you will receive strong professional, academic and mentoring support, helping you build the skills and confidence needed to pursue research with rigour, integrity and purpose.

Our PhD program is known for being very collegial, inclusive and deeply supportive. Each year, students come together at our annual symposium to share their work, strengthen peer networks and celebrate achievements. Many alumni reflect on their time here as one of the most rewarding periods of their career - and we are proud of that legacy.

This booklet offers a glimpse into the opportunities ahead of you. The projects featured are often flexible and can be shaped to match your interests and strengths. I encourage you to reach out to our faculty, explore all possibilities and find a project that inspires you. This is an important decision, and the right fit will fuel your enthusiasm and success.

I hope you will consider making QIMR Berghofer the place where you take the next step in your academic journey. Should you join us, I look forward to welcoming you to our Institute as you begin an exciting step in your career.

Professor Grant A. Ramm

Interim Director and CEO

QIMR Berghofer

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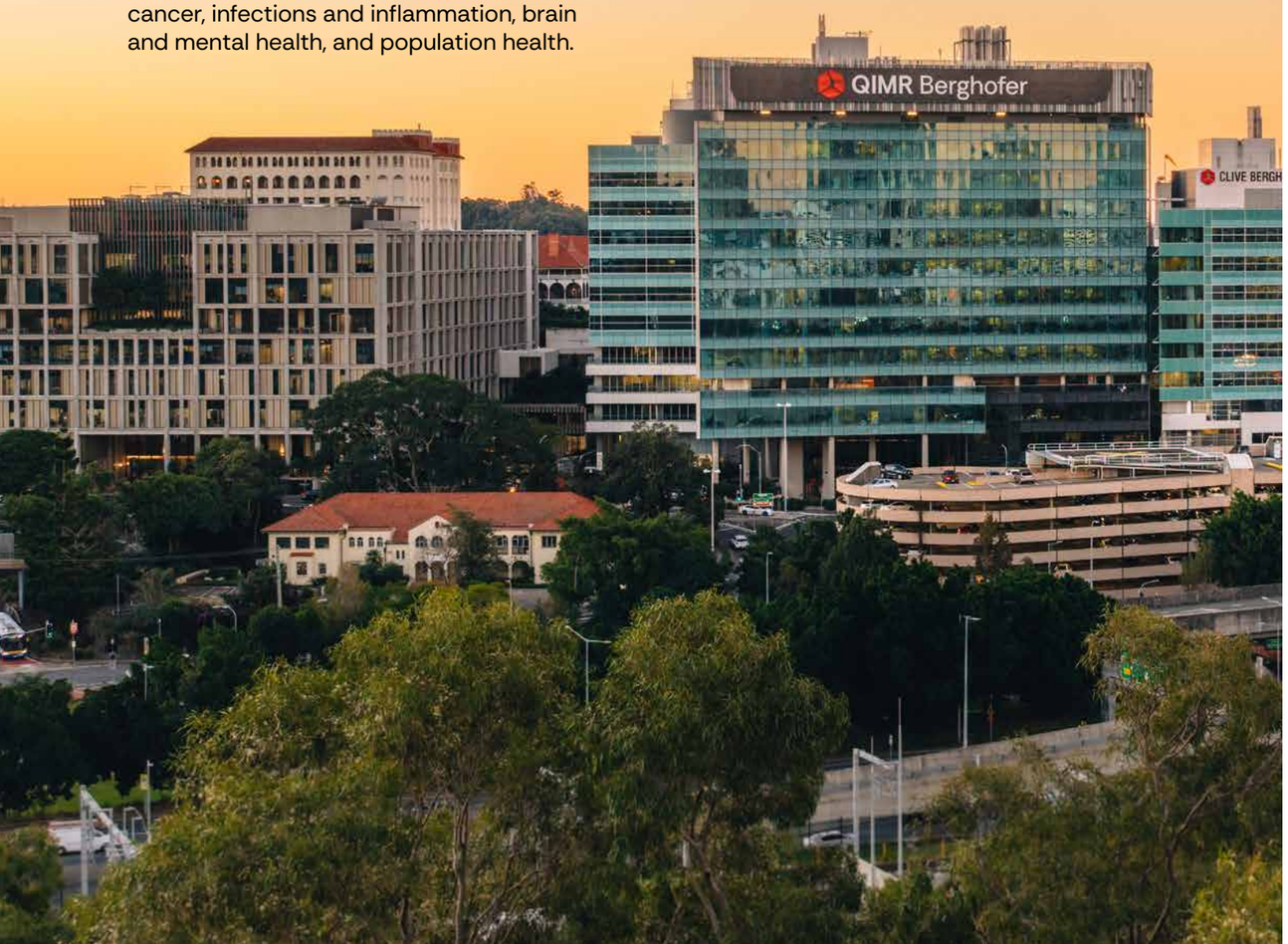
QIMR BERGHOFER 2026 – 2027 STUDENT PROJECTS

Quick facts about QIMR Berghofer

- QIMR Berghofer was established in 1945 as "The Queensland Institute of Medical Research" and celebrated its 80th year in 2025.
- 588 papers were published (2024-2025).
- The QIMR Berghofer student body is very multinational and is strongly supported by a Higher Degrees Committee dedicated to mentoring and guiding students through their candidature.
- QIMR Berghofer is a world-leading translational research institute focused on cancer, infections and inflammation, brain and mental health, and population health.
- The Institute is home to more than 700 scientists (of which approximately 150 are students) in >60 research laboratories.
- The Institute is located at the Herston Health Precinct, which is home to more than 30 health facilities, medical research institutes, universities and organisations.



QIMR Berghofer Students

The QIMR Berghofer Student Council is a dynamic organisation that serves as a support system, social hub, and a source of lifelong memories for students at QIMR Berghofer. It provides a network of support where students can connect with peers and mentors who share their research interests and offer academic resources and social support to help them excel in their research endeavours.

The Student Council consists of three student committees: Student Society, Higher Degrees Committee Student Representatives, and Early Career Researcher Convenors. These committees are responsible for organising a range of events, including lunch barbecues, trivia nights, bake sales, seminar series, annual symposiums, and even conference retreats. These activities create opportunities for students to make friends, establish meaningful connections, and foster a sense of community within the scientific community.

Moreover, through engaging events and activities, the QIMR Berghofer Student Council encourages students to create lasting memories that they will cherish throughout their scientific journey, adding a unique dimension to their overall research experience. We are excited for you to join us!

Above: (top) Students in one of the Institute's dining areas; (bottom) Attendees at the 12th QIMR Berghofer Biennial Postgraduate Student Conference – Mercure Clear Mountain Lodge, Spa & Vineyard, Brisbane Queensland.

Why study at QIMR Berghofer?

Studying at QIMR Berghofer provides students with a unique opportunity to have access to diverse clinical and cutting-edge research. Our proximity to the Royal Brisbane and Women's Hospital (RBWH) and the Herston Health Precinct makes us ideal for clinical research collaborations.

In addition to your research training, QIMR Berghofer is committed to your overall professional development. This includes expanding your skills in critical scientific writing, statistics, leadership, communication and protecting your intellectual property. After studying at QIMR Berghofer, your broader skill base will allow you to compete for your future desired career.

Advantages of studying at QIMR Berghofer include:

- Expert supervision from world leaders in their field of research.
- Access to and support from high-quality, purpose-built facilities and technical experts.
- Access to advanced technologies and equipment.
- Exposure to a wide range of interdisciplinary research encompassing everything from population studies to statistics, public health, tropical medicine, immunology and cancer.
- Opportunities for international collaboration and travel.
- Competitive Honours and PhD top-up scholarships.
- Travel support for attending international conferences to promote collaborations and future postdoctoral positions.
- Student mentoring and professional development.
- Dynamic process of review to monitor student progress and ensure timely completion of your degree.
- A regular student seminar program.
- A weekly seminar series presented by researchers, including national and international speakers.
- An active student society, symposium and retreat for networking and training.

The QIMR Berghofer student body is a diverse group of Australian and international students involved in a wide range of research endeavours. We are working to make a real difference to health issues affecting Australians and the rest of the world.

Clinician Researcher Academy

The QIMR Berghofer Clinician Researcher Academy ("the Academy") is designed to develop and coordinate research collaborations, career development, professional development, academic training, and mentorship with and for clinician researchers.

Participants at the Academy have access to cutting-edge resources, world-renowned scientists, key networks, and collaborative research opportunities through a range of visitor, affiliate, and student arrangements.

In turn, QIMR Berghofer aims to advance research impact and translation through clinically relevant and clinically informed research, and to promote achievement of our vision of better health and wellbeing through impactful medical research. Our Scientific and Core Services are world-leading and include genome informatics, statistics and research design, research software, programming and high-performance computing, metabolomics, sample processing, sequencing and NATA-accredited flow cytometry, and histology. Our Scientific and Core Services teams provide training in the use of specialist equipment, techniques, and research methodologies.

Our Good Manufacturing Process (GMP) accredited Q-Gen Cell Therapeutics facility has over 20 years of experience in T cell manufacturing supporting the immunotherapy industry and advancing patient outcomes with the manufacture of autologous and allogeneic therapies.

The facility is licensed by the Therapeutics Goods Administration for the manufacture of T cell therapies for clinical trials. The Institute offers a weekly faculty seminar series and regularly hosts national and international experts as guest speakers who share the latest research findings and methods across a range of health and medical research topics. Our clinical higher degree students are supported by a professional team that assist you to navigate the PhD journey and with mentoring advice and skill development to pursue a research career with the highest levels of integrity and scholarship.

Clinical Director:
Professor Elizabeth Powell

Elizabeth.Powell@qimrb.edu.au

qimrb.edu.au/our-research/clinician-researcher-academy

QIMR Berghofer Core Facilities

HISTOLOGY FACILITY

The QIMR Berghofer Histology Facility is a state-of-the-art NATA-accredited service and research laboratory dedicated to advancing histology through expert support and comprehensive services. We provide specialised histology offerings performed by our experienced staff, which include sample preparation, embedding, sectioning and a range of staining techniques, including immunohistochemistry and spatial biology platforms. Our facility is designed to meet the diverse needs of scientists and postgraduate students from QIMR Berghofer, as well as external and international institutions, creating a collaborative environment that fosters innovation and research excellence.

The strength of our facility lies in our team, known for their extensive expertise in both routine and specialised histological techniques. With specialists in tissue processing, embedding and sectioning, we can adeptly manage a wide variety of sample types and complexities such as mosquitoes, organoids, and hydrogel patches. Our team delivers rigorously optimised workflows tailored specifically for advanced spatial biology platforms. Our proficiency in antibody optimisation and advanced immunohistochemistry methods, including multiplex staining, allows us to deliver detailed insights into tissue morphology and function, which are essential for both research and diagnostics.

Our commitment to client success goes beyond service provision. Our team is always eager to offer guidance on project planning and development. Whether you need assistance with experimental design, training in specific techniques or troubleshooting existing methodologies, our staff are here to help. We take pride in providing responsive, tailored support that aligns with each client's research objectives.

Central to our mission is a dedication to achieving the highest quality results in a cost-effective manner. We recognise the pressures of research timelines and budget constraints, and we strive to deliver optimal outcomes without sacrificing quality. Our facility is equipped with cutting-edge technology and adheres to rigorous quality control measures, ensuring that all histological preparations meet the highest standards.

SAMPLE PROCESSING

Underpinning outstanding and reproducible science are consistent, high-quality samples. The quality of these samples largely depends on pre-analytical conditions, including the timing, collection, storage, and sample preparation techniques. The consistency of producing these samples is paramount in generating reliable and meaningful data.

Our NATA-accredited Sample Processing Facility provides service and expertise in pre-analytical sample handling, preparation and storage of biological samples, as well as post-processing analyses such as qPCR. Our processes are designed to efficiently and economically meet rigorous quality requirements.

We work alongside researchers and clients to design pre-analytical sample handling solutions for the collection, transportation, storage, aliquoting, blood fractionation, and cell isolation (including PBMC preparation and storage), nucleic acid extraction (DNA and RNA), nucleic sample QC, and PCR.

Our service accommodates both high-throughput and single sample processing. It integrates seamlessly with other Scientific Services - particularly the Genetic Analysis and Sequencing Facility - to deliver a streamlined workflow from sample collection to data generation.

Partner with a NATA-accredited facility for confidence, compliance, and quality in every sample.

FLOW CYTOMETRY

Our Flow Cytometry and Fluorescent Activated Cell Sorting (FACS) Facility use lasers and photon detectors to capture vital information about cells, cellular components and other particles. The technology relies heavily on the use of fluorescent probes to detect molecules of interest associated with normal or disease states. The technology is capable of providing data from over 40,000 cells per second and provides our researchers with a vast amount of information.

Flow cytometry is at the forefront of immunology, cancer and infectious disease research, with ever evolving innovative technology paving the way for scientific advancements. This allows for the rapid detection and identification of distinctive characteristics on individual cells based on light scatter and fluorescence emission.

Immunophenotyping and profiling of different immune cell populations is crucial in immunology research, making flow cytometry an indispensable tool that enables large amounts of complex and comprehensive data to be acquired in a short period of time.

MICROSCOPY & SPATIAL CELL BIOLOGY FACILITY

Our Microscopy & Spatial Cell Biology Facility is equipped with a comprehensive range of instruments for imaging both fixed or living cells and tissue. These include stereo microscopes, slide scanners, compound microscopes, confocal microscopes, intra-vital microscopes, cyclic immunofluorescence microscopy, spatial molecular imaging, and various analysis stations and software. We are equipped to capture images of cells or tissue stained with colourimetric dyes or fluorescent dyes at various resolutions from macro to super resolution.

We provide assistance and training on all instruments and software in the facility and can provide full service for some services if required.

Our Microscopy Facility is proudly supported by the Australian Cancer Research Foundation and operates microscopes in the ACRF-Centre for Comprehensive Biomedical Imaging.

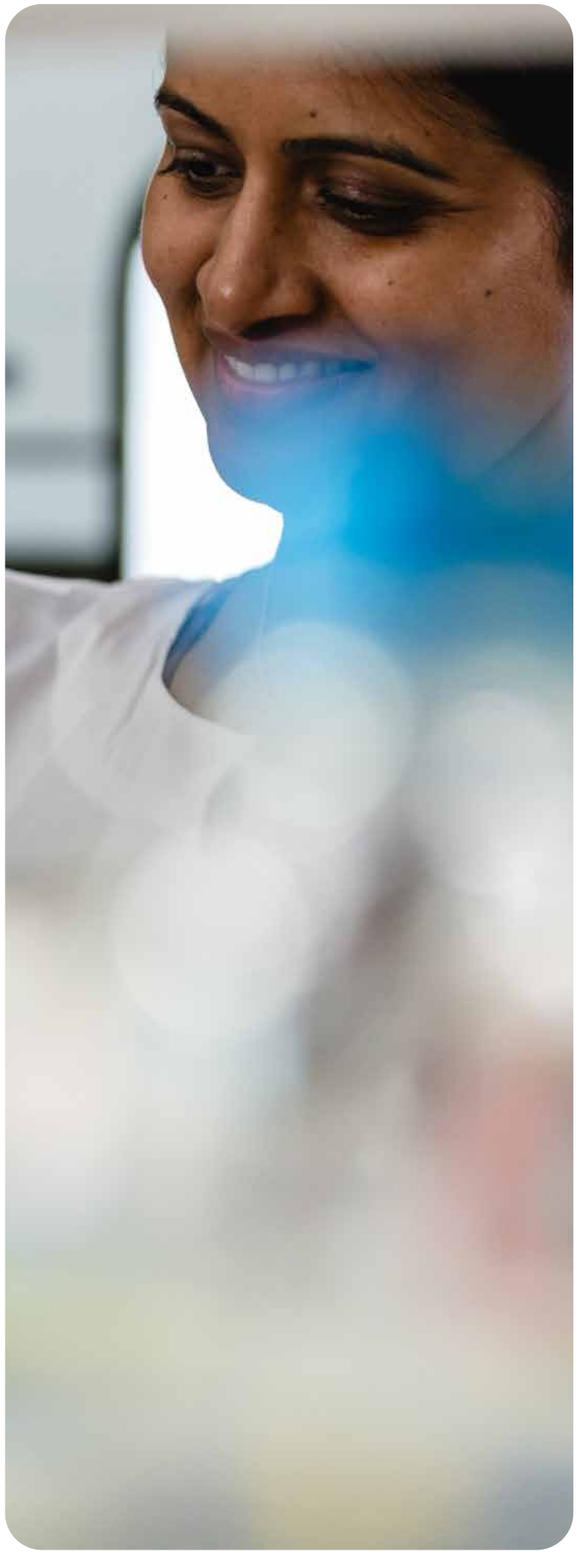
We also proudly support and interact with the:

- Australian Microscopy and Microanalysis Society (AMMS)
- Light Microscopy Australia (LMA)
- Microscopy Australia (MA)
- ACRF Cancer Biology Imaging Facility and the ACRF Cancer Ultrastructure and Function Facility at the Institute for Molecular Bioscience (IMB)
- Centre for Microscopy and Microanalysis-UQ (CMM)
- Microscopy Facility at Translational Research Institute
- Microscopy Facility at QUT
- Advanced Microscopy Facility at the Queensland Brain Institute (QBI).

GENETIC ANALYSIS AND SEQUENCING FACILITY

Our Genetic Analysis and Sequencing Facility includes Next-Generation and Capillary Sequencing, using several sequencing platforms and supporting auxiliary instruments. DNA Sequencing and Next-Generation sequencing are used in molecular biology to study genomes, transcriptomes and the proteins they encode.

Information obtained through sequencing allows researchers to identify phenotypes in cancers, diseases and complex disorders by changes in genes and gene associations. This data has the potential to help identify



potential drug targets and vaccine candidates and influence patient outcomes in clinical applications.

Our sequencing services employ capillary sequencing and both long read and short read next-generation sequencers to deliver consistent high quality genomics data.

METABOLOMICS

The QIMR Berghofer Metabolomics Facility measures the metabolome and lipidome using quantitative (QqQ) and qualitative (Q-ToF) liquid chromatography-mass spectrometry instrumentation.

Metabolomics can provide an overview of the metabolic status and global biochemical events association with a cellular or biological system, and in medical research in particular, provide mechanistic understanding of the biochemical and metabolic changes that occur during the onset, progression, or as a consequence of disease.

Metabolites include the nutrients we obtain from food, the lipids found in cell walls, the bases that make up DNA/RNA, and the amino acids that are coded for by genes and are subsequently assembled to form proteins. Metabolites are the small molecule compounds that are the substrates, intermediates, and end products of the multitude of metabolic pathways required for life.

PROTEOMICS

Our Proteomics Facility uses liquid chromatography mass spectrometry (LC-MS) to analyse samples from a variety of medical research projects and to measure the proteome. These highly sensitive instruments can provide impressive depth for proteomic analysis of complex samples.

Proteomics is the study of proteins in biological systems, encompassing their structures, functions, and interactions. While genomic data can provide a basic template for the proteins in a system, proteomics is required to truly evaluate protein expression and how it changes in response to various stimuli.

It is well established that transcriptomic sequencing expression levels do not always correlate to experimentally observed protein expression levels. As proteins are responsible for carrying out most of the activities within a cell, it is imperative to study them directly in order to properly understand how cells function, and how these functions can be dysregulated, to cause disease states.

Proteomics offers medical researchers an array of vital information on cellular processes to better understand their disease states of interest and how to treat them.

QIMR Berghofer Services

Q-Gen Cell Therapeutics

genomiQa

Q-GEN CELL THERAPEUTICS

As one of the largest cell manufacturers in Australia, we leverage our extensive expertise and state-of-the-art technologies to deliver high-quality products. Our team of highly skilled professionals work tirelessly to deliver exceptional customer service and technical support, ensuring that our clients receive tailored solutions that meet their unique requirements.

With specialist teams in manufacturing, quality control, quality assurance, supply chain, equipment engineering and regulatory compliance, we can assist in all aspects of your clinical trial project. Our dedicated project management support and an unwavering commitment to cell therapy development ensures Q-Gen is your preferred manufacturing partner.

GENOMIQA

GenomiQa is a start-up company that has grown out of QIMR Berghofer. We offer hospitals, clinicians, researchers, and biopharma companies high-quality analysis of data from whole genome sequencing. Founders, Associate Professor Nic Waddell and John Pearson, have more than 35 years' combined experience in genomics and bioinformatics. These areas of expertise blend powerfully within genomiQa's products and services, which are designed to support personalised treatment and better outcomes for patients.

We bring precision analytics to routine clinical practice. In practice, this offers:

- More accurate diagnostics;
- Better decision support for clinicians;
- Precision drug development.

Q-Gen
Cell Therapeutics

Q-Gen

Dr Balaji Somasundaram

Balaji.Somasundaram@qimrb.edu.au

qimrb.edu.au/commercial-collaborations/q-gen

Hands-on experience in patient-centric cell and gene therapy manufacturing.

This project is suitable for an Honours, Masters or PhD student.

BACKGROUND

Are you passionate about cutting-edge biotechnology and want to make a real impact in the future of healthcare?

Join Q-Gen, a leading cell and gene therapy (CGT) manufacturing facility, for an immersive industry placement where you'll gain hands-on experience in a patient-centric, cGMP-compliant environment.

This placement offers a unique opportunity to understand how life-changing cell and gene therapies move from the laboratory bench to patients—through real-world exposure to manufacturing, quality control, quality assurance, and supply chain operations.

PLACEMENT STRUCTURE

Duration: 6-12 months, full-time.

Supervision: Students will be supported by dedicated mentors across Q-Gen departments, with regular feedback and development sessions.

ROTATIONAL EXPERIENCE:

Manufacturing: Learn about cleanroom operations, aseptic processing, and GMP documentation.

Quality Control: Support testing, data integrity, and environmental monitoring activities.

Quality Assurance: Observe batch review, deviation handling, and regulatory compliance.

Supply Chain: Understand materials management, logistics, and supplier interactions in a highly controlled environment.

WHO SHOULD APPLY

We welcome applications from students currently studying:

- Biotechnology, Biomedical Science, Bioprocessing, or related life sciences fields.
- Chemical Engineering, Chemistry, or other STEM disciplines with an interest in advanced manufacturing or therapeutic production.

Applicants should demonstrate enthusiasm for hands-on learning, attention to detail, and a genuine interest in contributing to patient-focused innovation.

HOW TO APPLY

Submit your CV and a brief cover letter (max 1 page) outlining your motivation for joining Q-Gen and how this placement aligns with your career goals.

Apply now: Balaji.somasundaram@qimrb.edu.au

APPROACH

By the end of this placement, students will:

- Understand end-to-end cell and gene therapy manufacturing processes within a regulated cGMP facility.
- Gain insight into cross-functional collaboration between manufacturing, quality, and supply chain teams.
- Develop technical competencies in documentation, aseptic techniques, material management, and batch record review.
- Build transferable professional skills, including teamwork, communication, time management, and problem-solving in a dynamic, compliance-driven setting.
- Receive mentorship and coaching from experienced industry professionals to help shape your career path in biomanufacturing and biotechnology.

OUTCOME

Students will complete the placement with:

- A strong foundation in cGMP operations in biologics translation, particularly in cell and gene therapy manufacturing.
- A network of professional connections within the CGT sector.
- A clearer vision of career opportunities in biomanufacturing, quality, or supply chain functions.
- A certificate of completion and reference from Q-Gen upon successful completion of the placement.

Medical Research Opportunities

Join one of the largest medical research institutes in Australia.
The options for students to be part of QIMR Berghofer are:

A Research Higher Degree Student at QIMR Berghofer (PhD, MPhil, Masters Coursework or Honours)

We have a wide range of student projects, and many can be tailored to a student's research interests. Some projects have the flexibility required for clinical students.

B Clinical Research Rotation – Royal Brisbane and Women's Hospital

The clinical research rotation for Junior/Senior House Officers is a unique opportunity to gain insight and skills in research methodology, study design, data analysis and evidence-based medicine, while contributing to meaningful projects that can improve patient care and outcomes.

C Vacation Research Program

Through The University of Queensland, Queensland University of Technology, and Australian Catholic University, we offer vacation research experience. These are small projects carried out over a 4-8 week period during the university summer (November-February) breaks giving students research experience and some financial support.

D Volunteer Program

Students who have an interest in medical research and would like to gain some experience can apply to be a research volunteer. This is not association with any university course. These unpaid placements run for a limited period of time and acceptance is at the discretion of QIMR Berghofer.

General info: qimrb.edu.au
University students webpage: qimrb.edu.au/people-and-careers
Projects webpage: qimrb.edu.au/student-projects
Further enquiries: GraduateEducation@qimrb.edu.au

Quick Admissions Guide for Students

1. Check you are eligible for the degree you are interested in undertaking. This is specific to the university you are enrolling with.
2. Check the QIMR Berghofer website and identify a Student Project or Research Laboratory that matches your research interests.
3. Contact the QIMR Berghofer scientist via email providing the following information:
   i) Whether you want to undertake Honours, MPhil, or PhD study.
   ii) Discuss your research interests and any previous research experience.
   iii) Provide your academic CV and university transcript.
4. Arrange to meet in person or have a Teams/Zoom interview. If a supervisor accepts you as a student, then continue the rest of the steps below.
5. Enrol through an Australian university. *
6. Complete the admission process to QIMR Berghofer. An approval notification will be sent to you via email.
7. International students must also have an appropriate visa from the Australian Department of Home Affairs. #
8. Provide evidence of full admission/enrolment to an Australian university and scholarship (if applicable).

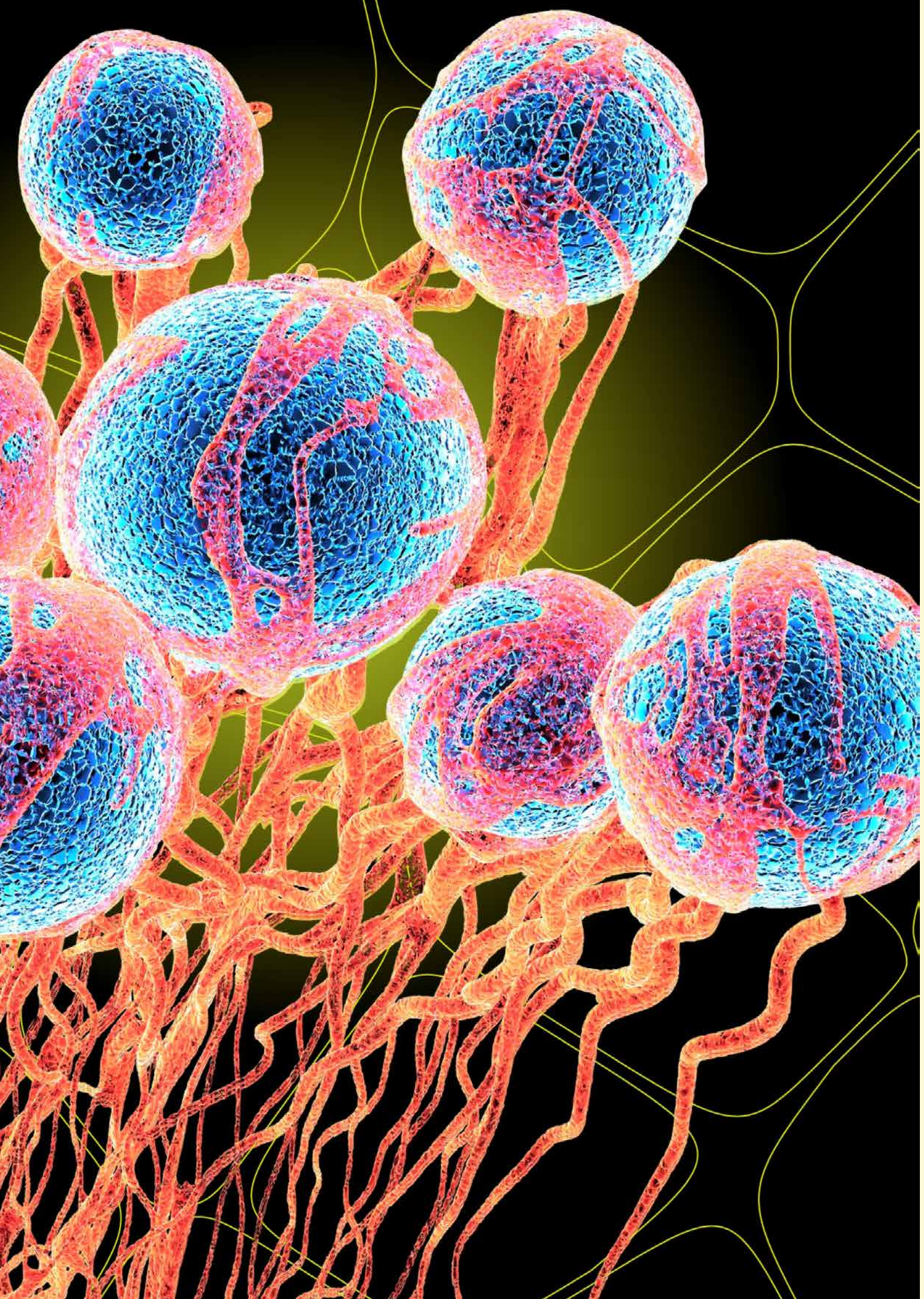
Congratulations, you are ready to begin your candidature!

PLEASE NOTE: This is only a BRIEF GUIDE and it is your responsibility to familiarise yourself with the details or requirements for each step.

**IMPORTANT: Apply for admission to QIMR Berghofer and your chosen university at the same time. Many university departments will not approve your application until you have at least provisional approval from QIMR Berghofer.*

 # This process may take up to 12 weeks to finalise, and this should be taken into consideration when determining your start date.

General info: qimrb.edu.au
University students webpage: qimrb.edu.au/people-and-careers/student-admission-process
Projects webpage: qimrb.edu.au/student-projects
Further enquiries: GraduateEducation@qimrb.edu.au



Cancer Program

At QIMR Berghofer, our leading cancer researchers are developing new techniques that will help us to understand, prevent, detect, and treat cancer, a leading cause of death in Australia.

Cancer cases are expected to grow to 185,000 per year over the next decade as Australia's population ages. It is the second most common cause of death, exceeded only by cardiovascular disease.

Our researchers are working on a number of projects that include:

- Prevention: identifying specific modifiable environmental and genetic factors that reduce a person's risk of developing cancer.
- Detection: developing better screening tests, so that cancer can be detected earlier.
- Treatment: identifying better treatments and conducting clinical trials to test for effectiveness.

Although overall cancer survival rates have improved in the past 20 years, several types of cancer have poor five-year survival rates. These include ovarian, brain, oesophageal, lung, pancreas and colorectal cancer. Our research at the Institute is aimed at developing a better understanding of who is at risk of particular types of cancer and how treatment options can be tailored and more effective.

Our researchers continue to pioneer novel strategies and treatments across a broad range of cancers to help save lives and improve the quality of treatment.

B-lymphocytes in Autoimmunity and Malignancies

Emeritus Fellow: Professor Fabienne Mackay

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qimrb.edu.au/researchers-and-labs/b-lymphocytes-in-autoimmunity-and-malignancies

The B-lymphocytes in Autoimmunity and Malignancies Laboratory studies the immunobiology of B-lymphocytes, particularly the B cell survival factors BAFF and APRIL and their receptors BAFF-R, TACI and BCMA.

Professor Fabienne Mackay has shown that excess BAFF leads to autoimmunity in mice and is associated with human autoimmunity, in particular systemic lupus erythematosus (SLE). This has encouraged the development of Belimumab, a therapeutic BAFF-blocking antibody that has been approved for use in SLE in the clinic. The laboratory's effort has been extended to understand how dietary interventions lower the risk of developing SLE and how diet/dietary metabolites can be used as therapeutic modalities.

Another research area of the laboratory is chronic lymphocytic leukaemia (CLL), a blood cancer caused by the clonal expansion of mature B cells. Patients with CLL show severe systemic immunodeficiency that results in death in a quarter of CLL patients despite therapeutic intervention. Our laboratory has shown that CLL cells rely on BAFF/APRIL to suppress the immune system through IL-10 production.

We aim to identify novel therapeutic targets that will be able to restore patient immune function in CLL and halt CLL progression. Hence, the laboratory is developing a therapeutic antibody against CLL which would not compromise the host's protective immunity.

In an attempt to identify a novel therapeutic target for CLL, we have identified that a fat-rich diet halts CLL progression. We are now investigating the cellular and molecular mechanism underlying this protection against CLL.

Functional Cancer Genomics and Functional Genetics

Senior Group Leader: Professor Stacey Edwards

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qimrb.edu.au/researchers-and-labs/functional-cancer-genomics

The Functional Cancer Genomics Group is focused on identifying new therapeutic targets for breast and ovarian cancer.

We are particularly interested in those targets that have genetic evidence linking a DNA variant to risk of the cancers. Most risk variants fall in noncoding regions of the genome and are enriched in DNA regulatory elements such as enhancers, which can be located hundreds of kilobases away from their target genes.

The noncoding genome also serves as a template for the transcription of long noncoding RNAs (lncRNAs), which often show cell-type-specific expression and function, making them exceptional drug targets.

We integrate genetic information with a diverse range of sophisticated molecular approaches to identify and evaluate protein-coding genes and lncRNAs that are driving cancer development.

Senior Group Leader and Program Director (Cancer): Professor Juliet French

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The Functional Genetics Laboratory combines genetics and functional genomics to pinpoint the key genes and pathways implicated in the development of both breast and ovarian cancers.

We are interested in understanding how inherited and/or acquired genetic variants located in noncoding DNA contribute to cancer development. More particularly, we investigate regions that are either transcribed into functional RNAs such as long noncoding RNAs (lncRNAs) or those that act as DNA regulatory elements such as enhancers.

Identifying the lncRNAs affected by noncoding genetic variants and the protein coding genes they regulate is necessary to identify therapeutic opportunities for primary and secondary cancer prevention. These can be achieved by identifying novel targets or using existing therapies that can be repurposed for the prevention or treatment of either breast and ovarian cancers.

Evaluation of new long-noncoding RNAs driving breast or ovarian cancer development.

This project is suitable for an Honours or PhD student.

BACKGROUND

It is now clear the majority of the human genome is transcribed from both DNA strands but only 2% encodes protein. Much of this transcription is derived from DNA sequences that do not encode functional proteins. The majority of these transcripts are long non-coding RNAs (lncRNAs) defined as being >200 bp in length. While it is generally accepted lncRNA transcription is functionally significant, the scope and function of lncRNAs in cancer is still not well understood.

Genome wide association studies (GWAS) have identified thousands of common variants association with an increased risk of breast and ovarian cancers. Large-scale genome sequencing projects have also identified regions of the genome that are frequently mutated in breast and ovarian cancers. Importantly, the majority of these disease-association variants and mutations lie within intergenic regions and introns of protein-coding genes, suggesting that undiscovered RNA transcripts such as lncRNAs, may play a direct role in cancer development.

AIM

We have recently used RNA sequencing and bioinformatic approaches to identify hundreds of new cancer-related lncRNAs. We now want to understand how these lncRNAs modulate breast and ovarian cancer development.

METHODS

Projects will use multiple in vitro approaches to determine how the variants and mutations alter lncRNA function, including CRISPR-based lncRNA editing and reporter assays. We will link lncRNAs to their target protein-coding genes using HiChIP chromatin assays and CROP-seq experiments. We expect that some of the lncRNAs will have cancer-related biological functions. We will therefore overexpress or silence lncRNAs in breast and ovarian cancer cells and examine their effects on cell growth, response to DNA damage, apoptosis, migration and tumour formation. We will also assess the function of lncRNAs in tumour formation using an explant assays in mice. The discovery of novel regulatory lncRNAs influencing cancer development may reveal entirely new avenues for breast and ovarian cancer therapeutics.

Students will have access to unique expertise and reagents, and will acquire skills in tissue culture, CRISPR-based methods, RNA and DNA manipulation, confocal microscopy, FACS analyses and other molecular biology techniques.

Molecular Oncology

Team Head: Associate Professor Olga Kondrashova

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qimrb.edu.au/researchers-and-labs/molecular-oncology

We utilise advanced bioinformatic and machine learning methodologies to analyse a variety of cancer data types, including genomic, transcriptomic and DNA methylation data. This analysis allows us to understand how different cancers respond to treatments and influence patient outcomes.

A large part of our work involves studying pre-clinical cancer models to ensure their accurate representation of human disease, thereby enabling the discovery of treatment strategies and biomarkers that can be translated into clinic.

Our research spans multiple solid cancer types, including ovarian, endometrial, breast and lung cancer. Our work is highly collaborative; we partner with several clinical and molecular cancer laboratories to facilitate the most translatable research.

Re-sensitising treatment resistant metastatic ovarian cancer.

Co-supervisor: Associate Professor Jacinta Simmons

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High grade serous ovarian cancer is most often detected after it has moved away from the ovaries and fallopian tubes, where it is harder to treat and almost always becomes resistant to current treatments. Standard therapy relies on tumour cells being unable to accurately repair DNA damage due to mutations in common DNA damage response genes. Resistance to treatment occurs when tumour cells gain further mutations to bypass or repair mutated genes to re-enable accurate DNA repair.

The project will employ CRISPR screening, cell and molecular biology techniques to investigate mechanisms of resistance and identify novel strategies for re-sensitising ovarian cancer to therapy.

Translational Cancer Immunotherapy

Group Leader: Associate Professor Siok Tey

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The Translational Cancer Immunotherapy Laboratory investigates the means by which the immune response can be harnessed to control cancer. Our team of biomedical and clinical scientists have a strong focus in translating basic science knowledge into new therapies that can be taken to clinical trial.

Bone marrow transplantation is the most established form of cancer immunotherapy and has been a longstanding interest of our lab. Its curative potential resides in the donor T cells, which are very effective in recognising and eradicating cancer cells. However, these T cells can also attack vital tissues, and the resulting organ damage. Known as graft-versus-host disease (GVHD) is a major source of transplant-related morbidity and mortality. Our research seeks to enhance the anti-tumour response and attenuate GVHD through T cell engineering. These include the use of "safety switches" to enable T cells to be deleted in the setting of GVHD and the use of regulatory T cells (Tregs) to attenuate GVHD.

Our above experience in T cell engineering has led to our current research focus in Chimeric Antigen Receptor (CAR) T cell therapy. CAR T cells are gene-modified immune cells (T cells) that can recognise specific surface proteins on tumour cells. They can be very effective in killing these tumour cells and can cure up to 50% of certain blood cancers. Our laboratory is developing new CARs with the aims of making them more effective and accessible. These include CAR T cells directed at blood cancers and childhood cancers. In collaboration with the Royal Brisbane and Women's Hospital, we are one of only a few groups in Australia with the capacity to make clinical grade CAR T cells on campus and take them to clinical trial.

CAR T cells - redirecting T cells for cancer immunotherapy.

This project is suitable for Honours, Masters and PhD students.

BACKGROUND

Chimeric Antigen Receptors (CARs) are genetically engineered molecules that can redirect T cells to recognise particular antigens, such as those expressed by cancer cells. T cells that are transduced by CAR targeting CD19 have been effective in treating B cell cancers, e.g. B-cell leukaemia and lymphoma, where conventional treatments have failed.

This exciting technology is one of the major breakthroughs in cancer therapy this decade. However, not all patients respond, not all responses are durable and there is limited success to date in CAR T cells targeting solid cancers.

This project involves developing and testing new concepts in CAR T cell engineering to make them more effective, safer and more able to target solid cancers. Our laboratory is involved in preclinical development, through to research translation and early phase clinical trials. There is also an opportunity for students to be involved in clinical correlative research to better understand the immunobiological determinants of clinical response and toxicity.

AIM

The overarching aim of this project is to develop safer and more effective CAR T cell therapies for blood cancers and solid cancers, and take these to early phase clinical trials.

This is achieved through several interrelated projects with the following aims:

- To investigate how CAR T cell function can be modulated by changing individual components within the CAR transgene.
- To optimise methods for the clinical scale manufacture of CAR T cells as a precursor to future clinical trials.
- To examine the longitudinal fate of CAR T cells and the bystander immune compartment in patients undergoing CAR T cell therapy.

APPROACH

We use a range of immunology, molecular biology and cell therapy approaches to achieve these aims. Not all projects will involve all these approaches. Immunology techniques include cell culture, multiparametric flow cytometry (including spectral cytometry), live-cell imaging and a range of in vitro immunological assays (e.g. ELISA, cytokine bead array). Some projects will involve in vivo experiments using mouse models, and some projects will involve analysis of clinical samples. Molecular techniques include CAR gene design and cloning, and CRISPR/Cas9 gene knock-out. Cell therapy technology includes generation of viral vectors, small-to-large scale cell processing, including the use of clean room suites within the Good Manufacturing Practice (GMP) facility.

PROJECT POTENTIAL

The project is suitable for biomedical scientists and clinicians who are interested in wet lab research.

Students will have the opportunity to work on different phases of the development of a novel cell and gene therapeutic. All students will have the opportunity to work on the preclinical development and testing of novel CARs. Masters or PhD students may have the opportunity to work on clinical scale-up and technology transfer to Good Manufacturing Practice facility. PhD students may also have the opportunity to take a technology through to early phase clinical trial.

Understanding the immunobiology of bone marrow transplantation.

Co-supervisor: Dr Andrea Henden

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This project is suitable for an Honours or Masters student.

BACKGROUND

Bone Marrow Transplant (BMT) offers cure to patients with aggressive blood cancers. Its efficacy lies in the ability of the newly transplanted immune system to recognize and destroy recipient malignant cells as foreign, a phenomena known as Graft-versus-Malignancy (GVM). However, if healthy cells and tissues are targeted the complication of Graft-versus-Host disease (GVHD) occurs. Post-transplant all patients are managed with immunosuppression to control the balance between GVM and GVHD, however immunosuppression brings risk of infection and poor response to vaccines. Each of these complications are mediated by immune control, and new therapies to manipulate immunity post-transplant are required. This project will examine a number of factors influencing T cell function in the context of transplantation and the effects on GVM and GVHD, with a focus on translational research and the development of potential new therapies.

AIM

- To examine the impact of the gastrointestinal microbiome on T cell function and GVHD.
- To examine the fate of T cell and non-T cell immune populations after BMT and the impact of viral infection and cytokines on immune reconstitution.

METHODS

- Immunophenotyping including flow cytometry and spectral cytometry.
- Measurement of soluble immune mediators.
- Correlation with clinical outcome data.

Cancer Genetic Susceptibility

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The Cancer Genetic Susceptibility laboratory primarily studies the role of genetics in endometrial cancer risk and development. Our team leads large-scale genetic studies for endometrial cancer and uses these data to answer a variety of research questions falling under three main themes: prevention, prediction and treatment.

Transplantation Immunology

Team Head: Associate Professor Antiopi Varelias

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Stem cell transplantation is considered the "gold standard" procedure for the treatment of blood cancers (including leukaemia, lymphoma and myeloma) in both adults and children. Globally, over 9,000 patients per year undergo this high-risk, life-saving therapy.

However, graft-versus-host disease (GVHD) occurs in 50–70% of patients, of which 20% will develop severe GVHD that is untreatable. Unfortunately, additional complications such as infection and cancer relapse are common.

Research conducted by the Transplantation Immunology Laboratory focuses on improving our understanding of the pathophysiology of complications following stem cell transplantation. Using unique pre-clinical models combined with innovative technologies, the group aims to define the immunological mechanisms that underpin these complex disease processes, with the view of translating the basic research findings into clinical practice.

Harnessing the gut microbiome to improve stem cell transplantation.

Aspects of this project would be suitable for Honours, Masters, MPhil, MD and PhD students. Email the supervisor to discuss suitability.

BACKGROUND

Haematopoietic stem cell transplantation (HSCT) is considered the gold standard procedure for the treatment of high-risk blood cancers. However, graft-versus-host disease (GVHD) remains a barrier to the success of this life-saving immunotherapy. GVHD occurs in 50-70% of transplanted patients, of which 20% will develop severe GVHD which is unresponsive to therapy and is eventually fatal. Thus there is an urgent need for new treatments. Systemic exposure to gut microbes (and their derivatives) which are normally sequestered in the lumen, are initiated by chemotherapy/radiation treatment prior to transplant and can have profound effects on GVHD severity. Antibiotic-based approaches to deplete the microbiome and prevent acute GVHD have been partially successful, however increasing antibiotic resistance and the realization that many bacteria have important anti-inflammatory properties severely limits this approach.

AIM

This project aims to improve our fundamental understanding of microbial-host interactions which regulate protective and pathogenic mechanisms after transplant.

Understanding infectious respiratory complications after stem cell transplantation.

Aspects of this project would be suitable for Honours, Masters, MPhil, MD and PhD students. Email the supervisor to discuss suitability.

BACKGROUND

Respiratory viral infections are a major global public health problem. RSV-induced bronchiolitis and pneumonia are the leading cause of hospitalization in infants and young children worldwide, while in adult allogeneic hematopoietic stem cell transplant (HSCT) recipients the incidence of progression from upper to lower respiratory tract infection is 40-60%, with mortality rates as high as 80%. With the lack of efficacious antivirals, new treatment options are needed. Given the paucity of mechanistic data to guide clinical studies or define the basis of disease, we established a murine model of RSV infection after SCT using pneumonia virus of mice (PVM), the murine homologue of human RSV, to address the knowledge gaps in the field.

AIM

This project aims to investigate fundamental immunological mechanisms which underlie the RSV-mediated post-transplant complication.

PROJECT POTENTIAL

This research will lead to the delineation of critical mechanisms which underpin fatal pneumonitis, and the identification of potential therapeutic targets to ameliorate RSV-driven HSCT transplant mortality.

Identifying novel MAIT cell expansion strategies to mitigate graft-versus-host disease.

Aspects of this project would be suitable for Honours, Masters, MPhil, MD and PhD students. Email the supervisor to discuss suitability.

BACKGROUND

Mucosal-associated invariant T cells (MAIT cells) are an important regulatory subset which possess potent antimicrobial functions, primarily due to their rapid, diverse and expansive cytokine production.

Initially, MAIT cells were shown to respond to vitamin Bderived microbial metabolites presented by the MHC class I-like molecule MR1, however increasing evidence now shows activation via MR1-independent mechanisms such as cytokine-mediated pathways. We have shown recipient MAIT cells control gut barrier function, in part via interleukin-17A, to attenuate pathogenic T cell responses in the colon and protect against the development of acute graft-versus-host disease.

AIM

This project aims to validate newly identified candidates that expand MAIT cells in vivo.

PROJECT POTENTIAL

This translationally-focused research builds on strong preclinical findings and is pertinent for the development of MAIT cell-based immunotherapeutic approaches to treat gut GVHD in the clinic.

In situ immune cell profiling using spatial transcriptomics in gastrointestinal graft-versus-host disease.

Aspects of this project would be suitable for Honours, Masters, MPhil, MD and PhD students. Email the supervisor to discuss suitability.

BACKGROUND

Acute gastrointestinal graft-versus-host disease (GVHD) is a common, life-threatening complication following allogeneic haematopoietic stem cell transplantation. Gut GVHD occurs when donor-derived T-cells traffic to host GI tract tissue in response to cytokine release during conditioning chemotherapy, resulting in T cell mediated apoptosis of GI tract mucosa. Early identification of patients at greatest risk of gut GVHD would allow for trials of early escalation of immune-suppressing treatment to prevent gut GVHD onset or ameliorate its severity. Currently, there is a lack of predictive tools for the early detection of acute gut GVHD. Although blood based biomarkers are relatively easily obtained, they are often less informative compared with tissue-based biomarkers.

AIM

This project aims to examine the feasibility of applying spatial transcriptomics in the diagnosis and prognostication of acute gut GVHD.

PROJECT POTENTIAL

This research will generate tissue specific cellular transcriptomic signatures that may serve as potential biomarkers to improve early acute gut GVHD diagnosis and prognostication.

Cancer Neuroscience

Team head: Associate Professor Lachlan Harris

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At the core of the Cancer Neuroscience Laboratory is a focus on researching cellular quiescence, a reversible hibernation-like state, adopted by brain cancer cells to evade chemotherapy and radiotherapy. By targeting these quiescent cells, we might overcome treatment resistance and improve outcomes for persons with glioblastoma.

To identify novel therapeutic approaches to target quiescence, the laboratory also focuses on understanding how quiescence is regulated in normal neural stem cells in the memory centres of our brains.

- Brain cancer – targeting treatment resistant, quiescent cancer stem cell populations through direct targeting, reactivation or suppression strategies.
- Modelling – determining the most effective approaches (direct targeting, reactivation, suppression) to target treatment resistant, quiescent cancer stem cell populations.
- Metabolism – its impact on quiescent brain cancer stem cells and normal adult neural stem cell populations.
- Healthy adult neural stem cell quiescence – identifying novel regulators, with a focus on calcium binding proteins.
- Dysfunction of adult neural stem cell quiescence during the aging process, and its possible role in cognitive disorders such as depression and anxiety.

Should I stay, or should I go? How brain stem cells decide to leave quiescence.

This project is suitable for an Honours or PhD student - multiple projects available.

BACKGROUND

Quiescence is a type of reversible cell-cycle arrest displayed by many resident tissue stem cell populations, which helps to ensure we have a lifelong population of stem cells to maintain tissue homeostasis, respond to injury and other stimuli. One region where these stem cells exist is in the brain. In mice, a major model organism, there are two main stem cell niches in the adult brain. These are the subgranular zone of the hippocampus and the subventricular zone lining the lateral ventricles of the forebrain. When quiescent neural stem cells in these regions activate, they generate neurons that function in memory, spatial navigation and odour discrimination. Similar neural stem cell populations with similar functions exist in the human brain.

AIM

This project aims to uncover novel molecular regulators of brain stem cell quiescence.

METHODS

One prism through which this will be explored, is by interrogating how brain stem cells enter deeper quiescence during the aging process. The project will employ a range of techniques using aged wildtype mice, genetically modified mice and primary neural stem cell cultures derived from the hippocampus and subventricular zone of postnatal/adult mice.

OUTCOMES

The outcomes of this project are expected to shed light on how quiescence is regulated. The genes/cellular processes we identify as being important in quiescence can then be explored in the context of diseases where adult neurogenesis is disrupted, for example during aging and major depressive disorder. Likewise, these findings will also be of interest to brain cancer research, where quiescence is frequently co-opted by cancer stem cells to evade therapies. Specifically, this project will:

1. Establish the role of a novel group of calcium-binding proteins in deciphering activation/proliferation cues using in vitro and in vivo models.
2. Determine if decreased expression of these proteins explains why quiescence deepens during aging and
3. Determine if these proteins are functionally important in the progression of brain cancers, with a specific focus on quiescence and treatment resistance.

Improving survival for adult brain cancer patients by targeting 'sleeping' cancer stem cells.

This project is suitable for an Honours or PhD student - multiple projects available.

Glioblastoma (GBM) is the most common malignant primary brain tumour in adults and is inevitably fatal, with a median survival of just 15-months after diagnosis. Standard treatment involves surgical resection, postoperative radiation and chemotherapy. Unfortunately, significant populations of resistant glioma stem cells remain after chemotherapy, these cells regrow the tumour, and patients ultimately succumb to the illness. Glioma stem cells resist treatment in part because they are in a state of cellular sleep, known as quiescence. The quiescence of glioma stem cells means they divide very rarely, whereas current chemotherapy preferentially targets fast-dividing tumour cells. A common strategy in cancer research is to combine chemotherapy with drugs that slow tumour growth. However, this approach often increases the resistance of tumours as it forces more cells into quiescence. The innovative research program Dr Harris is developing is to target quiescent GSCs by leveraging unique features of quiescence and turning them into therapeutic vulnerabilities.

Leukemia Research Laboratory

Group Leader: Professor Steven Lane

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The Leukaemia Research Laboratory is researching myeloid blood cancers that include acute myeloid leukaemia (AML), myelodysplastic syndrome (MDS) and myeloproliferative neoplasms (MPN) as part of its translational leukaemia research work.

These very aggressive and rapidly fatal blood cancers are among the most common types of cancer affecting Australians. The laboratory's efforts concentrate on understanding how leukaemia stem cells in AML and MPN are able to regenerate leukaemia (or cause relapse in patients), even after cytotoxic chemotherapy.

Research has focused on generating robust models of leukaemia and dissecting the pathways of self-renewal in leukaemia stem cells and normal blood stem cells.

The group aims to tailor treatments for individual patients, identify new drug pathways and explore repurposing existing drugs to target resistant leukaemia types.

Mapping the malignant niche: Uncovering vulnerabilities in myeloproliferative neoplasms driving stem cells.

Co-supervisor: Dr Jasmin Straube

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This project is suitable for Honours, Master's, MPhil, MD, or PhD students with a background in bioinformatics.

BACKGROUND

Myeloproliferative neoplasms (MPNs) are chronic blood cancers that are currently incurable and are driven by mutated hematopoietic stem cells (HSCs). Although patients can live with MPN for many years, the disease has the potential to progress to rapidly fatal myelofibrosis or acute leukemia.

Emerging evidence indicates that MPN-driving HSCs remodel their surrounding microenvironment. This alteration affects interactions with stromal, endothelial, and immune cells, creating a protective niche that supports malignant cell survival at the expense of healthy HSCs. Disrupting these pathogenic interactions may make MPN stem cells vulnerable to eradication.

To investigate these interactions, we conducted spatial transcriptomic profiling using the Xenium platform in our murine MPN model. These data capture cell-type-specific expression and spatial organization, providing a robust foundation for understanding MPN niche remodeling and identifying therapeutic vulnerabilities.

AIM

1. Define the MPN bone marrow niche cellular composition.
2. Locate MPN stem cells and their cellular neighborhoods.
3. Identify spatially-resolved molecular interactions between MPN stem cells and niche-supporting cells.

METHODS

We will explore cellular segmentation algorithms to deconvolute small and large cell types. You will integrate single-cell RNA sequencing and spatial sequencing (Xenium) data from the bone marrow of our MPN murine model using dimension-reduction methods to annotate cells and to create an MPN bone marrow atlas. We will determine the spatial proximity patterns between malignant HSCs and niche subsets using spatial statistics, such as spatial autocorrelation. We will assess how disease progression and treatment alter these spatial relationships. Additionally, we will evaluate ligand-receptor pairs that mediate malignant HSC survival and highlight potentially actionable interactions, such as cytokine signaling pathways and adhesion molecules. Finally, we will cross-reference our murine findings with human MPN datasets to prioritize interactions that are conserved in human disease for translational relevance.

PROJECT POTENTIAL

This project has the potential to transform our understanding of the MPN stem cell niche and identify therapeutic strategies that directly target disease-driving HSCs, addressing an unmet need in current clinical practice.

The Genome Variation and Regulation in Disease

Team Head: Associate Professor Jonathan Beesley

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My team in the Genome Variation and Regulation in Disease Laboratory are interested in how human genetics contributes to disease and how we can use these discoveries to find better treatments. We integrate large-scale genetic and functional genomics data to guide computational analyses and laboratory experiments. We are using a diverse array of approaches including pooled functional genetic screens, multiplex reporter assays, and genome editing to pinpoint the causal genetic changes, their target genes and pathways, and the cell types in which they act.

Identifying the causal genes at cancer risk loci.

This project is suitable for an Honours or PhD student.

BACKGROUND

Genome-wide association studies (GWAS) have identified thousands of genetic variants association with cancers and other complex diseases. However, most risk variants lie in non-coding regions of the genome, making it challenging to determine which genes they regulate and how they influence disease biology.

Our laboratory combines human genetics with functional genomics to uncover the molecular mechanisms underlying genetic risk. We integrate large-scale sequencing datasets (e.g. single-cell chromatin accessibility, transcriptomics, chromatin interaction data) with statistical and computational approaches to move from variant association to biological insight. The ultimate goal is to identify the genes, cell types, and pathways that mediate disease risk and may serve as therapeutic targets.

AIM

Depending on level and background, student projects may involve:

- Primary analysis of high-throughput functional genomics data (e.g. RNA-seq, ATAC-seq, single-cell multi-omics).
- Development and application of statistical and machine learning models to link genetic variants to regulatory function.
- Integration of genetic association data with multi-omic datasets to predict target genes at GWAS loci.
- Pathway and network analysis to identify biologically actionable mechanisms.
- Identification of candidate genes and pathways for therapeutic targeting or drug repositioning.

APPROACH

Students will gain training in:

- Statistical genetics and regulatory genomics.
- Reproducible bioinformatics workflows (R/Bioconductor/Python).
- Machine learning approaches for biological data.
- Interpretation of large-scale genomic datasets.
- Collaborative research across computational and experimental teams.

PROJECT POTENTIAL

Projects are embedded within an interdisciplinary environment, collaborating with both computational and wet-lab scientists. Findings from these studies directly inform downstream experimental validation and may contribute to identifying novel cancer genes and therapeutic strategies.

This project would suit a student with a background in bioinformatics, statistics, or genetics, with an interest in gene regulation and disease biology. Students would work closely with dry and wet lab scientists to identify cancer genes and pathways, which might represent targets for future drug development.

Functional evaluation of risk genes in early breast cancer.

BACKGROUND

Genome-wide association studies (GWAS) have identified numerous genetic loci association with breast cancer risk. However, translating these statistical

associations into biological understanding requires direct experimental interrogation of candidate genes and regulatory elements. Our laboratory investigates how inherited genetic variation contributes to the earliest stages of breast tumorigenesis. We focus particularly on early pre-invasive lesions and the cellular transitions that precede invasive disease. Using CRISPR-based genome engineering, next-generation sequencing, proteomics, and in vivo models, we functionally evaluate candidate risk genes to define their roles in epithelial transformation, cell fate, and tumour initiation.

By integrating human genetics with experimental cancer biology, this work aims to identify mechanisms driving early disease and uncover new opportunities for prevention and interception.

AIM

Depending on level and experience, student projects may involve:

- CRISPR-based gene perturbation (knockout, activation, or repression) in breast epithelial cell models.
- Functional assessment of candidate risk genes using in vivo mouse models.
- Multi-omic analysis following genetic perturbation (transcriptomics, proteomics).
- Characterisation of phenotypes relevant to early tumour development (proliferation, differentiation, invasion, immune interactions).
- Validation of candidate therapeutic vulnerabilities.

APPROACH

Students will gain hands-on training in:

- CRISPR genome editing and molecular cloning.
- Mammalian cell culture.
- In vivo models of breast cancer.
- Next-generation sequencing library preparation and analysis.
- Experimental design and translational research strategies.

PROJECT POTENTIAL

Projects are conducted within a collaborative environment that integrates genetic discovery with mechanistic experimentation. Students will work closely with computational biologists to prioritise candidate genes and with cancer biologists to evaluate functional outcomes.

This project would suit students with a background in genetics, molecular and cell biology with a strong interest in cancer biology and translational research.

Cancer Metabolism

Group Leader: Professor Nils Halberg

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The Cancer Metabolism Group is keenly interested in how the physiological state of a person affects cancers.

Over a person's lifetime, somatic cells will accumulate spontaneously occurring gene mutations, the majority of which do not cause disease. The global incidence of cancer has more than doubled over the past 30 years – primarily due to increasing living standards, modern lifestyles, and an aging population.

The common denominator for these is alterations to the physiological homeostasis of the individual at risk rather than a change in mutational burden. This strongly implies that the interaction of physiological conditions with cells harboring oncogenic mutations governs cancer risk.

The Cancer Metabolism lab utilises systems biology technologies to both clinical biobank and mouse models to dissect the molecular drivers of the intersect between physiology and tumorigenesis.

Mechanistic understanding of how obesity causes cancer.

These projects can be adapted in scope for Honours or PhD students.

Obesity increases the risk of developing thirteen types of cancer that normal weight individuals may not develop despite of harbouring the same cancer risk loci. Globally, overweight/obesity may account for 544,300 cancer cases every year and is currently implicated in 15-20% of cancer-related mortalities. This places obesity second only to smoking as the most prevalent preventable cause of cancer.

Project 1 - What are the properties of cancer cells adapted to aberrant physiological environments?

We have previously demonstrated that obesity is not association with additional oncogenic genetic alterations that could explain the increased cancer risk. Instead, we demonstrate that cancer cells undergo adaptive epigenetic remodelling and gain tumour initiating properties when exposed to prolonged periods of obese conditions. This interaction between metabolic, epigenetic, and tumorigenic events currently represents significant knowledge gaps.

AIM

- Uncover the relationship between systemic metabolic challenge as induced by physiological stressors and intracellular metabolite dynamics in cancer cells.
- Identification of the metabolites that are sufficient to drive tumour initiation – and how this is achieved.
- Determine how metabolite-driven epigenetic changes can display loci specificity.
- Discover the epigenetic, transcriptional and translational machinery required to that link physiological stressor to tumour initiation.

Key methodologies for this project are in vivo CRISPR loss- and gain-of-function screens, single cell transcriptomics and epigenomics, in vivo tumour modelling and metabolomic tracer studies.

Project 2 - How do physiological stressors affect the tumor ecosystem?

We know that stem cells are intrinsically connected to the cellular niche in which they reside and that these cellular interactions are particularly important and instructive for stem cell plasticity. In this project, we ask if an obese environment instructs the cancer stem cell niche to govern cancer cell dedifferentiation and enhanced stemness features.

AIM

- To develop a comprehensive cellular spatial map of the cancer stem cell niche in obese and non-obese cancer patients.
- To comparatively extract obesity-dependent deregulated cell abundancies and cellular interactions within such niches.
- To mechanistically dissect the causal importance of the obesity-dependent niche composition.

Key methodologies for this project are spatial interrogation of the tumour microenvironments (sequencing and proteome-based), in vivo tumour modelling and antibody-based therapeutics.

Project 3 - How does physiological stressors affect somatic fully differentiated cells of the body?

This project address two areas that we believe are currently severely understudied: 1) How does the obese phenotype affect male and female germ cells and thereby the intergenerational metabolic health and 2) How does a history of obesity affect future possibilities of cancer risk (epigenetic memory).

AIM

- Uncover the relationship between systemic metabolic challenge the epigenetic landscape of both male and female germ cells.
- Demonstrate how efficiently the obese phenotype is transferred between generations in mice.
- Conduct generational cancer studies.

Key methodologies for this project are single cell transcriptomics and epigenomics, metabolomics, mouse in vitro fertilization and advanced mouse cancer models (genetic and viral based).

Medical Genomics

Senior Group Leader: Professor Nic Waddell

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The Medical Genomics Team analyses next generation sequence data to address clinical challenges in a variety of diseases. The approaches we take include:

- Characterising cancer genomes with short and long read sequencing.
- Classification of tumours into significant subtypes.
- Identification of mutational processes that underlie tumour development.
- Determining genomic and transcriptomic features association with immune response.

Ultimately, we aim to take steps towards 'personalised medicine' to enable the diagnosis, management and treatment of patients.

Long read sequencing of cancers to identify somatic mutations and base modifications in cancer.

This project is suitable for Masters, MPhil, MD or PhD students. Preferred candidates would have some expertise in bioinformatics.

BACKGROUND

Genome sequencing of tumours has made pivotal advances in cancer research by identifying driver events mechanisms of tumorigenesis, revealing potential actionable targets and allowing researchers to begin to understand intra and inter tumour heterogeneity. Resources such as The Cancer Genome Atlas (TCGA) and the International Cancer Genome Consortia (ICGC) have sequenced thousands of cancer samples across many cancer types. These data are used extensively by researchers across the globe and have informed clinical trials into precision

medicine. Current genomic research has relied on short read sequencing technology, which typically produces sequence reads of 150 bases in length, and although valuable has some limitations. In contrast long read sequencing (LRS) is capable of producing sequence reads that are thousands of bases long.

This approach offers many advantages as it can detect and resolve mutation events that were not possible to see from short read sequencing. In addition, it enables simultaneous detection of base modifications in RNA and DNA. The role of many of these base modifications in cancer is not yet known.

APPROACH

This project will analyse long read whole genome and full-length RNA-seq data generated using a PronethION sequencer from Oxford Nanopore Technologies (ONT). The specific aims of this work are:

AIM

Aim 1 - Analyse long read whole genome sequence data from cancer samples to characterise the somatic mutations.

Aim 2 - Analyse base modifications in both whole genome and RNA-seq data..

Aim 3 - Determine whether there is an association with base modification in RNA and cell surface protein expression.

PROJECT POTENTIAL

This work will improve our understanding of cancer genomics. It will provide insights into how base modifications drive tumour development and whether they can inform cancer therapy. We anticipate this work will lead to multiple publications and conference speaking opportunities.

Sid Faithfull Brain Cancer

Group Leader: Professor Bryan Day

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Our direct focus is to investigate the biological processes critical for the development of these intractable tumours, commercialise our research findings and bring our novel antibody therapies to clinical trial to improve the lives of brain cancer patients.

The Sid Faithfull Brain Cancer Laboratory focuses on glioblastoma (GBM) which is the most common and aggressive form of adult brain cancer. GBM kills approximately 1,900 people per year in Australia. Survival rates are very poor with a median survival of approximately 15 months. Meaningful advancements in patient treatment and survival have not changed for decades. New and better treatment therapies are urgently needed.

The laboratory also studies a number of paediatric brain cancers including medulloblastoma and an incurable form of brain stem glioma called Diffuse Midline Glioma (DMG), previously known as Diffuse Intrinsic Pontine Glioma (DIPG). Our goal is to design therapies that specifically treat the tumour site while keeping the healthy developing brain intact in these young patients.

Targeting novel receptors in GBM.

Co-supervisor: Dr Rochelle D'Souza

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This project can be adapted in scope for an Honours or PhD student.

BACKGROUND

We have generated well-characterised monoclonal antibodies (mAbs) against two receptor proteins that are present on two discrete cell populations and propose to use these simultaneously to effectively target this devastating disease. By targeting two proteins specifically expressed on the tumour and not normal brain, we aim to reduce toxicity while effectively killing most of the tumour. We have conjugated the mAbs with a drug to make antibody drug conjugates (ADCs) and aim to test their killing efficacy *in vitro*.

AIM

To validate dual targeting using ADCs as an effective therapeutic strategy for GBM in vitro.

APPROACH

- *In vitro* killing assays to determine GBM cell killing and IC50.
- Apoptosis/Cell death assays.
- Flow cytometry and Western blotting.
- Immunofluorescence and confocal microscopy.

OUTCOME

Validation of novel ADCs that have anti-cancer effects in primary GBM cell line models which would then serve as a base for further validation in animal models. This would pave the way for translation into the clinic to improve outcomes for patients with GBM.

Cancer Drug Mechanisms

Group Leader and Chair of Higher Degrees Committee: Professor Glen Boyle

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The Cancer Drug Mechanisms Laboratory combines expertise in cell biology with understanding of drug mechanisms to treat cancers and other chronic diseases.

The group's cancer biology work currently focuses on understanding the development and progression of cancers of the skin and oral cavity.

Specifically, the laboratory is investigating the molecular mechanisms involved in the progression and metastasis of melanoma, head and neck cancer, as well as cutaneous squamous cell carcinoma. These mechanisms also affect drug resistance of cancers.

The identification and understanding of pathways in these cancers is crucial prior to the design or identification of suitable treatments. The group also uses its cell biology knowledge to assist in the development process for novel agents targeting cancer and other chronic disorders.

Developing small molecule inhibitors to target treatment refractory melanoma.

This project is suitable for an Honours, Masters, MPhil or PhD student.

BACKGROUND

Cutaneous melanoma is a neoplasm of melanocytes, the pigment producing cells in the skin, and is the most aggressive and lethal form of skin cancer. The incidence of melanoma has increased dramatically over the past three decades, including in Australia where it is now the fourth most commonly diagnosed cancer. It is estimated that over 16,800 Australians will be diagnosed with melanoma in 2025 and over 1,300 people will die. Metastatic dissemination of melanoma is a serious complication for the successful treatment of the disease, and represents the most common cause of death for melanoma patients.

We have identified a transcriptional program in melanoma tumour cells that triggers dissemination of melanoma cells and allows survival. The program simulates chronic interferon-γ exposure, and also results in extracellular matrix alterations. These changes have been observed in melanoma patients that are resistant to standard of care therapy. We have now linked the driver of this signature, the transcription factor BRN2, with worse patient outcome following this therapy. It is possible to directly target BRN2 binding to DNA using small molecule inhibitors. Targeting BRN2 directly increases specificity, as it is not widely expressed in normal adult tissue.

AIM

This project aims to develop novel small molecule inhibitors of BRN2 for single agent or combination therapy of patients with therapy refractory melanoma.

PROJECT POTENTIAL

Generation of novel BRN2 targeting agents could benefit melanoma patients, as well as additional cancer types where the transcription factor is highly expressed including glioblastoma and neuroendocrine prostate cancer.

Molecular Immunology

Group Leader: Associate Professor Michelle Wykes

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The Molecular Immunology Laboratory works on the immunology of infectious diseases such as malaria, as well as cancer and autoimmunity. In 2016, the laboratory discovered programmed cell death1 ligand 2 (PD-L2) was contrary to dogma, not a "brake" on the immune system, but actually an essential activator of immunity.

In 2023, the laboratory spun-out Fovero Therapeutics to develop novel immunotherapies for cancer and autoimmunity as well as diagnostics for these diseases. Fovero Therapeutics is focused on developing immunotherapies for cancers with the greatest unmet need such as MSS+ colon cancer and triple negative breast cancer.

Post-treatment Cancer Immunobiology

Group Leader: Associate Professor Jiajie (Jet) Hou

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In the light of therapy-induced or organ-specific cues in the cancer macroenvironment, the Post-treatment Cancer Immunobiology Laboratory leverages genetically modified mice and clinical samples for cellular-and-molecular immunology-based high-throughput analyses, thus delving into the mechanisms of how the acquired inflammation and epigenetic regulation impose therapy response or resistance.

In particular, they are looking at how post-treatment inflammation reshapes the function of anti-tumour T cells and other underrepresented immune populations, aimed to explore whether the underlying molecular traits can apply to tailoring T cell-based immunotherapy and new drug development.

Too much of a good thing: how post-immunotherapy inflammation compromises tumour immunity in the liver.

This project is suitable for all types of students.

BACKGROUND

Innovative immunotherapy drugs such as immune checkpoint inhibitors (ICIs) have replaced the first-line treatment for many cancers, however, their therapeutic effects on primary and secondary liver cancers are limited. Clinician researchers including myself have noticed that unwanted locoregional inflammation may lead to disease progression and therapy resistance in the liver. My research has identified a group of liver "inflammation checkpoints" that can diminish cancer-promoting inflammation and enhance anti-tumour immunity. I have also developed liver inflammation-targeted strategies to improve immunotherapy efficacy and resolve conventional therapy resistance. This project will take advantage of my years of clinical expertise in ICI resistance and my research experience in cancer-promoting inflammation, emphasising how CD8 T cells are regulated by ICI-induced liver-specific inflammation.

AIM

This project aims to investigate the post-ICI CD8 T cell trajectory in the liver and understand how intrahepatic inflammatory signals impose on T cell function. By identifying and leveraging new immune populations and molecular targets, we intend to design relevant combination strategies to orchestrate anti-tumour immunity in the liver.

APPROACH

Based on genetically modified mice and clinical samples, we will investigate the post-treatment cancer microenvironment using single-cell sequencing and multiplex immunohistochemistry. Different mouse strains will be used for tumour inoculation and drug administration. Mouse or human tissues will also be acquired for in vitro culture systems. In addition to high-throughput flow cytometry and other immunological analyses, molecular & cellular biology experiments and multi-omics methods will be applied to mechanistic exploration.

PROJECT POTENTIAL

This project will reveal a phase-and-context-dependent regulation of CD8 T cell anti-tumour immunity, potentially breaking the liver-specific barriers to immunotherapy response.

Conjoint Gastroenterology

Group Leader (Honorary): Professor Vicki Whitehall

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The Conjoint Gastroenterology Laboratory studies the molecular, clinical and pathological features of bowel cancers. Using genome wide transcriptomics, genomics and gene-editing, we have identified key drivers of bowel cancers subgroups with different clinical outcomes. Current projects are focussed on discovering new approaches to sensitising cancers to chemotherapy and immunotherapy, using in vitro patient derived organoid models and in vivo mouse models. We work closely with oncologists, surgeons and pathologists to progress our goal of developing personalised medicine strategies to inform therapeutic decisions and improve patient outcomes.

Gene Regulation & Translational Medicine

Senior Group Leader: Professor Sudha Rao

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Though all genes exist within every cell in the human body, only a defined gene expression program is executed at any time via reprogramming of the epigenome in response to environmental cues. These dynamic events are elegantly orchestrated by writer and eraser enzymes; generating a 'histone code' within the epigenetic landscape of genes. The therapeutic implications of targeting novel domains of epigenetic enzymes are beginning to be appreciated in immuno-oncology.

The laboratory's focus on immune-oncology is on metastatic cancers and potential implications for viral therapy and the immune response in the aged population. We are also addressing the potential implications for the utility of epi-therapy in combination with immunotherapy and chemotherapy for a variety of metastatic cancers. My team is in the process of developing sensitive liquid biopsies using our newly identified novel biomarkers for patient responsiveness to immunotherapy in the context of the tumour microenvironment. We are also in the process of developing clinical based epigenetic platforms for drug screening and biomarker discovery in collaboration with global technology partnerships.

Population Health Program

Our Population Health Program and its team is dedicated to understanding the factors influencing the health and wellbeing outcomes of all Australians and our regional neighbours.

Drawing on the expertise of our clinical scientists, epidemiologists, health economists, and specialist researchers, we examine the causes of disease, their transmission, and identify patterns and changes in the health of the population. This knowledge is used to develop measures to control and prevent diseases, increase early detection and improve treatments to ensure the best possible health outcomes.

The research we do is diverse. It ranges from examining the role of vitamin D supplementation in health outcomes to reducing the incidence of mosquito-borne illnesses and other tropical diseases, and from identifying environmental and genetic risk factors for disease to improving the wellbeing of those caring for cancer patients and evaluating the social and economic consequences of disease.

Our studies are helping develop treatment guidelines to ensure all patients receive the best possible care, prevent hospital admissions, improve well-being and reduce mortality.

The Population Health Program is guided by the ultimate goal of preventing ill-health in communities and improving patient care, quality of life, and survival rates, so that all Australians and our regional neighbours have the opportunity to enjoy good health.

Gynaecological Cancers

Distinguished Scientist: Professor Penelope Webb

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The Gynaecological Cancers Group studies the epidemiology of gynaecological cancers, particularly ovarian and endometrial cancers, from aetiology to diagnosis, patterns of care, quality of life and survival.

A particular focus is on the role of environmental (non-genetic) factors in the causation and prognosis of ovarian and endometrial cancer. Much of this work is conducted within two national record-linkage studies (OVARIAN and CURVVE), three national studies (AOCS, ANECS and OPAL) and two international consortia.

Genomics, Imaging, and AI

Team Head: Associate Professor Puya Gharahkhani

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The Genomics, Imaging, and AI Laboratory is part of the Population Health Program. With a primary focus on neurodegenerative disorders of the eye and brain, particularly glaucoma, macular degeneration, dementia, and Parkinson's disease, the lab employs statistical genetics and machine learning methodologies to advance gene discovery and improve risk prediction for these diseases.

Currently, the lab is leading groundbreaking projects that integrate diverse modalities through innovative multimodal AI approaches, aimed at enhancing risk prediction for various diseases. The lab also boasts exciting collaborations with industry partners in both clinical and machine learning analytical domains.

Early detection of neurodegenerative disorders using artificial intelligence.

This project is suitable for full-time PhD students with expertise in artificial intelligence and data analysis.

BACKGROUND

Research studies focused on neurodegenerative diseases affecting the eye and brain, such as glaucoma, dementia, and Parkinson's disease. Early detection and intervention play a crucial role in managing the risks for developing these conditions.

Our ongoing studies utilise machine learning and statistical methods to analyse existing ocular imaging, neuroimaging, genetics, and digital biomarkers. We aim to enhance the prediction of risks association with these conditions.

Cancer Control

Distinguished Scientist: Professor David Whiteman AM

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Research undertaken by the Cancer Control Group is conducted with a view to reducing the burden from cancer through identifying risk factors, then translating these research findings into policy and practice.

This includes research to identify the environmental and genetic factors that cause cancer, as well as research into early diagnosis, treatment and survival.

The group had two major areas of research focus: melanoma and skin cancer, and upper gastrointestinal neoplasia.

Cancer Aetiology and Prevention

Senior Group Leader: Professor Rachel Neale

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The Cancer Aetiology and Prevention Laboratory focuses primarily on understanding the health benefits of vitamin D supplementation, balancing the risks and benefits of sun exposure and reducing the impact of pancreatic cancer.

Sun Balance: Balancing the harms and benefits of sun exposure.

This project can be adapted in scope to suit honours, masters, MPhil, or PhD projects.

BACKGROUND

The sun has both harms and benefits. QIMR Berghofer led the development of a new position statement, that includes advice specific to people's risk of skin cancer and where they live. We now need to work out how best to communicate this advice. The Sun Balance project will use co-design methods to design educational materials specific to different settings and populations, then conduct a randomised controlled trial to test their effectiveness and implementation.

METHODS

The project will include qualitative and quantitative methods. We can devise projects that meet the interests of prospective students.

PROJECT POTENTIAL

Sun Balance will ultimately lead to new ways of helping people implement strategies to enable them to gain the benefits of sun exposure while avoiding the harm.

SUNWISE – Skin cancer, UV exposure, nutrition, and vitamin D in Australia.

This project is suitable for MPhil or PhD students.

BACKGROUND

Nonmelanoma skin cancer, almost all of which are keratinocyte cancers (KCs, squamous and basal carcinomas), is Australia's most frequent and costly cancer. Although the vast majority of KCs are localised and easily treated, about half as many people die from NMSC as from melanoma. Despite these sobering statistics, these cancers are not consistently included in cancer registries and we have little information about subgroups of the population that are at risk of developing and dying from NMSC. While most NMSCs are caused by exposing the skin to the sun, ultraviolet (UV) radiation also has benefits, most notably production of vitamin D. Despite Australia being the skin cancer capital of the world, approximately 20% of the population is vitamin D deficient overall, and over 40% of people in southern states are deficient in winter. Given the role of vitamin D in a wide range of health outcomes, it is vital to develop policy that avoids vitamin D deficiency in the majority of the population. Understanding factors influencing NMSC incidence and mortality and vitamin D in Australia is needed to inform decisions about who should undergo regular screening of their skin, and also to enable evidence-based recommendations about sun exposure, sun protection, and balancing the harms with the benefits of sun exposure.

AIM

We plan to use national linked data to explore the epidemiology of skin cancer and vitamin D deficiency in Australia.

METHODS

This study will involve analysis or large existing linked datasets.

Kidney Data Collaborative

Supervisor: Dr Eoin O'Sullivan

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Kidney Data Collaborative: Serological, spatial and clinical trajectories in ANCA-association vasculitis.

This project is suitable for an Honours, Masters, or MPhil student.

BACKGROUND

ANCA-association vasculitis is a relapsing autoimmune disease with substantial morbidity and mortality. While serological monitoring is routine, the longitudinal behaviour of ANCA titres and their geographic distribution across Queensland are incompletely characterised. Integration of laboratory, hospital, medication and spatial datasets within the Kidney Data Collaborative enables robust evaluation of disease trajectories and novel risk factors, at scale.

AIM

1. To characterise longitudinal ANCA serological patterns and phenotype stability.
2. To examine spatial clustering and geographic variation in ANCA positivity and confirmed vasculitis.
3. To evaluate associations between serological persistence, geographic factors and clinical outcomes including kidney failure and mortality.

METHODS

Retrospective study using linked pathology, hospital, medication and geographic datasets. Analyses will include survival modelling, state transition analysis and spatial mapping. Students will initially work with curated synthetic datasets before progressing to real-world data following governance approvals.

PROJECT POTENTIAL

This project offers strong training in clinical epidemiology, spatial modelling and translational nephrology, with clear publication potential.

BOOST-CKD: Rapid implementation of guideline-directed therapy in chronic kidney disease.

This project is a summer semester/short project for an Honours, Masters, MPhil or PhD student.

BACKGROUND

Despite strong evidence supporting renin-angiotensin system inhibitors, SGLT2 inhibitors, mineralocorticoid receptor antagonists and GLP-1 receptor agonists in CKD, real-world uptake remains suboptimal. BOOST-CKD is a structured, protocol-driven, virtual clinic model designed to rapidly initiate and optimise these therapies within routine nephrology care.

AIM

1. To evaluate feasibility and uptake of rapid, protocolised medication optimisation in CKD.
2. To assess changes in prescribing rates, dose optimisation and time to guideline-directed therapy.
3. To explore patient-level outcomes including blood pressure, albuminuria and kidney function trajectories.

METHODS

Prospective implementation study embedded within clinical practice. Students may undertake health service evaluation, quantitative outcome analysis, process evaluation, health economic analysis or qualitative assessment of patient and clinician experience, depending on level and interest.

PROJECT POTENTIAL

Direct clinical translation with strong alignment to health system improvement. Suitable for expansion into higher degree research and competitive grant pathways. High policy and implementation relevance.

Senescence signatures in chronic kidney disease.

This project is suitable for an Honours, Masters, MPhil, or PhD student.

BACKGROUND

Cellular senescence contributes to fibrosis, inflammation and progressive organ dysfunction in CKD. Transcriptomic datasets now allow interrogation of multiple senescence programmes, including cell cycle arrest, DNA damage response and inflammatory signalling, across kidney disease phenotypes.

AIM

1. To construct and validate a kidney-focused senescence scoring pipeline.
2. To compare senescence programmes across CKD phenotypes.
3. To identify candidate genes and pathways for translational targeting.

METHODS

Bioinformatic analysis of public and local single cell RNA sequencing datasets using R and Python. Pathway scoring will be applied across multiple senescence frameworks.

PROJECT POTENTIAL

Strong potential for publication and extension into multi-omics work. Suitable for computationally inclined students and higher degree research pathways.

Molecular Cancer Epidemiology

Senior Group Leader: Professor Amanda Spurdle

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The Molecular Cancer Epidemiology Laboratory is focused on translational genomics, aiming to increase the impact of genomics in health practice.

The laboratory primarily studies the epidemiology and genetics of breast, ovarian, and endometrial cancer and conditions of inherited cancer risk. Our research identifying molecular signatures of normal and tumour tissue can point to the genetic and environmental causes of these cancers.

Through studying approaches to diagnostic processes and genomic variant interpretation, our lab is improving clinical genomics application for improved patient management for other diseases.

The laboratory covers a range of projects with the themes of clinical genetics, cancer epidemiology and molecular pathology.

Evaluation of variants in known or candidate high-risk cancer genes.

Co-supervisor: Dr Aimee Davidson

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This project can be adapted in scope for an Honours or Masters student.

BACKGROUND

Panel gene testing is increasingly applied to identify the underlying genetic cause of cancer in patients with suspected hereditary cancer. Identification of a pathogenic variant directly influences clinical management for patients and their at-risk relatives, setting the path for preventative and increasingly chemotherapeutic options. Unfortunately, such testing often identifies variants with uncertain impact on function and clinical phenotype. Such variants of uncertain clinical significance create considerable difficulties for counselling and clinical management. A range of methods can be useful for assessing variants, including bioinformatic analysis, assays of mRNA and protein function, and also investigating association with clinical features such as segregation in families, age at onset /phenotype in case-control studies and tumour pathology.

AIM

To use statistical and laboratory methods to assess the clinical relevance of rare cancer gene sequence variants identified by clinical genetic testing of patients with suspected hereditary cancer, identified in Australia or through the international consortia such as ENIGMA.

APPROACH

This project will assess the effect of variants on gene/protein function using a variety of bioinformatic predictions, molecular biological assays and/or statistical analyses. Techniques may include RNA analyses using LCLs and/or constructs, protein assays in collaboration with other laboratories, pedigree analysis and simple statistical analyses of clinical factors predictive of pathogenic variant status, to develop calibrated measures of association with disease for use in multifactorial likelihood analysis.

OUTCOME

Analysis of specific variants will provide evidence regarding their pathogenicity for translation in the clinical setting. Comparison of assay results with risk will form the foundation for improving bioinformatic prediction tools and incorporating predictions and/or biological assay results in statistical models of risk prediction.

Expanding genetic diagnoses into non-coding regions of the genome.

Co-supervisor: Dr Rehan Villani

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This project is suitable for an Honours, Masters, or MD student.

BACKGROUND

A molecular diagnosis informs many aspects of treatment for a patient with an inherited condition, however current techniques provide a diagnosis in only around 25% of cases. Non-coding regions of the genome remain underrepresented in clinical cases and variants in these regions are therefore a potential source of diagnoses for undiagnosed patients. Non-coding variants remain elusive as there is insufficient evidence to predict their impact and/or disease-causality. In order to improve diagnosis in these regions, we are working to determine which of the current research tools provide sufficient evidence to predict disease-causality in a clinical setting. We are testing methods to determine how to apply bioinformatic tools with best predictive power; to provide evidence based clinical recommendations for clinical diagnostics inclusive of non-coding regions. This work will increase diagnostic yield for patients undergoing genetic testing.

AIM

To improve diagnostic yield for patients with inherited disease by evidencing new methods for applying computational and experimental evidence in variant curation across expanded areas of the genome.

METHODS

We use a range of computational methods and statistics, but can support across levels of skill and experience. Using clinical and public data, we investigate research tools to determine if they can be applied in clinical genomic diagnostics and evaluate their predictive power and impact to determine clinical recommendations. We will access a variety of publicly available data and software, with analysis techniques including those used in health quality assessment and diagnostic evaluation.

PROJECT POTENTIAL

The projects that we offer are very applied and translate well for clinical understanding of genomics and genetic variant curation. We also support building bioinformatic, coding skills, statistics along with research translation and implementation projects aligned with this area. This project has real world translational potential as it will provide results enabling improved clinical diagnostic practice, to improve health care for patients.

Statistical Genetics

Senior Group Leader: Professor Stuart MacGregor

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The Statistical Genetics Laboratory studies the role that genetic variation plays in determining risk of disease and its risk factors.

The laboratory develops and applies statistical genetic methods to gene mapping studies across a wide range of traits and diseases.

One major focus is understanding genetic variation in various cancers, including melanoma, ovarian cancer and oesophageal cancer. This work will lead to a better understanding of why particular individuals are affected by cancer or why they respond poorly to cancer treatment.

Another major interest is ophthalmological genetics, with ongoing work to identify the specific genes involved in both eye disease and their underlying quantitative risk factors.

Eye disease genetics.

This project is suitable for an Honours, Masters, MPhil, MD or PhD student.

BACKGROUND

Glaucoma is the leading cause of irreversible blindness worldwide. While there is no cure once visual loss occurs, progressive visual loss and blindness can usually be prevented by timely treatment. This means early detection is vital. Unlike many other common complex diseases, the heritability of glaucoma is very high (70%) and traditional epidemiology studies have not identified any means by which risk can be decreased (e.g. via modifiable risk factors). The major role of genetic factors in glaucoma make understanding the molecular mechanisms fundamental to improve screening and develop better therapies. We have developed genetics-based risk prediction tools for glaucoma, and are now exploring how to implement these to prevent blindness.

AIM

To apply risk prediction tools for glaucoma based on genetic data. To translate these genetic findings into improved screening for the disease. To integrate genetics-based prediction approaches with methods harnessing artificial intelligence. The project may also consider gene-mapping and prediction analysis for other eye diseases such as myopia, age-related macular degeneration and dry eye.

PROJECT POTENTIAL

The QIMR Berghofer Genetics of Glaucoma Study is one of the largest studies of its kind internationally, with large scale genetic data recently collected on thousands of Australians. This will be supplemented with very large-scale genetic data sets (genome wide association studies, exome/genome sequencing, proteomics) which are available in the lab. The student will employ a range of statistical genetic approaches to interrogate these data and to determine the genes and pathways underlying glaucoma and use these in prediction models.

Bridging gaps on the genetics of age-related disorder among under-represented populations.

Co-supervisor: Dr Jue Sheng Ong

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This project is suitable for PhD students only.

Some experience in biostatistics and data analysis is essential, and a background in statistics, engineering, health sciences, epidemiology, health economics, computer science and/or public health is recommended. Crucially, candidates must demonstrate adequate interpersonal skills, critical thinking and cultural competence to effectively engage with stakeholders from diverse backgrounds. Special attention will be given to ensuring the respectful engagement of under-represented populations and safeguarding their rights throughout the research process.

BACKGROUND

Genomics research stands as a pivotal domain providing insights into the genetic foundations of human diseases, paving the way for personalized treatments. However, it is increasingly evident that this research has not been conducted equitably across diverse populations.

The historical Eurocentric bias in genomics has resulted in a notable lack of representation for non-European populations in significant genetic discoveries. Such disparity holds profound implications for health equity and precision medicine, underscoring the necessity to address hurdles in genomics research among diverse populations.

AIM

This project meticulously examines opportunities and challenges in human genetic research on age-related disorders across diverse ancestries. It involves identifying factors affecting statistical genetics techniques, evaluating feasibility of genetic screening programs, and addressing disparities in research capacity.

The PhD candidate will analyse multi-ancestry genetic data on various age-related human diseases, contributing to diversity in genomic research. They'll have the opportunity to work on genomic data from large established biobanks and co-design pilot genetic studies focused on under-represented populations. The project is flexible, allowing candidates to focus on specific/multiple disease endpoints or ethnicities; or focus on specific research question of interest.

PROJECT POTENTIAL

This project offers an innovative opportunity to address the need for equitable representation in genomic research. Through co-designing pilot studies and leveraging emerging technologies, the candidate will advance genomic knowledge, promote health equity, and guide capacity-building efforts in diverse communities.

Genetics and Skin Cancer

Team Head: Associate Professor Matthew Law

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In the Genetics and Skin Cancer laboratory, we determine how genetic variation leads to melanoma and basal or squamous cell carcinoma. We then use this information to work out how we can best detect and manage these cancers.

Genetics of skin cancer project.

Co-supervisor: Dr Mathias Seviiri

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BACKGROUND

Genetics, together with sun exposure, play an important role in the development of skin cancers. The Genetics and Skin Cancer lab studies the genetics of these skin cancers. Melanoma is the deadliest skin cancer and is responsible for >1,800 deaths a year in Australia. While keratinocyte cancers are rarely deadly, their high incidence still results in ~600 deaths a year, and that same high incidence means overall they are the most expensive cancer in Australia. The goal of this project is to dissect the genetics of skin cancers and work out how we can use this information to improve health outcomes.

Our resources include large cohort studies based at QIMR Berghofer, including the Queensland Study of Melanoma: Environmental and Genetic associations[1], the Queensland Twin Registry[2], and the QSkin Sun and Health Study[3] with genetic data on over >40,000 people across the cohorts. Through access to large public datasets like the UK Biobank and international collaborations, we have data linking genetics to skin cancer risk and outcomes for over 1,500,000 people[4-7].

Through these large-scale resources, we are able to dissect the genetics of skin cancers and their risk factors, and use this information to better understand how to predict, manage, and treat these serious diseases.

AIM

- To use computational statistics approaches to dissect the genetics of melanoma, keratinocyte cancers, and their risk factors.
- To use this genetic information in risk prediction models and to identify factors important for outcome and prognosis.
- To use this genetic data to understand how genetic differences cause skin cancer.

METHODS

The project will focus on characterising the role of germline genetic variation in skin cancer. Genome-wide genetic information will be married with data on cancer susceptibility traits and cancer outcomes[4-7]. The overlap of skin cancer and its risk factors will be used to identify new genetic risks common to all traits[4,8,9]. Fine-mapping, bioinformatics, and post-GWAS approaches (e.g., transcriptomics data) will be used to fully interpret identified genetic variants[6,10,11].

The resulting genetic data will be used to develop prediction models, and these models will be calibrated against in-house datasets such as QSkin to determine how they can best help predict disease risk[12–15]. Mendelian randomisation may be used to determine if potential risk factors association with skin cancer are causal[16].

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Global Precision Health

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The Global Precision Health Lab investigates a broad spectrum of human complex traits, with the overarching aim of strengthening the footprint of precision health research on the global stage. We focus on data-driven strategies and collaborative research to address critical knowledge and capacity gaps in precision health, particularly within diverse and under-represented populations.

Our lab is disease-agnostic: we welcome research proposals across any complex human disease, as long as they align with our core research philosophy—that impactful research should have the potential to benefit not only patients, but also one or more of the following stakeholder groups:

(i) researchers

(ii) policymakers, and

(iii) early adopters within diverse healthcare systems.

In Australia, our work includes exploring the opportunities and challenges of engaging culturally and linguistically diverse (CALD) communities in biomedical research. We are particularly interested in evaluating and deploying cutting-edge methods for delivering and validating precision health solutions tailored to these populations, using also our learnings from international collaborative work to inform unique cultural and ethical considerations within these CALD communities.

Globally, we contribute to shaping precision medicine ecosystems through strategic partnerships, capacity-building initiatives, and cross-border research collaborations. Our work aims to develop adaptable frameworks and sustainable strategies that support the advancement of inclusive and equitable precision health research worldwide.

Wellness in the tropics – Translating ideas into innovations for non-communicable diseases.

This project is suitable for an Honours, Masters, MPhil, MD, or PhD student.

BACKGROUND

Tropical regions have traditionally faced significant health challenges due to infectious diseases. However, with shifting disease patterns, non-communicable diseases (NCDs) such as diabetes are becoming increasingly prevalent, largely driven by lifestyle changes, including rising sugar consumption. While genomic and multi-omics technologies offer transformative opportunities for precision medicine, many tropical communities remain underrepresented in genomic research. Addressing this gap is crucial for ensuring equitable access to cutting-edge healthcare innovations.

AIM

This project aims to review, evaluate, and develop data-driven strategies for integrating genomic science into precision medicine initiatives for tropical communities. Candidates will have the flexibility to focus on a specific disease of interest or explore multiple diseases within this framework, gaining valuable expertise in disease biology, genomic data analysis, and translational research.

METHODS

The project will involve a comprehensive literature review of genomic and precision medicine applications in tropical health, as well as an analysis of existing genetic, omics, and biomarker data to assess their relevance for disease prevention, diagnosis, and treatment. Candidates will also have the opportunity to develop innovative data solutions to address unmet clinical and research needs. For those interested in policy and implementation science, there will be an option to engage with key stakeholders, including healthcare professionals and policymakers, to identify barriers and opportunities for integrating genomic medicine into existing healthcare systems. Findings from this research will inform the development of strategic recommendations, tools, or frameworks to enhance genomic research and precision health initiatives in tropical regions.

PROJECT POTENTIAL

This project offers a unique opportunity to contribute to global health equity by advancing precision medicine in underrepresented populations while building research and technical capacity for genomic innovation in communities with a limited research footprint. Through collaborations with leading tropical health researchers facilitated through the Centre for Tropical Health and Emerging Diseases, the candidate will gain hands-on experience in genomic research, multi-omics integration, translational science, and stakeholder engagement. Additionally, this work will support the development of data-driven strategies to strengthen healthcare systems in low- and middle-income tropical countries (LMICs), fostering sustainable and impactful genomic research efforts.

Global Health & Tropical Medicine

Group Leader and Program Director (Population Health): Professor Darren Gray

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The Global Health and Tropical Medicine Lab investigates the transmission and control of tropical infectious diseases and diseases of poverty. These diseases are some of the most prevalent and important infections worldwide, and their effects on human health are the cause of much suffering and economic loss. We aim to understand the spatial distribution and risk factors for these diseases, and to develop public health interventions that will lead to their sustainable control and eventual elimination.

In particular, our research focuses on:

- Soil-transmitted helminth (STH) infections - a group of parasitic diseases with an estimated global prevalence of 650 million people.
- Schistosomiasis - another highly prevalent parasitic disease that causes severe morbidity, including bladder cancer, liver disease, and stunted growth.
- Opisthorchiasis - a foodborne parasitic disease that is a major contributing factor to bile duct cancer in the endemic regions of Southeast Asia.
- Strongyloidiasis - a particular type of STH infection that is highly prevalent in remote northern and western regions of Australia.

Cardiovascular Disease Prevention

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The Cardiovascular Disease Prevention Group focuses on generating epidemiological evidence to guide policy and practice decisions to improve the prevention of cardiovascular and related chronic diseases. A particular focus is on using big data and modelling to enhance disease risk prediction to guide treatment decisions in primary care and generating evidence to address gaps in implementation of preventive interventions.

Mosquito Genomics

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Better control of mosquito-borne diseases through mosquito genomics:

New technologies to control mosquitoes and diseases they transmit are developing rapidly – from the natural pathogen-blocking symbiotic bacteria to the engineered "selfish genes".

In creating and assessing new mosquito control technologies, we take the approach "from the field – to the lab – back to the field". This means that we study natural mosquito populations, do laboratory experiments, and aim to produce practical solutions for field deployment. In doing so, we generate and analyse genomic and other "omics" data from a single mosquito cell to a system of mosquito populations.

We use spatial population genomics and simulation modelling to understand how mosquitoes move, mate and survive in different environments so that we can apply optimal control strategies. We also investigate mosquito genomes to identify and test genes that can be targeted for genetic control, so that we can move away from chemical insecticides.

We collaborate with the leading scientists in Australia, USA, Asia-Pacific and Europe to address the current challenges and predict future obstacles in protecting the communities in Queensland, Australia and around the globe from the mosquito-borne diseases.

Cancer & Chronic Disease

Group Leader: Associate Professor Patricia Valery

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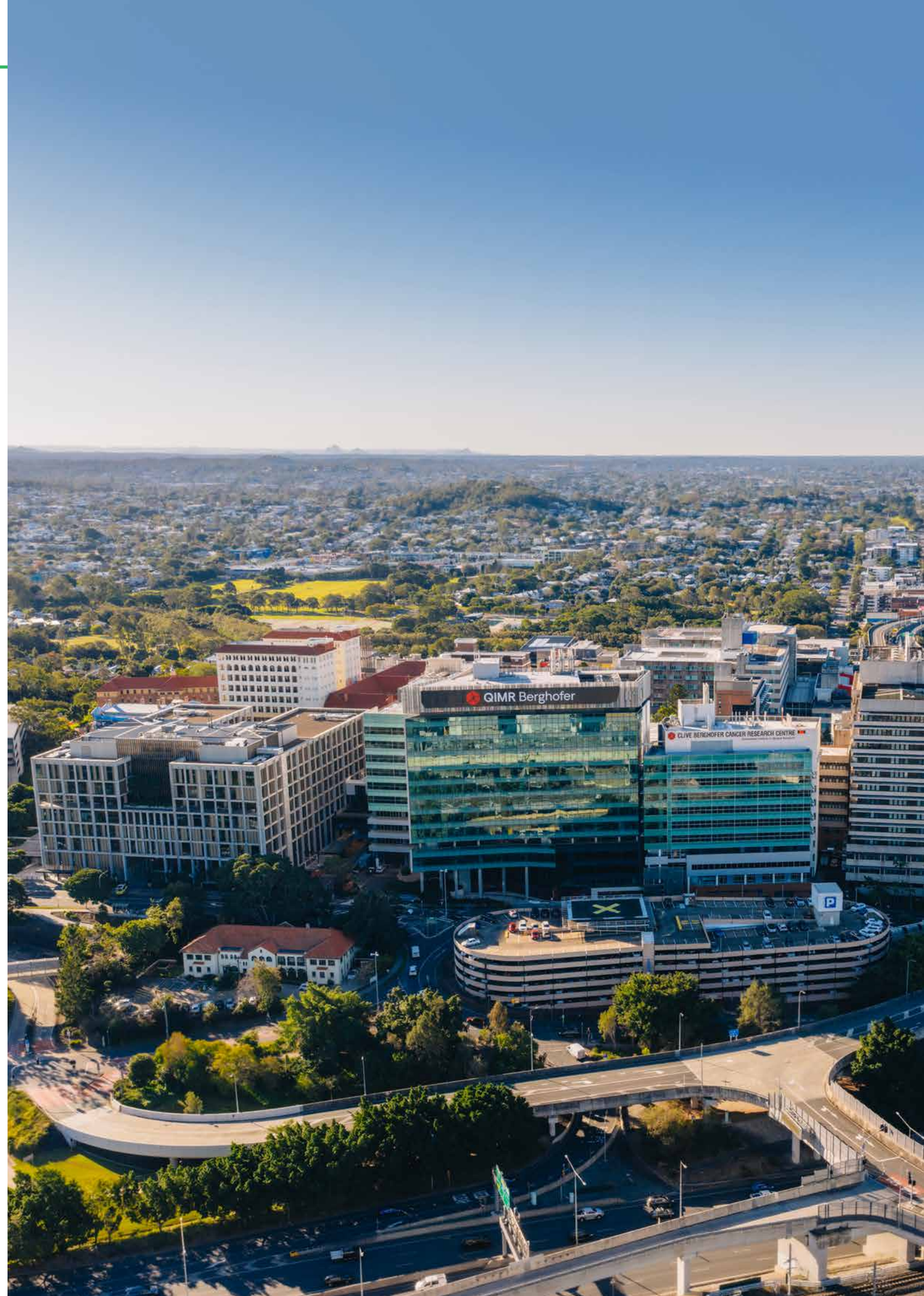
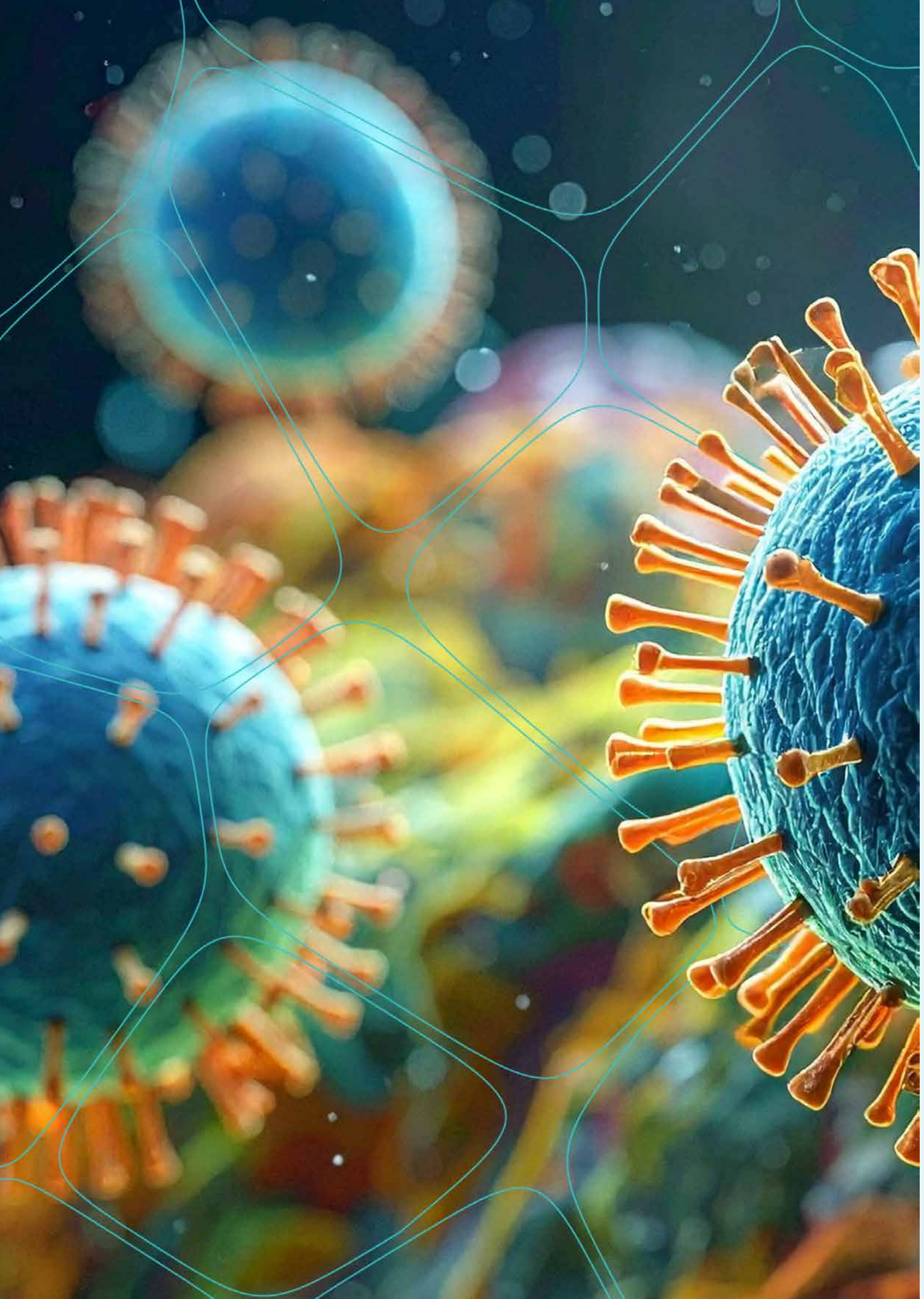
We lead QIMR Berghofer's research on the epidemiology of chronic liver disease and liver cancer. To achieve our vision, our research has focused on three broad areas, namely:

1. Through data linkage studies, our research targets the disparities in healthcare use and patient outcomes. We focus on regional areas, First Nations people, and the use of clinical and health service data to identify individuals at highest risk of progression of liver disease and liver cancer.
2. Through mixed-methods studies, including qualitative interviews with patients and health professionals, we are examining patients' perspectives and preferences about their care, and their practical, psychosocial and information needs.
3. Through interventional studies we are exploring new models of care aimed at improving early identification of patients at risk of liver disease progression and liver cancer, reducing barriers association with their diagnosis and management, and improving patient outcomes.





Infection and Inflammation Program

The Infection and Inflammation Program at QIMR Berghofer is a globally recognised research program dedicated to understanding, preventing, and treating diseases driven by infection and immune dysregulation. Our work spans viruses, bacteria, parasites, and chronic inflammatory conditions, with a strong focus on translating discovery science into vaccines, therapeutics, and public health impact.

We have an international reputation in infectious disease research, particularly in viral immunology, malaria, and parasitology. Our controlled human malaria infection studies are world-leading, enabling rapid evaluation of new anti-malarial drugs and providing unique insights into host immunity. Our expertise also underpins the development of cellular immunotherapies for cancer and infectious diseases.

The Program delivers impactful research in vector biology, helminth control, and neglected tropical diseases, including scabies, an important condition affecting Aboriginal and Torres Strait Islander communities. Complementing this, our work on chronic inflammation is advancing new treatments for cardiovascular, liver, lung, brain, and gastrointestinal diseases using cutting-edge organoid and multi-omics technologies.

Our integrated capabilities, from high-containment laboratories and advanced spatial and single-cell platforms through to clinical trials, enable seamless translation from discovery to patient outcomes.

The Program contributes to improving health equity by addressing infectious and chronic diseases that disproportionately affect Aboriginal and Torres Strait Islander peoples, while aligning with national priorities in remote and tropical health.

Together, these strengths position the Program to deliver innovative, scalable solutions that improve health outcomes locally and globally.

Immunology and Infection

Group Leader and Program Director (Infection & Inflammation): Professor Christian Engwerda

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The Immunology and Infection laboratory studies malaria and leishmaniasis, two important parasitic diseases that affect millions of people around the world every year. Our research focuses on CD4+ T cells because of their central role in controlling anti-parasitic immunity. We use our discoveries to improve immune responses following vaccination or drug treatment with the aim of generating long-lasting immunity in communities to reduce the numbers of infections, and ultimately eliminate these diseases. Our findings relate to inflammation, and as such, our work also has important implications for developing treatments for infections, cancer and autoimmune diseases that impact thousands of Australians.

Characterising CD4+ T cell responses during parasitic infections.

This project is suitable for an Honours or PhD student.

BACKGROUND

Inflammation is a complex biological response of the body to injury, infection or other harmful stimuli. It is a protective mechanism that helps to remove the cause of injury and initiate the healing process. Immune regulation refers to the mechanisms that control inflammation to ensure that it functions properly and does not cause damage to the body's own tissues. The immune system has a delicate balance between being responsive to pathogens and harmful invaders, while also avoiding overreaction or autoimmunity. CD4+ T cells play critical roles in coordinating immune responses and differentiating into functional subsets best suited to control pathogen growth, as well as controlling resulting inflammation. We hypothesise that the composition of anti-parasitic CD4+ T cells subsets that develop during parasitic infection determines the outcome of disease. Furthermore, CD4+ T cell subset composition can be manipulated to improve vaccine and drug efficacy to establish long-term immunity.

AIM

To test this hypothesis, we will address the following aims:

1. Define CD4+ T cell molecular and phenotypic signatures association with parasite control.
2. Develop strategies to modulate CD4+ T cells to improve their anti-parasitic functions.
3. Test host-directed strategies in pre-clinical disease models and primary human CD4+ T cells.

CD4+ T cell memory in malaria and visceral leishmaniasis.

BACKGROUND

Protective immunity to chronic parasitic infections such as malaria and visceral leishmaniasis (VL) depends on the generation, maintenance and functional programming of long-lived CD4+ T cell memory. Malaria and VL represent two distinct paradigms of immunity. In malaria, protection against severe disease (clinical immunity) develops relatively quickly in endemic populations, even though sterilising immunity is acquired slowly and often remains incomplete[1]. In contrast, most individuals infected with *Leishmania donovani*, a causative agent of VL, remain asymptomatic, with only a minority (~one in nine in India), progressing to clinical disease[2]. This suggests that a single exposure to Leishmania can generate durable immune responses that prevent disease progression, although sterilising immunity is rare[3,4]. Instead, asymptomatic or drug-treated individuals often harbor persistent parasites yet effectively control infection through long-lived CD4+ T cell–mediated responses, a phenomenon termed concomitant immunity[5,6]. Leveraging these contrasting immune trajectories provides a powerful framework to dissect the development and maintenance of long-lived, protective CD4+ T cell responses. Understanding how CD4+ T cell memory is formed, maintained, and functionally remodelled in these settings is a critical barrier to developing more effective vaccines and host-directed therapies.

AIM

This project will investigate how CD4+ T cell memory develops in malaria and VL, and how inflammatory cues shape memory cell fate and protective capacity. Using samples from controlled human malaria infection (CHMI) studies, well-established pre-clinical mouse models of malaria and VL, and cutting-edge single-cell multi-omics (scRNA-seq, scTCR-seq, and spatial transcriptomics), students will help define memory-association CD4+ T cell states. The project will also examine how inflammatory mediators and host-directed immunomodulation influence CD4+ T cell memory quality, durability, and recall responses.

PROJECT POTENTIAL

Students will gain hands-on training in advanced immunology techniques (spectral flow cytometry, antigen-specific T cell assays, single-cell sequencing analysis) and work with unique human clinical samples and translational infection models. The outcomes will provide fundamental insight into how protective CD4+ T cell memory is established during parasitic infection and identify strategies to improve vaccine durability and therapeutic immune modulation for malaria and VL.

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Barrier Immunity

Team Head: Associate Professor Amanda Oliver

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The Barrier Immunity Laboratory studies how epithelial cells maintain immune homeostasis and barrier integrity at mucosal surfaces, with a focus on the lung and gut. The lab investigates how epithelial cells support and orchestrate immune responses by forming a physical and biochemical barrier, sensing pathogens and communicating with innate and adaptive immune cells.

A particular interest is the role of epithelial antigen presentation via MHC class II in modulating local CD4 T cell responses, an area that remains poorly understood in humans. Using human tissue-derived organoid models and integrative single-cell and spatial transcriptomic approaches, the lab bridges in vitro and in situ systems to uncover the cellular and molecular pathways underpinning barrier-immune interactions.

By understanding how these tightly regulated processes are disrupted in inflammation, infection, and chronic diseases such as inflammatory bowel disease and chronic obstructive pulmonary disorder, the lab aims to identify new mechanisms and therapeutic targets to restore barrier integrity and immune homeostasis.

The barrier atlas: Cross-tissue insights into homeostasis and dysfunction.

This project is suitable for Honours, Masters, MPhil or PhD students and can be adapted to suit.

BACKGROUND

Single-cell RNA sequencing (scRNA-seq) has revolutionised our understanding of human tissue biology by enabling the characterisation of cellular diversity and function at unprecedented resolution. To date, billions of cells have been profiled across organs, developmental stages, disease states, and populations. Large-scale tissue profiling and data integration efforts have produced tissue-specific atlases such as the Pan-GI Cell Atlas[1], led by the primary supervisor of this project, Dr Amanda Oliver and cross-tissue atlases, focused on profiling specific cell lineages across the body [2,3].

This project will extend these efforts by constructing a unified atlas of mucosal barrier tissues, such as the lung and gut. These organs are critical interfaces with the external environment, balancing protection against pathogens and toxins with essential physiological functions including respiration, digestion, and symbiosis with the microbiome.

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AIM

By pooling and harmonising single-cell datasets across barrier tissues, the student will:

- Identify conserved cellular programs and regulatory networks that underpin shared barrier functions, especially related to immunity.
- Discover tissue-specific specialisations that enable organs to meet unique physiological and environmental demands.
- Integrate multi-modal data, including spatial transcriptomics and metagenomics, to map cellular niches and their interactions with the microbiome.

APPROACH

Candidates are expected to have a strong bioinformatics background and will gain extensive experience with large-scale data integration as well as deep biological knowledge of barrier tissues. The project will require

the student to adapt and streamline integration, quality control, annotation, and spatial mapping methods into a robust pipeline capable of handling millions of cells across thousands of samples and hundreds of donors. Once the atlas is assembled, advanced computational approaches, including gene regulatory network inference, foundation models, and neural networks, will be applied to uncover novel biological insights.

OUTCOME

By combining large-scale single-cell data with spatial and microbiome profiling, this project will generate the first cross-tissue single-cell atlas of barrier biology. The outcomes will provide mechanistic insights into how barrier tissues maintain homeostasis and adapt to unique environmental challenges, laying the foundation for understanding diseases of barrier dysfunction such as inflammatory bowel disease and chronic respiratory conditions.

Investigating epithelial immunomodulation in barrier tissues.

This project is suitable for Honours, Masters, MPhil or PhD students and can be adapted to suit.

BACKGROUND

Barrier tissues such as the gut and lung form dynamic interfaces with the external environment, balancing immune defence with tolerance to commensal microbes and environmental exposures. While epithelial cells have traditionally been viewed as passive structural barriers, emerging evidence suggests they actively instruct local immune responses and contribute to immune homeostasis.

Major histocompatibility complex class II (MHCII) enables the presentation of processed peptide antigens to CD4+ T cells, orchestrating antigen-specific adaptive immunity. Although this function is classically attributed to professional antigen-presenting cells (APCs), epithelial MHCII expression has been observed in mucosal tissues and is upregulated in chronic inflammatory diseases such as inflammatory bowel disease (IBD). However, the molecular mechanisms regulating epithelial antigen presentation and its functional consequences remain poorly understood.

AIM

This project will define how epithelial cells regulate antigen presentation and directly shape adaptive immune responses in barrier tissues by:

- Defining the inflammatory and microbial signals that regulate epithelial MHCII expression.
- Identifying molecular pathways controlling epithelial antigen-presentation machinery.
- Determining how epithelial antigen presentation influences CD4+ T cell activation.

APPROACH

Candidates are expected to have a strong foundation in laboratory-based research and a genuine interest in immunology and/or intestinal biology. The student will employ sophisticated epithelial culture systems, including mammalian cell lines and patient derived intestinal organoids (3D mini-gut cultures), alongside organoid-immune cell co-culture models to perform perturbation and functional assays. These experiments will be complemented by immunophenotyping approaches, including flow cytometry and immunofluorescence microscopy, together with bulk, single-cell, and spatial transcriptomic profiling. There will also be opportunities within the lab to gain experience in bioinformatic analysis of high-dimensional transcriptomic datasets, enabling integration of experimental and computational approaches.

PROJECT POTENTIAL

This project addresses a fundamental question in mucosal immunology: do epithelial cells instruct adaptive immune responses at barrier surfaces? By combining mechanistic experiments with patient derived organoid-immune co-culture systems, this work aims to define epithelial-specific pathways that regulate immune activation and tolerance.

Outcomes from this research have strong translational relevance for diseases characterised by barrier dysfunction and chronic inflammation, including inflammatory bowel disease. The project forms part of a broader Barrier Immunity research program integrating experimental and computational approaches, with strong potential for high-impact publications and future therapeutic discovery.

Genomics and Machine Learning

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The Genomics and Machine Learning Laboratory (GML) studies cancer and infected tissues in patient samples and mouse models. They generate novel data from spatial and single cell technologies and develop new computational and statistical methods to find clinically important patterns from this complex data.

They pioneered the merging of two big data fields, sequencing and imaging, to advance understanding of pathological processes one cell at a time and across all cells within a diseased tissue.

By mapping cell types, their spatial organisation and cell-cell interactions in tissues, GML focuses on discovering new patterns and cellular regulation mechanisms that are hidden from traditional research approaches.

Examples of outcomes include cell and gene markers for predicting cancer progression risks, stratifying disease subtypes, discovering new drug targets to modulate the immune systems, and adding new capabilities for prioritising drugs most effective to each patient.

Gut Health

Honorary Group Leader: Associate Professor Graham Radford-Smith

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Gut Health is a critical part of our mental and physical health. With the increasing knowledge and understanding of our gut microbiome and how it is influenced by our dietary and other lifestyle choices, there is growing interest in how we can improve our health by making more informed decisions about our daily activities. This supports the concept of the brain-gut axis.

The Gut Health research group focuses on the development of knowledge, understanding and then practical tools that allow us to monitor gastrointestinal health. These provide us with increasingly sensitive systems to make earlier diagnoses of gut disorders such as Crohn's disease, ulcerative colitis, colonic polyps, and colorectal cancer. The group uses a range of approaches to investigate these complex disorders including the analysis of large, longitudinal datasets containing clinical, laboratory, and omics data, bulk gene expression analysis, single cell and special technology, and both prospective cohort studies and interventional clinical trials. We have published several applications that can be used in clinical practice to optimize patient care and use the latest technologies to update and improve these together with additional tools.

The Gut Health research group has direct links with the Gastroenterology unit at the Royal Brisbane and Women's Hospital, and with multiple collaborating clinical and basic science centers across Australia and internationally.

Molecular Parasitology

Honorary Group Leader: Malcolm Jones

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The Molecular Parasitology Laboratory was founded by the late Professor McManus, and is now headed by Professor Malcolm Jones. The laboratory leads the world in parasitic worm research with the goal of global control of neglected tropical helminthiases. The group translates laboratory findings into effective disease interventions paving the way for improved health outcomes. Along with a multidisciplinary collaborative team, the laboratory pioneers research on the development/application of schistosomiasis vaccines, in diagnostics, genomics and in tropical/international health, contributing a cohesive and remarkable body of 650 publications in an extensive career. Many are transformational, shaping policy/practice leading to improved treatment/control of worm infections with wide-scale application for informing government agencies, including Australian, globally on intervention options in other parasite-endemic communities.

Molecular Helminthology

Team Head: Dr Hong You

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The Molecular Helminthology lab focuses on CRISPR-based diagnosis for helminth infections, vaccine development and novel drug discovery against schistosomiasis.

The Molecular Helminthology Laboratory focuses on the identification and characterisation of vaccine, drug, and diagnostic targets for helminth infections—particularly schistosomiasis—through the application of cutting-edge gene functional technologies. These include CRISPR-based systems (CRISPR/Cas9, Cas12/13, and CRISPRi/a), single-cell and spatial transcriptomics, bulk transcriptomics, proteomics, and RNA interference. We have established CRISPR/Cas technologies in schistosomes, creating unique opportunities for functional genomics, improved diagnostics, and translational research. Identified targets are validated using in vitro parasite culture systems and in vivo animal challenge models for therapeutic and vaccination studies. The team has pioneered mRNA vaccine development for schistosomiasis and has

extensive experience evaluating vaccine and drug efficacy across laboratory and field settings. In parallel, we have developed portable, field-friendly point-of-care CRISPR-based diagnostic tools for schistosomiasis, strongyloidiasis, and other helminth infections in Asia, Africa, and Australia.

Development of CRISPR-based diagnostic technology for helminth infections.

This project is suitable for an Honours, Masters, MPhil, MD or PhD student.

BACKGROUND

Intestinal parasitic worms (helminthiases) cause debilitating diseases, afflicting >1.5 billion people globally. Major global endemic hotspots include: SE Asia, South America, Africa and the Pacific. Current diagnostic tests for worm infections are neither sufficiently sensitive nor field-friendly for use in low-endemic and resource-poor settings, leading to underestimation of true infection rates. Advanced tools are urgently needed for rapid mapping of helminthiases and monitoring control efforts as mass drug administration programs are unsustainable.

AIM

We aim to develop and evaluate accurate, easy-to-use and low-cost point-of-care diagnostic tools by using CRISPR/Cas12 and Cas13 based system, for the diagnosis of neglected tropical diseases, including schistosomiasis, strongyloidiasis, hookworm, lymphatic filariasis and other infectious diseases.

PROJECT POTENTIAL

The development of CRISPR-based diagnostic tools for various helminths aligns with the urgent WHO need for ultra-sensitive, portable, point-of-care technologies. These tools can facilitate rapid disease mapping, enhance the monitoring of helminth control programs, and support the assessment of elimination targets.

Drug discovery against schistosomes and schistosome-association pathogens.

This project is suitable for an Honours, Masters, MPhil, MD or PhD student.

BACKGROUND

Schistosomiasis is a serious global problem and the second most devastating parasitic disease after malaria. Currently, there is no effective vaccine available and treatment is entirely dependent on praziquantel chemotherapy, which raises significant potential threat to public health should drug resistance develop. The paucity of molecular tools to manipulate schistosome gene expression has made an understanding of molecular pathways in these parasites difficult, increasing the challenge of identifying new potential drug candidates.

AIM

We will use edge-cutting approaches, including spatial profiling tools, CRISPR- mediated gene editing platform, to identify novel drug targets and to characterise their functional roles in parasite development and host–pathogen progression.

PROJECT POTENTIAL

Harnessing those powerful technologies in helminth research will enhance our ability to better understand the mechanisms of parasite–host interactions and to identify novel drug targets, with the potential for translation into real-world strategies to improve the control of parasitic diseases and enhance well-being in developing countries.

Emerging Viral Diseases

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The Emerging Viral Diseases Laboratory focuses on deciphering the molecular mechanisms underlying viral infection and disease, as well as developing effective interventions to combat emerging viral pathogens. Emerging viruses include newly identified viruses, such as SARS-CoV-2, as well as previously known viruses that are experiencing a rapid rise in incidence or geographic range, such as Japanese encephalitis virus (JEV), Chikungunya virus (CHIKV), and Oropouche virus (OROV).

The Emerging Viral Diseases Laboratory has three core research themes:

1. Discovering the molecular mechanisms of viral replication and virus-host interactions for the development of antivirals.
2. Defining pathogenic versus protective virus-induced inflammation for the development of new anti-inflammatories.
3. Development and pre-clinical evaluation of new vaccines.

The Emerging Viral Diseases Laboratory focusses on four emerging viral genera:

- Orthoflaviviruses (Japanese encephalitis, Murray Valley encephalitis, Zika, Dengue, and West Nile viruses).
- Alphaviruses (Chikungunya, Ross River, Mayaro, Getah, and O'nyong'nyong viruses).
- Orthobunyaviruses (Oropouche and Trubanaman viruses).
- Coronaviruses (SARS-CoV-2).

Mosquito Control

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There are no effective vaccines against malaria or most arboviruses. There are no chemotherapeutants for the treatment of arbovirus infection. Mosquito surveillance, management and manipulation remain the mainstays of most mosquito-borne disease control programs. The Mosquito Control Laboratory (MCL) manages state-of-the art pathogen and insect containment facilities with the capacity to undertake studies on all aspects of vector biology and disease transmission. We work on innovations in mosquito surveillance and control that might help interrupt parasite and pathogen transmission.

We are unique in the Southern Hemisphere with regard to our size, capacity and expertise. This makes us a key partner in a national, regional and international network. Our presence significantly enhances Australia's ability to investigate emerging vector-borne disease threats in the region. A major remit of the refurbished (2013), MCL is to exploit this unique facility through building strong collaborative links with parasitology, virology and vector biology laboratories throughout the world.

The MCL has permission to hold a number of exotic mosquito species in addition to native Australian mosquitoes. These include insecticide-resistant and susceptible Aedes aegypti strains, Aedes albopictus and Anopheles stephensi. The MCL has local access to real-world mosquito-virus transmission systems through a number of native mosquito vectors and their association alphaviruses (including Ross River and Barmah Forest). We have field work in progress in Asia, Europe and the Americas.

Mosquito-borne disease transmission in a changing world.

Co-supervisor: Dr Brian Johnson

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BACKGROUND

In recent decades, arthropod-borne viruses (arboviruses) have emerged or re-emerged as human and animal pathogens with important implications for public health. These include dengue, Zika and chikungunya viruses, which circulate between humans and the urban mosquitoes, Aedes aegypti and Aedes albopictus, as well as zoonoses with complex transmission pathways that involving multiple vectors and vertebrate hosts. These include Japanese encephalitis virus (JEV), Murray Valley encephalitis virus (MVEV) and Ross River virus (RRV).

We are particularly interested in incriminating transmission pathways, and the factors that drive human spill-over for JEV, MVEV and RRV. The former is vaccine preventable, but in Australia we do not know where and when to target vaccination campaigns because the disease is highly unpredictable in its spatial and temporal prevalence. MVEV is endemic to Australia and Papua New Guinea, but in this case there are no vaccines or therapeutants for a disease whose appearance is also impossible to predict across regions or years. Both MVEV and JEV are deadly and untreatable in a small proportion of human cases. RRV is Australia's commonest mosquito-borne disease (ca 5000 cases per annum) causing debilitating arthritogenic symptoms. It has caused explosive epidemics in the Pacific countries and territories, involving > 100,000 human cases. Recent sero-surveys suggest that it may now be endemic across the Pacific and that transmission is becoming more common in urban Australia.

Globally, anthropogenic and ecological changes, particularly those related to climate and extreme weather events, may increase vector and host prevalence, expose new reservoirs to infection or induce arboviruses to adapt to new maintenance cycles. These factors may favour the emergence and spread of human zoonotic infectious diseases. Detailed studies on JEV, MVEV, RRV, and their vectors and its hosts are required to 1) track the diversity and evolution of viruses across habitats, 2) understand their key transmission dynamics, and 3) determine the risks of human spill-over.

OBJECTIVES

- Demonstrate how new surveillance technologies (mosquito trapping, and molecular xeno-monitoring)

can incriminate vectors and vertebrate reservoirs of disease.
- Identify key pathways of arbovirus transmission and human spill-over in urban and rural environments in Australia.
- Apply these new insights to prioritise future research and to target interventions (i.e. health communication, insecticidal control, and vaccines).

SUB-OBJECTIVES
- Gain a fine-scale understanding of how specific virus variants emerge, spread and dominate particular habitats.
- Support the longitudinal collection and identification of mosquitoes (including blood-fed individuals) and vertebrates around areas association with virus transmission.
- Employ a range of diagnostic tools (serology of mosquito blood meals, metabarcoding and virus sequencing of trap collections) to identify transmission pathways.
- Application of modelling techniques (SIR or matrix models) to explore the impacts of different vectors and hosts on transmission.

PROJECT POTENTIAL
- This work will draw on recent developments in arbovirus surveillance, molecular xeno-diagnostics, and risk mapping to define key transmission pathways (virus variants, habitat, vectors and reservoirs) for mosquito-borne zoonoses.
- The resulting "toolbox" of methods, and their interpretation, will have relevance for risk prediction and control campaigns.
- The project is pertinent, not only for Australia, but for the emergence of zoonotic arboviruses in the Pacific.

Exploiting commensal micro-organisms for the control of pathogen transmission by mosquitoes.

Arthropod-borne viruses (arbovirus) transmitted by mosquitoes cause thousands of disease cases each year in Australia and remain a leading cause of morbidity and mortality internationally. Currently, there are no widely effective vaccines for most of the arboviruses, making mosquito population control the primary strategy for managing disease transmission. In addition to carrying human-pathogenic viruses, mosquitoes also harbour a variety of microbes that can be beneficial; including the intracellular bacteria Wolbachia and insect-specific viruses (ISVs), which are passed vertically from female mosquitoes to their offspring via the eggs. Mosquito infection with these microbes have been shown to inhibit infection of the mosquitoes with pathogenic arboviruses. Wolbachia are now applied worldwide as biological control agents for the control of dengue. Native mosquitoes harbour a range of uncharacterised Wolbachia strains, with untapped potential for disease control. While much work has been performed on ISVs in cell culture, mosquito infections have not been evaluated for most ISVs. In partnership with The University of Queensland, we are characterising native ISV infections in globally important mosquito vectors.

Projects on these microbes aim to establish new infections in mosquitoes and explore the mosquito host range, vertical transmission and inhibition of pathogenic infections. Procedures performed would include mosquito microinjection, cell and mosquito culturing, histology and microscopy and applied virology testing procedures. Results from this project will inform regulatory applications for the development of these beneficial microbes as biological control agents against arboviruses.

Scabies

Senior Group Leader: Professor Katja Fischer

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Scabies is one of the most common infectious skin disorders worldwide, particularly among children and in tropical regions. In Aboriginal and Torres Strait Islander communities of remote northern Australia, scabies prevalence is high and there are extreme rates of scabies-association streptococcal and staphylococcal infections.

Scabies mites are host-specific, 'obligatory' parasites without environmental reservoirs. Chemotherapy is the only way to combat scabies and its transmission in humans. There is no vaccine and the broad-spectrum anti-parasitic drugs available fail to control the disease.

Emerging mite resistance against leading drugs is of growing concern. Another problem is diagnosis. There are numerous skin conditions with similar symptoms but no reliable, simple methods to detect scabies. This makes efficient therapy, management and surveillance at individual, household and community levels very difficult.

Novel drugs and diagnostic tools to treat scabies are urgently needed. A central challenge is to comprehend mite biology and scabies pathogenesis, which are poorly understood, resulting in a lack of knowledge of specific drug targets in the parasite.

The Scabies Research Group is focused on understanding the molecular interactions of scabies mite molecules with host defense systems in the skin. The group, which has been working on scabies since the early 2000s, aims to develop new options for reducing scabies incidence and improving disease outcomes.

Disease mechanisms, novel therapeutics and molecular diagnostics for scabies.

Co-supervisor: Dr Deepani Fernando

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This project is suitable for an Honours, Masters, or PhD student.

Prospective students will learn a wide range of molecular biology techniques, protein technology, including protein expression and purification techniques, microscopy, animal work and more.

BACKGROUND

Scabies and association co-infections cause substantial illness and a major health burden in Indigenous communities of Northern Australia. In particular scabies-caused childhood pyoderma (bacterial skin infection) can cause severe complications in later life. Scabies-association Streptococcus infections for example, significantly contribute to an immune complication of streptococcal infection that can leads to heart and kidney disease (rheumatic heart disease and post-streptococcal glomerulonephritis).

Diagnosis of scabies relies mostly on epidemiological and clinical algorithms rather than pathogen detection. Incorrect diagnosis can result in rapid community transmission and pathology exacerbation. New scabicides are urgently needed, as current drugs often fail because they do not kill parasite eggs and/or have short half-lives. Drug resistance is emerging.

Several research projects are underway in our laboratory:

1. Recognising the health risk of scabies-association pathogens, we have commenced dissecting the link between scabies and bacterial infections at a molecular level and we lead the international scabies microbiome program to define the impact of scabies on the healthy skin flora and examine the synergy between mites and bacteria.
2. Drug resistance is an emerging problem in controlling the mites (causing scabies) and the bacteria (causing secondary infections). Our current research program combines cutting-edge basic research and unique pre-clinical studies, to compare the efficacy of several new candidate drugs that kill all stages of the scabies parasite including eggs to develop new candidate drugs.
3. Early and accurate diagnosis of scabies is critically important, as it can help prevent transmission and/or stop scabies outbreaks, it can improve the effectiveness of treatment and clinical management and avoid long-term disease complications in patients. Inappropriate treatment of undiagnosed scabies can cause further serious disease and contribute to emerging parasite resistance. For these reasons, we are developing the first Scabies Rapid Antigen Test (RAT) System for Point-of-Care.
4. Understanding the molecular mechanisms underpinning this disease is crucial to the development of diagnostics, treatments and cures. Therefore, we are also studying key aspects of mite biology and scabies pathogenesis. These more basic research projects are for example aimed at understanding the skin immune modulation by the parasitic mites or the severe itching, which is the main debilitating symptom of scabies infection. We have generated comprehensive integrated multi-omics databases from which we hope to identify and analyse molecular mechanisms unique to scabies. We have a powerful in vivo model and supporting technologies for pre-clinical work. We collaborate nationally and internationally with researchers and clinicians with a wide range of expertise.

Our program was developed in consultation with consumers and in response to concern over persistent high rates of scabies in remote A&TSI communities across Australia.

Translational and Human Immunology

Group Leader: Associate Professor Corey Smith

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The Translational and Human Immunology Group focuses on understanding the mechanisms that regulate human immune responses in health and disease. We have a keen interest in understanding how persistent viral infections contribute to a range of diseases, including autoimmune diseases and cancer. We aim to develop a deep understanding of differences in our immune systems that contribute to the susceptibility to different viral-association diseases. Knowledge gained from these studies forms the basis for developing novel immune interventional and diagnostic strategies that can be implemented in clinical settings.

Tumour Immunology

Distinguished Scientist: Professor Rajiv Khanna AO

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The major goal of the Tumour Immunology Laboratory is to obtain a deeper understanding of the mechanisms by which an immune response to tumours may be generated, augmented and applied to the inhibition of tumour growth. The members of this laboratory share the expectation that such insight will be applicable to the treatment and/or prevention of cancer.

Cellular immunotherapy – engineering "custom built" cells to treat cancer.

Co-supervisor: Dr Paulo Martins

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This project is suitable for Master's or PhD work and is flexible for clinical students.

BACKGROUND

Current standard approaches for the treatment of human cancers typically employ broad acting radiotherapeutic and chemotherapeutic approaches. There has been growing interest in approaches using immunotherapy with adoptive cell transfer (ACT): using patient's immune cells to treat their cancer. A specific type of ACT uses chimeric antigen receptors (CARs). These are genetically engineered molecules, which are custom built to specifically target protein antigens expressed on malignant cells. There are three FDA-approved CAR T cell-based therapies targeting CD19 on certain B-cell malignancies. CAR19 treatment, of children with relapsed or refractory acute lymphoblastic leukaemia (ALL), and of adults with advanced lymphomas, has demonstrated remarkable success and complete remission in some patients. Although approved therapies are limited to blood cancers, a growing number of CAR T-cell therapies are being developed and tested in clinical studies in multiple solid tumours. There are promising clinical data targeting tumour-association antigens in melanoma, lung, liver, breast, and brain cancers.

There are major differences between CAR therapies, mostly at the tumour-antigen recognition site, but CARs share similar components known as signalling domains that can affect the cells' overall function, such as their ability to produce more cells after infusion into the patient (expansion), and to survive longer in circulation (persistence). The ability to manipulate these domains to custom build CAR T cells to specifically target certain tumours, and avoid toxicity, is critical for the success of CAR T cell therapy.

AIM

The CAR T cell program at the Tumour Immunology Laboratory aims to design and test novel CAR T cell therapies for virus-association cancers. We have designed a CAR T cell, which targets a glioblastoma (GBM)-specific antigen A3 that is being tested for the treatment of GBM, an aggressive form of brain cancer. In our clinical trial of ACT to treat GBM ① we identified a distinct T cell expression signature association with potency and favourable long-term survival in GBM patients. This project will use this knowledge and expand the potential of the A3-specific CAR T cell product. We will customise the signalling domains to engineer a CAR with a similar expression signature to that of T cells with known GBM-killing potential. We will ultimately build a CAR better suited for the treatment of GBM.

Hepatic Fibrosis

Interim Director and CEO and Chief Scientist: Professor Grant Ramm

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The Hepatic Fibrosis Laboratory investigates the cellular and molecular mechanisms of scar tissue formation in the liver. This leads to fibrosis and cirrhosis in adult liver diseases such as haemochromatosis and in children in diseases such as cystic fibrosis and biliary atresia. If left untreated chronic liver disease can lead to liver cancer.

Molecular Nutrition

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The Molecular Nutrition Laboratory studies the processes responsible for nutrient homeostasis and how they relate to health and disease. We focus predominantly on disorders of iron homeostasis and we are passionate about improving the health of people with iron-related conditions, such as iron deficiency and the iron loading disorder hereditary haemochromatosis, both of which affect a surprisingly high number of Australians. In fact, iron-related disorders represent some of the most common conditions affecting humans worldwide. In the Molecular Nutrition Laboratory, we are working hard to understand the molecular basis of these disorders and to use this knowledge to develop better treatments for affected individuals.

Iron homeostasis during pregnancy and the effect of iron supplements.

This project is suitable for PhD students.

BACKGROUND

Adequate dietary iron intake is vitally important during pregnancy as the consequences of iron deficiency at this time can be severe. Complications can include pre-term delivery, intrauterine growth restriction and irreversible neurological damage in the developing infant. With a recent study suggesting that a staggering 60-70% of pregnant women in Australia are iron deficient, it is not surprising that oral iron supplements are widely consumed. What is surprising, however, is that the effect of such supplements has not been well studied, and while the benefits of supplementation on maternal iron stores and haemoglobin levels are well accepted, any benefit to pregnancy outcomes and fetal development is less evident, with many studies showing little or no improvement in a range of parameters, including prematurity and birth weight. In addition, the supplementation of iron replete pregnant women has been shown to be detrimental to both maternal and infant health, increasing the risk of both preterm delivery and small for gestational age births.

AIM

To investigate how iron homeostasis is regulated during pregnancy and to determine the effect of various forms of iron supplementation, with particular emphasis on the placenta and fetus.

PROJECT POTENTIAL

With iron deficiency affecting so many pregnant women, it is critical that we determine the cause of these effects so that optimal supplementation regimens can be implemented to reduce the prevalence of iron deficiency and maximise the health and safety of both mother and infant.

Iron homeostasis in developing red blood cells.

This project is suitable for PhD students.

BACKGROUND

Most of the iron in the body is contained within red blood cells in the form of haemoglobin, which is important for the transport of oxygen around the body. During development, red blood cells must have a highly efficient iron uptake pathway to obtain sufficient iron for haemoglobin synthesis. While many proteins involved in this pathway have been identified, recent data from our laboratory has shown that our understanding of this process is incomplete, particularly in utero. Many red blood cell disorders also detrimentally affect systemic iron homeostasis, although, again, the molecular pathways are incompletely understood.

AIM

There can be a range of aims association with this project, broadly split into the following: 1. Determining the molecules involved in red blood cell iron uptake in adulthood and during development. 2. Investigating how red blood cell development affects whole body iron homeostasis.

PROJECT POTENTIAL

Many red blood cell disorders are association with pathological changes in iron homeostasis. A greater understanding of how developing red blood cells handle iron, and the association effects on systemic iron levels, could lead to the development of more effective treatments for these conditions.

The regulation of body iron homeostasis.

This project is suitable for PhD students.

BACKGROUND

Human conditions with disrupted iron homeostasis are very common and most involve the inappropriate production of the peptide hormone hepcidin, which regulates body iron metabolism. Hepcidin is produced by the liver and secreted into the bloodstream where it acts as a negative regulator of intestinal iron absorption and storage iron release. Prominent examples of conditions association with altered hepcidin production are the anaemia of inflammation and the iron loading conditions hereditary haemochromatosis and β-thalassaemia.

AIM

To investigate the pathways regulating hepcidin production and to develop ways to manipulate these pathways to treat disorders of iron homeostasis.

PROJECT POTENTIAL

Inherited iron loading disorders, such as hereditary haemochromatosis and β-thalassaemia, represent some of the most prevalent genetic disorders known and the anaemia of inflammation is the most frequent anaemia in hospitalised and chronically ill patients. The development of new treatments for these conditions would have a major impact on the quality of life for those afflicted with these disorders.

Mucosal Immunology

Team Head: Associate Professor Severine Navarro

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The Mucosal Immunology group seeks to develop innovative treatments for inflammation and chronic illnesses, like allergies, asthma and inflammatory bowel diseases, with a particular focus on children. We work in collaboration with other academics, clinicians, paediatricians, dietitians, chemists, and computational biologists to translate our efforts to the clinic and bring our findings to the public. We are interested in the mechanisms of immune dysregulation, the role of the microbiome and its interaction with the different immune compartments to understand disease onset.

Respiratory Immunology

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The Respiratory Immunology Laboratory focuses on identifying pathogenic pathways that underpin the onset, progression, and exacerbations of asthma and chronic obstructive pulmonary disease. To achieve this, high-fidelity preclinical models of disease are developed that recapitulate key gene-environment interactions and allow for elucidation of cellular and molecular mechanisms. Where possible, scientific findings are translated with ex vivo model systems using primary human cells and by analysing clinical material.

Insights into the influence of a maternal high-fat diet on infant susceptibility to severe lower respiratory tract infections.

Viral bronchiolitis is an infection of the small airways (bronchioles) characterised by the infiltration of neutrophils, oedema, and shedding of the epithelial cells that line the airway. A recent population study found that the offspring of mothers who ate a poor diet in the third trimester were predisposed to severe viral bronchiolitis. We have modelled this association in mice, and established that the maternal diet affects the nascent microbiome in the offspring and association immune development. This project will explore the cellular and molecular mechanisms by which the microbiome affects immune development and susceptibility to infection in the lungs.

Understanding the mechanisms by which the assembling neonatal microbiome promotes neonatal immune development.

The microbiome is known to affect immune development. For example, germ-free mice have fewer Peyer's patches in the gut wall, suggesting that the gut microbiome regulates the formation of this lymphoid tissue. Other studies have shown that germ-free mice have fewer natural killer T cells. Both the microbiome and the immune system develop postnatally (predominantly if not exclusively), and there is considerable bi-directional crosstalk. In this project, we will study this relationship, with a focus on the seeding of innate lymphoid cells in mucosal tissues such as the gut and the lungs.

Clinical Malaria

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The focus of the Clinical Malaria Group is the evaluation of the safety and efficacy of candidate antimalarials, using the induced blood stage malaria (IBSM) model in healthy human volunteers. Developed by the previous group lead Professor James McCarthy, the model has been used to evaluate 10 investigational medicinal products. Models have been established for an artemisinin-sensitive and an artemisinin-resistant P. falciparum strain, and other Plasmodium species including P. vivax and P. malariae. The model has also enabled the conduct of studies to evaluate transmission-blocking interventions, and has enabled the conduct of exploratory studies to evaluate immunological and pathophysiological response to infection.

Immunopathology

Team Head: Associate Professor Kate Gartlan

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The Immunopathology Laboratory is focused on understanding the cellular and molecular mechanisms that drive immune-mediated pathologies. Our recent focus is on adaptive immune polarisation following allogeneic stem cell transplantation and its influence on graft versus host disease (GVHD). Donor stem cell transplantation is an important curative therapy in the treatment of blood cancers, however its application is limited by serious complications such as GVHD that have a significant impact on patient mortality and quality of life.

Early inflammatory responses during preparative transplant conditioning initiate a cascade of adaptive immune responses that manifest as acute and/or chronic tissue damage in >50% of transplant recipients. GVHD treatment options are relatively limited and focused on immunosuppression and steroidal therapy, which are problematic due to opportunistic infection and refractory disease, therefore new therapies are urgently needed.

Designing better T cells for use in stem cell transplantation.

BACKGROUND & HYPOTHESIS

Donor stem cell/bone marrow transplantation (allo-SCT/BMT) is an important curative therapy in the treatment of blood cancers, however its application is limited by serious complications such as graft-versus-host disease (GVHD) that have a significant impact on patient mortality and quality of life. Early inflammatory responses during preparative transplant conditioning initiate a cascade of adaptive immune responses that manifest as acute and/or chronic tissue damage in >50% of transplant recipients. GVHD treatment options are relatively limited and focused on immunosuppression and steroidal therapy, which are problematic due to opportunistic infection and refractory disease, therefore new therapies are urgently needed. Donor-derived T cells are known to be the key drivers of GVHD pathology but are also critical to maintain ongoing anti-tumour immunity, also known as Graft-versus-leukaemia (GVL) effects, which prevent cancer relapse in these patients. Identifying novel ways to target GVHD whilst maintaining GVL is key to improving patient outcomes. We propose that in vivo screening of potential therapeutic targets via manipulation of donor T cells pre-transplant will accelerate therapeutic development in this area.

AIM

In this study, we will utilise recent advances in CRISPR-mediated gene therapy to modulate T cell function in naïve primary T cells for allo-SCT.

APPROACH

This will involve optimisation, testing and validation of CRISPR gene editing of novel targets in naïve mouse T cells in vitro prior to transplant into allogeneic mice.

PROJECT POTENTIAL

Students will develop new skills in techniques relevant to immunology research such as immune cell isolation, gene modification and exposure to in vivo models of inflammatory disease. This research has the potential to develop novel treatment approaches for blood cancer patients.

Molecular Virology and Viral Therapeutics

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Our focus is the discovery of key viral or cellular molecules required for HIV to grow, and then to target their action so that HIV growth can be effectively blocked.

We are also interested in dengue and SARS-CoV-2 virus replication. Our dengue and SARS virus research includes development of novel inhibitors called defective interfering particles.

We have uncovered and developed defective interfering RNAs (DI RNA) from dengue virus and SARS-CoV-2.

DI RNAs are created by RNA viruses due to replication errors, resulting in incomplete viral genome copies lacking crucial replication genes. DI RNAs block parent virus replication in several ways:

- They compete for limited host cell resources, such as enzymes and nucleotides.
- They obstruct replication by serving as a template for RNA synthesis, generating more DI RNAs instead of viral genomic RNA.
- DI RNAs hinder viral particle assembly and release, and their innate immune responses.

We've created virus-like particles called DIPs and nanoparticles to deliver DI RNA, inhibiting virus growth in cells and animal models of human viral diseases. Our goal is to develop potent antiviral agents based on DI RNA to reduce virus spread and disease.

Cardiac Bioengineering

Senior Group Leader: Professor James Hudson

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The Cardiac Bioengineering Laboratory aims to develop state-of-the art bioengineering approaches for human myocardium. The team uses our screening platforms in house, in collaboration with research partners, and together in industry partnerships for a variety of different discovery science and therapeutics development applications. These include understanding the mechanisms of cardiac maturation, interactions between different cell populations in the heart, the role of metabolism in maturation and regeneration and development of new therapeutics for patients to prevent heart failure.

Cardiac Drug Discovery

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The Cardiac Drug Discovery Laboratory aims to develop new drugs to treat cardiac fibrosis and heart failure by understanding the signalling networks that regulate heart function. Our lab uses classical pharmacology and cell signalling approaches with an innovative combination of cutting-edge 'omics and advanced microscopy in human heart tissue and stem cell-derived human cardiac organoids. Our team's work is driven by a major unmet need, as one in three deaths in Australia are due to cardiovascular disease. In particular, heart failure has become a major clinical burden and this is only expected to worsen in our aging population. We have a particular focus on cardiac fibrosis, observed in >90% of heart failure patients, which is characterised by excessive production of extracellular matrix proteins that can prevent the heart from contracting effectively. However, the mechanisms that regulate these processes are unclear and there are currently no effective treatments for cardiac fibrosis.

Lung Inflammation & Infection

Group Leader (Honorary): Associate Professor David Reid

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A major focus of the Lung Inflammation and Infection program is to investigate the interaction between bacterial pathogens and the host innate immune response within the lung. Chronic respiratory diseases characterised by chronic infection are highly prevalent in Australia and globally.

We are especially interested in the role of iron and other biologically active metal ions in promoting bacterial infection in the lungs of patients with the genetic disease cystic fibrosis (CF) and other suppurative lung diseases. To do this, our group is studying bacterial and host immune system interactions in vivo using a number of biochemical, molecular and cell imaging methods and also modelling these interactions using mouse models.

Using this knowledge, we aim to develop more targeted treatments that are widely applicable to many severe chronic airway diseases, including asthma, chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis.

Investigating the effect of iron overload in a murine model of cystic fibrosis.

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Co-supervisor Dr Pramila Maniam

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This project is suitable for an Honours student.

BACKGROUND

Cystic fibrosis (CF) is a genetic disorder caused by mutations in the cystic fibrosis transmembrane regulator (CFTR) gene, which impairs chloride transport across cells and leads to the excessive secretion of sweat and mucus, particularly affecting the lungs. As a result, CF lungs are highly susceptible to chronic bacterial infections, which contribute to disease exacerbations. Elevated iron levels have been observed in the airways of CF patients, and this iron overload is association with increased bacterial infections. Iron is a biologically active metal required for normal physiological processes, but it can also produce damaging reactive oxygen species that may contribute to disease pathogenesis. We have a mouse model of CF (CftrG551D/G551D) that has been treated with iron dextran to mimic human disease. CF animals have also been crossed with Hemochromatosis mice, a genetic model of iron overload caused by mutations in the HFE gene, to determine how the presence of these mutations also contribute to disease phenotype.

AIM

- Quantify iron and mediators of iron homeostasis in lung, liver and spleen tissue.
- Investigate immune responses to changes in iron levels.
- Investigate the microbiome and effect of iron and HFE mutations on the microbiome.

APPROACH

To achieve this aim, we have already collected tissues, serum, and bronchoalveolar lavage fluid (BALF) from G551D CFTR mutant mice and wild-type (WT) controls. These samples will undergo a range of analyses, including protein and gene expression studies, histology, immunohistochemistry, iron assays, and ICP-MS. Additionally, serum and BALF will be analysed for cytokine levels to assess inflammation and immune responses.

PROJECT POTENTIAL

This project has significant potential to advance our understanding of iron dysregulation in CF. By investigating the mechanisms of iron overload in the G551D CFTR mouse model, the findings could reveal novel therapeutic targets to reduce oxidative damage and improve lung function in CF patients. Ultimately, the project has the potential to influence both CF treatment strategies and the broader understanding of iron-related pathologies in other diseases.

Cystic fibrosis in the age of CFTR modulators.

This project is suitable for a PhD student.

BACKGROUND

Cystic fibrosis (CF) is a debilitating, life-threatening disease characterised by airway inflammation, oxidative stress, persistent airway exacerbations and abnormal lung microbiome. CF is caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene, and predominantly affects the lungs, gastrointestinal tract, liver and pancreas. Several drugs have been developed in the last few years to treat CF with varying degrees of success, but we still need in-depth studies of how these therapies perform over time in a wide range of patients.

AIM

- Investigate markers of immune regulation, inflammation and iron status over time.
- Characterise how confounding factors, such as HFE mutations, affect disease progression and response to treatment.
- Investigate how CFTR therapies have changed the microbiome over time.

METHODS

We have collected thousands of patient samples (including whole blood, plasma, sputum, saliva, urine and PBMCs) in a Biobank to examine disease progression, mechanisms of how treatments work and how treatment has improved patient outcomes. These samples will be analysed using techniques such as gene expression studies, iron assays, proteomics and microbiome sequencing to address the above aims.

PROJECT POTENTIAL

This research is vital in order to contribute to the understanding of how these CFTR modulator drugs work in CF patients, how they can be changed to improve patient outcomes and potentially help to identify new therapeutic targets in the future. All this data will contribute to several papers that we hope to publish in the near future.

Applied Tropical and Molecular Parasitology

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The Applied Tropical and Molecular Parasitology Laboratory focuses on developing new diagnostics for, primarily, helminth infections and utilising molecular tools to investigate epidemiology of disease. We have a particular focus on zoonotic parasites such as Schistosoma sp., Strongyloides sp., and hookworm, applying a One Health lens to research projects with an aim for prevention of parasite infection. We collaborate closely with the Global Health and Tropical Medicine group to develop multifaceted control programs to achieve this goal.

Detection of Capillaria spp. in bio banked human samples from the Philippines and China using molecular methods.

This project is suitable for Honours students only.

BACKGROUND

Capillaria species are neglected parasitic nematodes that can cause significant morbidity but are often under diagnosed due to non specific clinical presentation and limited routine diagnostics. Bio banked samples from endemic regions provide an opportunity to retrospectively assess the presence and distribution of Capillaria infections using sensitive molecular tools. This project will apply DNA based methods to detect Capillaria spp. in stored samples from the Philippines and China.

AIM

Aim 1: To design and test a real-time PCR assay for detection of Capillaria spp.

Aim 2: To detect and characterise Capillaria spp. DNA in bio banked samples from the Philippines and China.

a) Optimise and validate DNA extraction and qPCR protocols for Capillaria detection in stored samples.

b) Determine the prevalence of Capillaria in the available sample sets.

c) Sequence positive samples to confirm species identity and explore genetic diversity.

Innovative point-of-care diagnostic tools for schistosomiasis.

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This project is suitable for an Honours and Masters student.

BACKGROUND

Schistosomiasis is a severely debilitating and often fatal chronic parasitic disease caused by agents of the genus Schistosoma, afflicting more than 250 million people worldwide. Sub-Saharan Africa accounts for 93% of the world's cases of schistosomiasis. The two main Schistosoma species affecting people in Africa are Schistosoma haematobium and Schistosoma mansoni. In Asia, S. japonicum is present in China, the Philippines and small foci of Indonesia, while S. mekongi is prevalent in the Mekong River basin. Both are highly zoonotic species, posing significant challenges for elimination.

By identifying communities with accurate schistosomiasis prevalence, diagnostic tests could help guide the allocation of resources and interventions to where they are needed most. Affordable diagnostic tools, especially used at point-of-care, for rapid mapping of schistosomiasis in the context of integrated control programmes are urgently needed.

AIM

Develop molecular-based POC assays by combining rapid DNA extraction, multienzyme isothermal rapid amplification (MIRA) and Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) with a CRISPR-association protein 12a (Cas12a) system.

Develop immunological POC tests through antigen screening and incorporating the best antigen into lateral flow immunoassays (LFIAs).

PROJECT POTENTIAL

If successfully developed and deployed, both POC assays will have a significant impact on the monitoring aspect of parasitic control programs, with potential to replace the far less sensitive Kato-Katz procedure currently used to facilitate the control of schistosomiasis in endemic areas.

Integrated epidemiology and disease prevention of Schistosoma mekongi and opisthorchis viverrini in the Mekong region.

BACKGROUND

Parasitic helminth infections such as schistosomiasis and opisthorchiasis continue to pose significant public health threats in the Mekong region. While Schistosoma japonicum has been the focus of much research in South-East Asia, Schistosoma mekongi—a zoonotic species endemic to Thailand, Lao People's Democratic Republic (Lao PDR), Cambodia, and Myanmar—remains neglected. Similarly, Opisthorchis viverrini, a liver fluke endemic to the same region, causes opisthorchiasis, a major risk factor for cholangiocarcinoma (bile duct cancer), yet remains under-addressed in integrated control strategies.

S. mekongi is transmitted by snails of the genus Neotricula and is known to infect humans, dogs, and pigs. Community-level prevalence in Cambodia and Lao PDR ranges from 0.6% to 33%, although recent data—especially on zoonotic reservoirs—remain limited. O. viverrini infections, on the other hand, are strongly association with consumption of raw or undercooked freshwater fish and are endemic in northeast Thailand and Lao PDR, where they affect millions of people.

The Mekong basin is recognized as one of the regions most vulnerable to climate change. Predicted increases in temperature (0.4°C to 3.3°C by 2060) and altered rainfall patterns (up to ±17%) are expected to influence the distribution and intensity of helminth transmission, including both S. mekongi and O. viverrini which are reliant on molluscan hosts. As climate conditions shift transmission zones, understanding the zoonotic and environmental drivers of infection is critical.

This project seeks to develop an integrated, multi-helminth control and elimination program in the Mekong region. The broader initiative will incorporate mass drug administration (MDA), health education, community-led water, sanitation and hygiene (CL-WASH), precision diagnostics, environmental monitoring, and targeted treatment strategies. Within this program, the PhD project will focus on both S. mekongi and O. viverrini, with emphasis on zoonotic transmission, diagnostics development, baseline epidemiological mapping, and post-intervention assessment—including the emerging threat of drug resistance in opisthorchiasis.

AIM

Aim 1: Identify and characterize animal reservoirs of S. mekongi and O. viverrini in Cambodia and Lao PDR.

Aim 2: Develop and validate novel diagnostic tools for S. mekongi and O. viverrini for use in both human and animal populations.

Aim 3: Conduct baseline prevalence surveys of S. mekongi and O. viverrini in humans and animals in selected endemic sites using newly developed diagnostics.

Aim 4: Evaluate the impact of an integrated intervention (MDA and health education) on the prevalence and transmission of S. mekongi and O. viverrini at 12–18 months post-intervention.

Aim 5: Investigate the presence and genetic markers of potential drug resistance in Opisthorchis viverrini, particularly in areas with long-standing praziquantel use.

PROJECT POTENTIAL

This project will contribute significantly to our understanding of multi-helminth epidemiology in the Mekong region and provide scalable tools and strategies for integrated parasite control in a changing climate.

Epidemiology of soil-transmitted helminths (STH) and strongyloides in Sarawak province, Malaysia.

This project is suitable for a PhD student only.

BACKGROUND

Parasitic worms are a major global health concern, infecting millions worldwide and causing chronic, potentially lifelong infections leading to significant disease and disability including growth and mental stunting in children, anaemia, and malnutrition. Intestinal helminths infect billions, with the majority of infections caused by soil-transmitted helminths (STH) (1.5 billion), schistosomiasis (250 million), and strongyloidiasis (600 million). A significant concern are zoonotic which complicate control and elimination programs due to animal reservoirs present, and potential increases in prevalence and changes in distribution of these parasites due to climate change.

There is also decreasing expertise in morphological parasite diagnosis despite their significant health burden. Microscopy with Kato-Katz (KK) is a mainstay of national surveys for STH and schistosomiasis but lacks sensitivity, particularly in low prevalence areas, and is highly dependent on microscopist skill. This has led to under-reporting of parasite prevalence and missing new or rare parasites. Molecular tools have greater sensitivity and have been used in prevalence surveys to identify parasites, while an AI-based microscope platform recently demonstrated increased sensitivity over human slide readers while decreasing slide read time to only 10 minutes for STH.

Sarawak province in Malaysia is a heavily forested area with unique biodiversity with increasing deforestation for farming, plantations and residential development

leading to increased risk of parasitic zoonoses infections. Few helminth surveys have been performed in Sarawak province, however small cohort studies on longhouse communities report prevalence >14% for STH, 11% for strongyloidiasis, and 4–11% for schistosomiasis. Non-human primates are also present in Sarawak and have previously been found to be infected with a range of zoonotic helminths including Capillaria, Oesophagostomum, Strongyloides, Trichuris, Ascaris and Hookworm.

There is great potential for increased transmission and emergence of new zoonotic helminth disease in Sarawak, and epidemiological surveys of humans, animals, and the environment utilising new diagnostic tools and genetic analysis will be crucial to understanding transmission and controlling infection there.

AIM

Aim 1: To collect stool samples from humans and animals (dogs, cats, non-human primates), along with soil and water samples, in endemic villages of Sarawak.

Aim 2: To perform molecular diagnostics on collected stool and environmental samples to identify helminth parasites.

Aim 3: To develop and optimise a method for an AI-based microscopy platform detection of Strongyloides spp. and compare with conventional microscopy and molecular diagnostics.

Aim 4: To perform haplotyping and population genetic analysis for Strongyloides spp., Hookworm, and Schistosoma spp. identified in human, animal, and environmental samples.

Aim 5: To identify environmental, economic, and social characteristics of high helminth prevalence areas combined with results of parasite surveys to map transmission hot-spots in Sarawak province.

Systems Virology

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The Systems Virology Laboratory investigates virus-host and virus-vector interactions at molecular, cellular and organism levels using a combination of advanced multi-omics techniques, bioinformatics, molecular virology and RNA structural biology.

We utilise advanced model systems such as stem cell derived organoids to study viral pathogenesis and apply single-cell and spatial transcriptomics combined with computational modelling to map cellular responses to arboviruses and uncover viral strategies for immune evasion. We aim to identify regulatory pathways driving viral replication, transmission and pathogenesis that can be targeted for development of effective defence strategies against medically significant arboviruses like Dengue, Zika, West Nile and Japanese encephalitis viruses.

Brain and Mental Health Program

The research is critical with about half of all Australians experiencing mental ill-health at some stage in their lives. This program focuses on a range of mental health areas including anxiety, depression, ADHD, autistic spectrum disorder, bipolar disorder, eating disorders, and schizophrenia.

Our neuroscientists, geneticists, epidemiologists, and clinical researchers are devoted to developing treatments, finding the causes, and working out how to prevent these conditions. This includes investigations into innovative neuro-stimulation and psychopharmacological interventions for people with serious mental disorders. Our understanding in the areas of psychiatric genetics, neuroimaging and neuroscience will inform new strategies for prevention, early intervention, and the treatment of complex syndromes.

Neurological conditions such as Parkinson's disease, multiple sclerosis (MS), motor neuron disease, epilepsy, and dementia, including Alzheimer's disease, are a growing health issue in Australia, often with limited treatment options. Our researchers are providing a broad interdisciplinary expertise in advancing understanding of this area from infancy to the elderly.

Psychiatric Genetics

Distinguished Scientist: Professor Sarah Medland OAM

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The Psychiatric Genetics Group focuses on investigating the genetic and environmental factors that influence mental health conditions and the impact of non-psychiatric conditions on mental health across the lifespan. The group also have a strong focus on the genetics of brain structure and on women's health.

The role of genomics in understanding psychiatric and neurological disease.

This project is suitable for PhD students only. Applicants with backgrounds in Psychology, Psychiatry, Statistics or Public Health are preferred.

Over the past decade, large-scale collaborative projects have significantly increased our knowledge and understanding of the genetic risk factors for mental health and neurological conditions across the lifespan.

Translation of genetic findings is usually conceptualised as a process involving the characterisation of implicated loci, identification of treatment targets, drug development and clinical trials. However, the accurate communication of the promises and limitations of new research findings is an essential part of research translation as is examining the utility of analytic techniques such as polygenic risk scores.

This project will focus on examining the ways genomic data could be used in clinical practice and the accuracy and specificity of these techniques. The project will require a strong background in statistics and research methodology.

Please note this is a dry lab analysis focused project.

Health and wellbeing in people with bipolar disorder.

This project is suitable for PhD students only.

Bipolar disorder is a lifelong and severe psychiatric illness characterized by recurrences of episodes of depression and hypomania or mania. Lithium is the first option in the pharmacotherapy of bipolar disorder. However, only one third of patients have a good response to this treatment, i.e., they often recover and remain well as long as they continue taking Lithium. The rest have a partial or deficient response.

QIMR Berghofer is part of an international effort to identify individual differences in Lithium response. We are collecting data across Australia on mental health, wellbeing and treatment response on bipolar disorder. We offer a project to analyse Lithium response in bipolar patients, comorbidity with other disorders and quality of life.

Please note this is a dry lab analysis focused project.

Identifying risk factors for problematic internet use and video gaming in Australian adults.

Supervisor: Associate Professor Penelope Lind

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This project is suitable for Honours students only. This project is most suitable for students with a strong background in Psychology/Psychiatry and statistical analysis.

The proliferation of computers, gaming consoles and widespread use of the internet in the last 15 years has resulted in the emergence of behavioural addictions to digital technology, namely the internet and video games, and the rise of cyberbullying. Pathological internet use and video gaming have been association with mental health issues (such as anxiety and depression), increased rates of obesity, introversion, a high degree of loneliness, disrupted family relationships and academic problems. Similarly, victims of cyberbullying can experience significant emotional and physical harm as well as social isolation.

I have previously recruited a cohort of Australian adults who completed an online questionnaire in order to (i) identify risk factors association with these behaviours, (ii) investigate the emotional and educational or occupational impacts of these behaviours, and (iii) examine the co-occurrence of these behaviours with other personality characteristics and psychopathologies such as substance use and mental health disorders.

I offer a project to analyse the collected online questionnaire data, and to provide the Honours student access to the online questionnaire in order for them to potentially recruit a second cohort.

Novel efficient statistical methods for biobankscale prediction from brain imaging.

Co-supervisor: Dr Baptiste Couvy-Duchesne

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This project is suitable for PhD students.

BACKGROUND

The field of neuroimaging is at a turning point, owing to the availability of several large datasets such as the UK Biobank, which comprises more than 50,000 volunteers from the general population with deep phenotyping, multimodal MRI and genotyping data. In comparison, clinical samples currently comprise a few thousand individuals at most, though larger samples should be available soon. Such large data promise a finer understanding of the brain association with disorders as well as improved risk prediction, though they also raise computational and methodological challenges.

AIM

This project aims at building prediction algorithms able to deal with the large number of features that still far exceeds the number of participants. This requires efficient algorithms and models that can scale up to the data (UKB sample is expected to grow to 100,000 participants) and that can combine information from different samples. Prediction often relies on penalised regression or convolutional neural networks (CNNs) that become extremely costly to train or update on large sample sizes, lack interpretability (black boxes), and often require pulling raw data together from different studies. Summary statistics such as brain association maps represent a condensed, meaningful and de-identified set of information, which could facilitate the analysis of big-data.

PROJECT POTENTIAL

Summary statistics are a promising way to jointly analyse multiple datasets (federated learning) without having to share or pull together the individual-level data, which often poses important ethical and legal difficulties, in particular in the case of clinical data. Lastly, methods based on summary statistics can be computationally savvy as they do not require large memory and long calculations, unlike most analyses performed on individuallevel data

Genetic and environmental influences on brain structure and function.

Co-supervisor: Dr Baptiste Couvy-Duchesne

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This project is suitable for an Honours student.

BACKGROUND

Genetic and environmental factors influence the structure and function of the human brain. Disentangling and quantifying these sources of variation (genetic and environmental) may be crucial to understanding the brain's genetic architecture and how it relates to typical and atypical brain function.

AIM

To provide a normative reference of healthy brain structure for future studies of neurological and psychiatric disorders by establishing a robust map of genetic and environmental influences on the brain.

METHODS

This project uses brain structure and function measures collected in genetically informative datasets. Statistical approaches such as twin modelling and polygenic risk scores will be applied to neuroimaging measures to elucidate genetic and environmental influences on brain structure and function.

PROJECT POTENTIAL

To identify the factors contributing to differences in brain structure and function between individuals and highlight brain regions especially vulnerable to genetic and environmental influences.

Brain Modelling

Group Leader: Associate Professor James Roberts

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The Brain Modelling Group models and analyses brain structure and dynamics in health and disease. This work currently follows two major themes: developing new diagnostic methods for infant and child brain health and modelling large-scale brain activity across the lifespan.

In infants and children, the group uses techniques from physics and machine learning to extract more information than ever before from intensive

care monitoring of babies born prematurely or with complications, and children at risk of adverse developmental outcomes. The goal is to enable early detection of injuries and early prognosis of developmental outcomes, so that clinicians can optimise care with personalised markers of brain health, potentially opening the window for new treatments.

On the modelling side, the group is harnessing the rapid developments in neuroimaging technology and connectomics to develop new mathematical models of brain activity, in particular at the spatial scales most relevant to human health. The goal is to fill in some of the large gaps in our knowledge of how neuroimaging brain signals emerge from brain structure, on how this relationship varies as we grow and age, and how things can go wrong leading to neurological and psychiatric disorders.

Modelling brain dynamics across the lifespan.

This project is suitable for PhD or Honours students. This project would suit students with a background in physics, maths, or a related discipline, and an interest in computational neuroscience, with some experience in programming (e.g., in MATLAB).

A major challenge for neuroscience is to understand how the brain's densely interconnected network of neurons—the "connectome"—gives rise to the rich repertoire of brain activity. The overarching aim of this project is to reveal how complex patterns of neural activity emerge from the connectome across the lifespan. This will entail using a novel combination of cutting-edge large-scale modelling of brain dynamics and state-of-the-art neuroimaging data (both structural and functional). There will be numerous applications depending on interests, examples include:

- How ageing brain structure changes our brain activity.
- How non-invasive brain stimulation perturbs brain network activity.
- How disorders such as epilepsy, schizophrenia, or ADHD may emerge from biologically-plausible changes to model parameters.
- Modelling sleep dynamics.
- Developing novel analysis methods for complex spatiotemporal dynamics.
- Model the early development and maturation of brain networks (collaboration with experimental neuroscientists at UQ).

Brain and physiological signal analysis from infancy to adolescence.

This project is suitable for PhD, Masters or Honours students.

BACKGROUND

The advent of precision medicine demands better tools for measuring human structure and function. The period from infancy to adolescence is a particularly important period of the lifespan where this lack of diagnostic and prognostic tools is felt in earnest. We measure signals from the brain and body (e.g. heart, lungs) to reveal important information on human health. The rise of machine learning and AI has delivered powerful new methods for data analysis, with which we develop tools that can track developmental trajectories more accurately and in more detail than ever before. We aim to evaluate these tools as developmental biomarkers and diagnostic tools to detect disease and monitor the response to interventions.

AIM

There are several opportunities for student-led projects across multiple large-scale datasets spanning EEG, neuroimaging (MRI), sleep physiology, cognitive performance, behavioural measures, and environmental factors. Projects are available for students at Honours, Masters, and PhD levels, and can be tailored in scope and methodological depth accordingly.

APPROACH

Students will have access to large, multimodal datasets including:

- Resting-state and sleep EEG.
- Structural and functional MRI.
- Brain–Cardiorespiratory physiological coupling during sleep.
- Cognitive and behavioural measures including psychological profiles (where available).
- Environmental and developmental risk/protective factors.

These datasets span infancy through adolescence and include both typically developing and atypically developing cohorts (e.g., Healthy Brain Network).

PROJECT POTENTIAL

Depending on interests, topics could include:

- Development of age-maturing head models for EEG source reconstruction.
- Brain connectivity across childhood neurodevelopmental disorders.
- Brain Age applications to understanding cognitive and behavioural development.
- Brain–heart–lung coupling during sleep as a marker of developmental maturation.
- Investigation of environmental factors that shift developmental brain trajectories toward vulnerability or resilience.

Translational Neurogenomics

Senior Group Leader: Professor Eske Derks

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The Translational Neurogenomics Laboratory is headed by Professor Eske Derks. The group currently includes 10 members (two postdocs, two visiting scientists, two PhD students and three undergraduate students). The Translational Neurogenomics Laboratory has identified genetic risk factors for a range of neuropsychiatric conditions, including substance use disorders, schizophrenia, depression, and obsessive compulsive disorder. Researchers in this group use genetic data to address questions, such as: Which genetic variants in the DNA increase the risk of developing a neuropsychiatric disease? What is the genetic overlap across different psychiatric disorders? What are the downstream molecular consequences underlying statistical genetic associations? Which existing drugs may be repurposed for prevention and treatment of neuropsychiatric diseases?

Investigating the role of OCD risk genes in human brain cell function.

Supervisor: Dr Lotta Oikari

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BACKGROUND

Obsessive compulsive disorder (OCD) is a psychiatric illness that affects approximately 1% of the population. OCD is responsible for profound personal and societal costs, including a substantial risk of suicide as well as an increase in general mortality. OCD is highly heritable, with twin based heritability estimates ranging between 27-47% in adults and 45-65% in children. Professor Derks (Translational Neurogenomics) recently led a study that identified 249 potential effector genes for OCD, with 25 of these classified as the most likely causal candidates. In a joint study between the Translational Neurogenomics and Cellular and Molecular Neurodegeneration groups, this project will investigate the roles of OCD risk genes on human neurons.

AIM

The expression of OCD risk genes will be modulated in healthy human stem cell-derived neurons. Following gene modulation, effects on neuron function will be investigated. This will include assessing the effects on neuron viability, marker expression and key functional proteins to understand how OCD risk genes affect neuron function.

Key assays will include:

- tissue culture,
- RNA-interference (RNAi),
- gene and protein expression studies and
- confocal microscopy.

OUTCOME

This project will reveal new information of the roles of OCD risk genes in human neurons. This will allow us to better understand cellular changes associated with OCD and ultimately develop new treatments.

Investigating the genetic relationships of Alzheimer's disease and sleep apnea.

This project is suitable for an Honours student. Required Skills or Experience: Possess a basic understanding of genetics, molecular biology and bioinformatics. Have a keen interest in neurogenetics and familiarity with R programming language will be advantageous but not necessary.

BACKGROUND

Alzheimer's disease is the most prevalent forms of dementia in elderly people characterised by cognitive impairment and loss of memory, affecting the quality of life. Unfortunately, there is no cure for Alzheimer's disease yet, therefore, identifying risk factors and the molecular factors that underlie increased susceptibility to Alzheimer's disease, will help early diagnose risk individuals to offer preventive care. Burgeoning evidence, particularly from animal and human studies, is pointing towards an intricate comorbid association between sleep disorder, particularly obstructive sleep apnea (OSA)-most prevalent forms of disorder in mid to elderly people. In this project, we aim to establish whether OSA has any causal association with risk of Alzheimer's disease leveraging genome-wide association studies (GWAS). Next, the project will also seek to discover molecular factors i.e., gene regulation that underlie this relation between Alzheimer's disease and OSA via integrating GWAS with molecular quantitative trait loci (QTLs) datasets. This will be an ideal project for a motivated and enthusiastic Honours student to study role of OSA (if any) on the risk of Alzheimer's disease and molecular factors that underlie this association.

APPROACH

We will offer hands-on training to students on various methods, particularly, analysis of GWAS and molecular QTLs datasets, required for successful completion of this project. Students will be highly skilled and efficient on handling large-scale genomics datasets and analysis of such datasets using bioinformatics and statistical genetics methods.

OUTCOME

The anticipated outcomes of this project are to assess whether sleep disorders contribute to induce or accelerate the risk of Alzheimer's disease and identify molecular factor that could serve as potential biomarkers for this association. The findings from this study are expected to provide new insights into the genetic relationships between sleep disorders and Alzheimer's disease. The student will gain valuable computational and analytical skills by applying bioinformatics and statistical genetics methods.

Brain age, epigenetic age, and neuropsychiatric disorders.

Co-supervisor: Dr Phoebe Imms

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We are looking for highly motivated Honours or PhD students with an interest in studying neuroscience, genetics, and mental health using advanced statistical and quantitative techniques.

BACKGROUND

Ageing is among the strongest risk factors for many neuropsychiatric diseases. However, ageing is not uniform across the body. Our organs (e.g., brain), our bodily systems (e.g., cardiovascular, metabolic), and even our DNA ages at different rates according to internal and external factors. This variability in biological ageing needs to be understood to make sense of how ageing influences, or is influenced by, neuropsychiatric disease. Importantly, some of the variability in biological ageing can be explained by our genetics.

Artificial intelligence and machine learning models can be used to derive the biological age of the brain from MRI scans. The difference between biological age and chronological age is the 'age gap', and it represents deviation from the normative trajectory of ageing. Similarly, epigenetic age refers to an estimate of biological age based on patterns of DNA methylation, which is a chemical modification of DNA that influences gene expression without changing the underlying genetic sequence. Unlike chronological age, epigenetic age reflects how your body is aging at a molecular level. Such biologically-informed ages can be used as a measure of internal system integrity, and a marker of dysfunction.

Physical and mental health are fundamentally linked: As one is affected, the other is too. For example, accelerated biological ageing in later life is associated with greater risk of depression and anxiety. Ideally, epigenetic clocks and neuroimaging-derived brain age gaps could be harnessed to monitor and stratify risk of neurological and neuropsychiatric disease. However, because they each measure ageing very differently, there is conflicting evidence that brain age and epigenetic age are phenotypically associated. Nevertheless, both older-than-expected brain ages, and faster paces of epigenetic ageing, have been related to psychiatric conditions (e.g., Schizophrenia), mood disorders (e.g., depression) and neurodegenerative disorders (e.g., Alzheimer's disease). Despite the (mixed) evidence of phenotypic relationships between brain age, epigenetic age, and neuropsychiatric disorders, their shared genetic bases remain incompletely understood.

AIM

Some example research questions that can be explored in this project are:

- What are the genetic similarities between neuroimagingderived brain ageing and epigenetic ageing?
- How do the genetic architectures of brain ageing and epigenetic ageing relate to external traits of interest, including (but not limited to): psychiatric traits (schizophrenia, autism spectrum disorder, attention-deficit hyperactivity disorder, obsessive-compulsive disorder), neurodegenerative traits (Alzheimer's disease, Parkinson's disease, fronto-temporal dementia), and ageing traits (frailty, longevity)?
- What are the conditionally independent genetic associations between each external trait and a network representing epigenetic and brain ageing?
- How do polygenic scores for brain ageing and each epigenetic clock relate to neuropsychiatric factors?
- Are there shared phenome-wide associations between brain ageing and epigenetic ageing? If so, do these point to shared biological pathways determining brain age and epigenetic age?
- How much of 'brain age' and 'epigenetic age' measure system-wide integrity and how much is brain specific?

APPROACH

This project involves analysing clinical, genetic, and neuroimaging data (mostly tabular, with the potential for preprocessing of raw data if needed). Students will have the opportunity to perform genetic analyses including (but not limited to) genomic structural equation modelling, linkage disequilibrium score regression, and genetic network analysis. If required, students also can learn how to implement machine learning algorithms to estimate brain ages from large-scale neuroimaging datasets. Skills will be developed in the use of language-based environments for statistical computing (e.g., RStudio and bash).

PROJECT POTENTIAL

This project offers the development of hard and soft skills necessary for a career in psychological, biomedical, or healthcare research. Students will gain invaluable experience in working among a team of peers while taking charge of their own independent project. There is strong potential for publication.

Understanding the shared and unique genetic risk factors between neuropsychiatric disorders and their comorbidities.

This project is suitable for an Honours student. Required Skills or Experience: We seek motivated Honours students interested in genetics, statistics, and bioinformatics. Some background in psychology or genetics may be helpful, but is not required for success.

BACKGROUND

Neuropsychiatric disorders have been demonstrated to have strong heritable components, allowing research to focus on, and differentiate between, the genetic and environmental risk factors which contribute to these disorders. The diagnosis of one europsychiatric disorder is association with an increased risk that someone will also have other diagnoses, including both physical diseases and other neuropsychiatric disorders. Examining the shared and unique genetic risk factors underlying the relationship between these comorbidities can break down variations in genetic influences, elucidate shared aetiology, and improve treatment options and outcomes. In this project, students can build their research question around neuropsychiatric disorders they have an interest in and choose which comorbidities to explore.

APPROACH

Students will develop their ability to identify gaps in the literature and formulate an appropriate research question to fill this gap with assistance from supervisors, and be trained to use a diverse set of methodologies in bioinformatics in addition to coding languages.

- Genome-Wide association Studies
- Genomic Structural Equation Modelling
- Linkage Disequilibrium Score Regression
- RStudio & Bash

OUTCOME

Students will identify shared and/or unique genetic risk factors of their chosen comorbidities. Students will gain proficiency in versatile skill sets, including bioinformatics approaches, statistical analysis, problem-solving, and communication. The project offers strong potential for the publication of the research in a journal, while working with a diverse team passionate about supporting new researchers.

Integrating genomic data to characterise inherited risk factors for mental health disorders.

This project is suitable for an Honours or PhD student. We are seeking a highly motivated student with a strong interest in statistics and quantitative studies.

BACKGROUND

Mental health disorders, including depression, anxiety, and substance abuse disorders, afflict around half of the individuals at some point in their lives and account for a substantial proportion of the global burden of disease. Recently, significant progress has been made in identifying genetic (i.e., inherited) risk factors associated with mental health disorders through genome-wide association (GWA) studies of large, population-based cohorts.

Although these GWA studies have implicated many genetic risk factors for mental health disorders, identifying the exact causal genes remains challenging. This is due in part to complex interactions between multiple cellular data types in specific tissues that are likely to mediate susceptibility. Integrated studies of multiple cellular data, such as DNA sequence variation, gene expression, and DNA methylation, in relevant tissues are therefore required to understand the impact of genetic risk factors on mental health.

This project will use high-quality gene expression and DNA methylation data measured in whole blood to characterise genetic risk factors underlying mental health disorders. Analyses will then be conducted across tissues using several publicly available multi-tissue genomic compendia. This study will provide a unique resource to identify and characterise novel genetic factors underlying susceptibility to mental health disorders. The identification of such causal genes is the next crucial step in elucidating the complex molecular pathways of mental health disorders and may help in the development of diagnostic tests and more rational treatment strategies.

What do we offer:

- A position in a dynamic research environment and the opportunity to conduct high-quality studies.
- Access to large-scaled datasets through (inter) national collaborations.

AIM

- To characterise genetic risk factors for psychiatric disorders in a large population-based sample.
- To prioritise causal tissues and mechanisms using independent multi-tissue genomic compendia.

Neurogenetics and Dementia

Team Head: Associate Professor Michelle Lupton

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Dementia is the second leading cause of death for all Australians. Alzheimer's disease is the most common form of dementia, predicted to affect 152M globally by 2050.

Common late onset Alzheimer's disease is caused by age-related failure of clearance of toxic proteins (β-amyloid and tau) from the brain leading to an immune response. Successful treatment or prevention relies on the ability to identify those at high risk or the earliest disease stages.

We run one of the largest cohort studies in the world focused on those at high risk and in the earliest disease stages of Alzheimer's disease, for the identification of affordable, accessible and scalable biomarkers for dementia diagnosis and screening, to be prepared for the best use of newly developed drugs and lifestyle interventions as they become available.

In addition, we carry out large scale genetic studies, including the use of genetic risk prediction and the identification of causal disease processes in Alzheimer's disease and dementia.

Accessible biomarkers for early-stage Alzheimer's disease.

This project is suitable for Honours, Masters, MPhil, or PhD students. For those with experience in statistics and an interest in dementia, genetic epidemiology, psychology, bioinformatics and machine learning.

BACKGROUND

Dementia affects an estimated 353,800 Australians, with up to 80% diagnosed with Alzheimer's disease (AD). Newly developed anti-amyloid drugs are set to revolutionise the treatment of AD. These are likely to have the most significant impact at the earliest stages of disease. Therefore, there is an urgent need for early-stage biomarkers that are affordable, accessible, and scalable.

AIM

To investigate genetic risk prediction and biomarkers for early-stage Alzheimer's disease, including the combination of traditional and digital biomarkers, which opens up opportunities for simple, accurate, and effective screening to identify early-stage AD.

METHODS

The student will build on our current work in PISA (the Prospective Study of Aging, Genes, Brain, and Behaviour) in this data analysis project (dry lab). They will test the integration of genetic risk prediction, blood-based protein biomarkers, and digital biomarkers, such as online cognitive testing, speech analysis and hand movement patterns. Predictive algorithms will be developed using statistical and machine-learning approaches.

PROJECT POTENTIAL

Accessible screening for early-stage Alzheimer's disease will identify individuals suitable for more in-depth diagnostic tests, treatment, interventions and participation in clinical trials.

Shared genetic architectures of epilepsy, frailty, and Alzheimer's disease: Causal inference, cognitive decline, and drug repurposing.

This project is suitable for Honours, Masters, MPhil, or PhD students.

BACKGROUND

Alzheimer's disease (AD) is one of the leading causes of dementia in older adults. The global burden of AD is projected to grow substantially, with an estimated 139 million people affected by 2050. AD is highly heritable (60–80%), and genome-wide association studies (GWAS) have identified over 70 associated genetic loci. Despite this, the complete genetic architecture and mechanisms underlying AD remain poorly understood. Emerging evidence highlights the role of additional risk factors—including epilepsy and frailty—in the progression of AD.

Individuals with epilepsy appear to be at greater risk for developing AD and experiencing frailty, potentially through pathological neuronal hyperexcitability pathways that accelerate cognitive decline, particularly in frail individuals. However, the causal relationships between these conditions and whether they share underlying molecular genetic factors have yet to be established.

AIM

This project will investigate the shared and unique genetic relationships between epilepsy, frailty, and Alzheimer's disease.

APPROACH

This project involves analysis of genetics and cognitive datasets.

Students will have the opportunity to perform statistical genetics analyses including (but not limited to):

- Linkage disequilibrium score regression (LDSC) and genetic correlation analyses.
- Mendelian Randomisation to test causal relationships between epilepsy, frailty, and AD.
- Polygenic risk score (PRS) analyses to predict domainspecific cognitive decline in the Prospective Imaging Study of Aging (PISA) cohort.
- Computational drug repurposing to prioritise therapeutic targets from shared genetic mechanisms.

No prior bioinformatics tools for genetic data analysis or R programming skills are not required as training to work on those platforms will be developed during honours.

PROJECT POTENTIAL

Outcomes of this project are expected to:

- Provide evidence of causal relationships between genetic risk for epilepsy, frailty, and AD.
- Identify individuals at increased risk of cognitive decline through polygenic risk prediction.
- Prioritise repurposable drug compounds targeting shared genetic mechanisms.
- Support the development of personalised prevention strategies for ageing populations.

There is strong potential for publication arising from this work.

Markers of bushfire smoke associated neurological impact.

This project is suitable for Honours, Masters, MPhil, MD or PhD students.

BACKGROUND

International evidence shows a strong association of air pollution exposure to increased risk of neurological disorders, and specifically Alzheimer's disease. Fine particulate matter (PM) less than 2.5 micrometres in diameter (PM2.5) is especially dangerous due to its ability to penetrate into the respiratory system and bloodstream. PM2.5 constitutes a significant proportion of bushfire smoke. Climate change is increasing exposure with substantial health risks, including the entry of ultrafine particles into the brain. Vulnerable populations include frontline rural firefighters and ageing populations.

APPROACH

The student will work on data collected as part of our R-FIRE (Rural Firefighter Investigation of Risk & Exposure): Brain Health cohort study, in this data analysis project (dry lab). They will test for associations of long term PM2.5 exposure with general health outcome measures and comprehensive brain health measures (including Ecog HBA Functional Assessment tool, and our online cognitive testing battery assessing memory, reasoning, concentration, and planning).

PROJECT POTENTIAL

The study aims to enable targeted screening and intervention efforts to mitigate the neurological consequences of smoke exposure, thereby improving health outcomes for affected individuals.

Cellular and Molecular Neurodegeneration

Senior Group Leader: Professor Anthony White

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qimrb.edu.au/researchers-and-labs/cellular-and-molecular-neurodegeneration

The Cellular and Molecular Neurodegeneration Laboratory investigates the cause and potential treatments for brain diseases including dementia (Alzheimer's disease), motor neuron disease (amyotrophic lateral sclerosis) and Parkinson's disease. These disorders (collectively known as neurodegenerative diseases) are a growing health issue in Australia and worldwide, with few treatment options available. In order to gain a better understanding of these diseases and develop new therapeutic approaches, the research team is currently developing new human brain cell culture methods for microglia, brain endothelial cells, organoids (mini-brains), and olfactory (nasal) cells.

The laboratory is utilising these new 2D and 3D human brain cell models to understand brain disease pathways, and the impact of environmental factors such as air pollution, SARS-CoV-2, and bushfire smoke on brain health. We have also established platforms for drug screening to identify potential new therapeutics for treatment of brain diseases.

Development of metal-based therapeutics for neurodegenerative diseases.

Co-supervisor: Dr Lotta Oikari

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This project is suitable for a PhD student but may also be considered for an Honours student.

Biological trace elements, also known as trace minera, or biometals include copper, zinc, iron, selenium and manganese. These and other biometals have essential roles in many areas of brain function including energy metabolism, transcription factor activity, antioxidant regulation and synaptic signalling. During ageing and brain disease, regulation of biometals is dramatically altered with changes to cellular and subcellular handling and localization. This leads to impairment of brain cell function, in both neurons and surrounding cell types (astroglia and microglia) and contributes to neuronal cell death in disorders such as Alzheimer's, Parkinson's and motor neuron diseases, as well as in lysosomal storage disorders such as Batten disease (childhood brain disorder). Our research has uncovered some of the processes involved in the loss of biometal regulation and found this to be an early event in many disorders. We are also developing compounds that can help restore biometal stasis in the brain.

This project involves the investigation of new metal-based compounds as potential therapeutic or diagnostic agents for Alzheimer's disease and other brain disorders. These compounds have unique properties including modulation of brain cell signalling, control of anti-oxidant function, and regulation of neuro-immune responses. The project examines the action of the compounds on a range of cell types including animal and human neurons, astrocytes and/or microglia, and we aim to understand the molecular pathways that contribute to therapeutic action. Longer-term projects will involve the examination of the compounds as therapeutics in specific animal models of brain disease to determine if they are suitable for further therapeutic or diagnostic development towards the clinic.

The wet lab project will utilize a range of tools and techniques including brain cell culture, analysis of immune response (cytokine analysis), phagocytosis assays, anti-oxidant assays, X-ray analysis of biometal distribution and metalloproteomic studies on metal-protein interactions.

Drug repurposing to treat childhood dementia.

Co-supervisor: Dr Lotta Oikari

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This project is suitable for an Honours, Masters, MPhil, MD or PhD student.

BACKGROUND

Childhood dementia is caused by a group of genetic disorders which have effects on infants and children that include dementia (loss of normal brain function). There are no cures, and treatments limited effects. We are collaborating with Professor Eske Derks and Dr Zac Gerring at QIMR Berghofer to screen currently used drugs to determine if any have therapeutic effects on childhood dementia.

AIM

Drugs and drug targets are identified using computational approaches, and the leading drugs will be tested for effectiveness in pluripotent stem cell derived brain cell models of childhood dementia.

METHODS

Growth of human stem cell-derived brain cell cultures.

PROJECT POTENTIAL

Potential to identify new drugs to treat childhood dementia.

Generating patient-derived microglia to investigate neuroinflammation in MND.

Co-supervisor: Dr Lotta Oikari

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Co-supervisor: Dr Hazel Quek

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This project will build important new tools for understanding the role of the immune system in amyotrophic lateral sclerosis (ALS), a form of motor neuron disease (MND). Inflammatory responses by the resident brain and spinal cord immune cells (microglia) have an important role in ALS/MND and are key targets for therapy. Until now, research on microglia has been largely restricted to cells of animal origin. We now have new techniques to generate microglia directly from ALS/MND patients to help understand the disease and test patient-specific drugs to modulate the immune response in the brain and spinal cord. This project will provide a new approach to investigating and treating inflammation in MND.

Generating Alzheimer's microglia for testing patient responses to immune-modulating compounds.

Co-supervisor: Dr Lotta Oikari

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Co-supervisor: Dr Hazel Quek

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Alzheimer's disease is anticipated to affect 100 million patients with an annual cost of US$1 trillion by 2050. Promising amyloid-clearing therapies have failed to translate to clinical outcomes, and new approaches targeting the underlying molecular pathways of Alzheimer's disease are urgently required. There has been a 're-awakening' to the critical role of microglia in Alzheimer's disease pathology. However, our ability to translate abnormal microglial biology into clinically relevant advances has been greatly impaired by inadequate cell models. Microglia-like cells can now be routinely generated from human peripheral blood monocytes. The approach is cost-effective and rapid, and these induced microglia reveal a remarkably close relationship to mature human microglia in terms of cell surface marker expression, functional assays, and gene expression.

In this project, we will generate microglia-like cells from blood samples collected from Alzheimer's patients, and people who are considered at high risk for Alzheimer's disease. We will compare the cultured microglia to identify patient-specific immune abnormalities using a range of assays currently established in our lab. We will then screen individual patient microglia for the efficacy of immune-modulating compounds to identify effective patient-specific neurotherapeutics in 'real-time'. This project will produce highly significant advances in patient-specific drug targeting for neuroinflammation in Alzheimer's disease, leading to the development of real-time, individual therapeutic approaches with major clinical benefits, including identifying patient-specific drugs, selecting suitable patients for clinical trials, and monitoring drug efficacy during trials.

Olfactory stem cells for investigating the causes and progression of dementia.

Co-supervisor: Dr Lotta Oikari

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Co-supervisor: Dr Hazel Quek

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BACKGROUND

With no clinical success yet achieved from amyloid-targeting strategies, there is an urgent need to gain new insights and develop effective treatments for people who have dementia. New stem cell-based approaches have generated much excitement in dementia research with the potential to study patient-derived neurons and supporting cells. However, the commonly used 'pluripotent' stem cells are artificially generated and do not possess all needed cell types, which makes them unsuitable as tools to understand the disease process in the majority of late-onset (sporadic) cases of dementia.

Olfactory (nasal) tissue contains a unique population of naturally occurring stem cells that renew the nasal receptor neurons and supporting cells in the nose throughout life. These exceptional stem cells can be collected through a routine procedure with local anaesthetic and readily grown in a culture dish in a laboratory to produce neurons and other key brain cell types that accurately reflect the same types of brain cells that occur in the patient of origin. These cells provide a unique tool to study patient-specific disease processes and develop therapeutics for personalised dementia medicine.

OBJECTIVE

Our plan is to collect nasal tissue from people with dementia and from people who are at high risk for dementia (together with matching control samples). The olfactory stem cells will be grown in our lab and studied using a range of molecular approaches to provide unique insights into the early disease changes in a person's brain cells. We are also attempting to grow brain 'organoids' from stem cells. These are 'mini-brains' that represent the 3-dimensional structure of a small part of a human brain and allow a much more accurate understanding of how brain cells work (or fail to work) in dementia. This will enable us to understand how brain cells are affected by dementia differently for each patient (i.e., derived neurons will retain patient-specific epigenetic markers) and will allow the screening of potential therapeutic drugs on an individual basis.

The potential impact of bushfire smoke on brain health.

Co-supervisor: Dr Lotta Oikari

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Co-supervisor: Dr Hazel Quek

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This project is suitable for an Honours, Masters, MPhil, MD or PhD student.

BACKGROUND

In this project, we are using our monocyte and pluripotent stem cell-derived brain cell models to understand how bushfire smoke affects the human brain, particularly its ability to include neuroinflammation. We are also working with Associate Professor Michelle Lupton, and Dr Jodi Thomas at QIMR Berghofer to determine if exposure to bushfire smoke affects the likelihood of being diagnosed with neurodegenerative diseases such as dementia.

AIM

1. Determine the impact of bushfire smoke on human brain cells.
2. Determine if exposure to bushfire smoke increases risk of dementia or other brain diseases.

PROJECT POTENTIAL

Potential to understand the impact of bushfire smoke exposure on human brain health.

Impact of bushfire smoke (haze) on childhood cognitive function in Indonesian schools.

Co-supervisor: Dr Hazel Quek

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This project is suitable for an Honours or Masters students.

BACKGROUND

Join an international research team at QIMR Berghofer, CSIRO, University of Canberra, and University of Indonesia, to study how seasonal bushfire smoke (haze) affects children's learning in Indonesia, and whether simple air filters in classrooms can make a measurable difference.

You'll help run validated attention testing in schools, work with local partners in Indonesia, and analyse how improved indoor air quality influences cognitive performance.

Your role as an Honours/Masters student:

- Travel to Indonesia for the initial testing period and assist with teacher training.
- Coordinate test administration and record classroom conditions (temperature, ventilation, haze levels).
- Support data entry and analysis, working closely with Indonesian collaborators.
- Contribute to interpretation of results, reporting, and publications.

AIM

Each year, haze from landscape fire impacts air quality across Southeast Asia, infiltrating classrooms and affecting children's health and learning.

This project - part of the HEAL HAZE initiative - will assess how haze exposure influences attention and whether classroom air filtration systems improve outcomes.

We'll use the d2 Test of Attention (d2/d2-R), a quick and wellvalidated measure of processing speed and concentration that is language-independent and easy for trained teachers to administer.

Cognitive Fitness

Group Leader and Program Director (Brain and Mental Health): Professor Murat Yücel

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qimrb.edu.au/researchers-and-labs/cognitive-fitness

The Cognitive Fitness Group uses cognitive neuroscience to create digital tools that measure, monitor and help optimise brain health.

Professor Murat Yücel's work primarily focuses on developing innovative approaches to Digital Medicine. This includes:

i. A gamified measurement tool for assessing cognitive and brain function for use in clinical research, aiming to comprehend the cognitive mechanisms of clinical dysfunction and guide mechanism-targeting interventions to enhance them;

ii. An ultra-brief tool for measuring cognitive fitness in clinical conditions, which can be used to build resilience against mental ill-health and improve performance in high-stakes situations, such as those faced by first responders, military professionals, and competitive athletes.

The novel Digital Medicine also includes an interactive virtual reality platform that delivers exposure/response prevention interventions for disorders like obsessive-compulsive disorder (OCD) and gambling disorder.

Professor Murat Yücel is also involved in clinical trials in Lifestyle Medicine, focusing on the neural and cognitive effects of physical exercise and mindfulness meditation. Additionally, he participates in clinical trials of Psychedelic Medicine, examining the cognitive and mental health effects of psilocybin and MDMA.

Child & Youth Mental Health

Honorary Group Leader: Professor James Scott

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qimrb.edu.au/researchers-and-labs/child-and-youth-mental-health

The Child and Youth Mental Health Group conduct research with a particular focus across four areas.

The first are studies of the causes and consequences of mental ill-health and suicidal behaviour in children and young people. This enables the identification of factors that influence mental health in childhood and adolescence. Modifying these factors can prevent the onset of mental illness and improve the wellbeing of children and adolescents.

The second research area addresses bullying victimisation and perpetration in school-aged children. Bullying victimisation is association with mental illness and poor academic performance.

The third is psychoneuroimmunology. Our research in this area has demonstrated the interplay between the nervous system and the immune system where we have shown some people have psychosis arising from inflammation in the central nervous system.

The fourth research area focuses on clinical trials and health service research. These studies evaluate the effectiveness of innovative treatments for young people at risk of or living with, mental illness and the outcomes following the implementation of clinical services and lifestyle support for young people living with mental illness.

Computational Neurogenomics

Team Head: Associate Professor Miguel Renteria

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qimrb.edu.au/researchers-and-labs/computational-neurogenomics

At the Computational Neurogenomics Laboratory, we use genomics, neuroscience, epidemiology, and data science to explore the complexities of the human brain.

Our research investigates the biological factors influencing cognition, behaviour, brain structure, and the risk of neuropsychiatric diseases. By analysing natural DNA variations across populations, we aim to uncover the mechanisms that shape brain function and mental health.

To achieve this, we apply advanced statistical and computational methods, collaborate across disciplines, and analyse large-scale datasets from international consortia and biobanks. We aim to deepen our understanding of human behaviour, neuroanatomy, and brain disorders, paving the way for better treatments.

We study a wide range of conditions, including Parkinson's disease, chronic pain, migraines, self-harm behaviours, depression, and sleep disorders.

Our team is committed to advancing scientific knowledge and improving human health by unlocking the brain's secrets.

Genetic architecture of glial responses to α-synuclein pathology in Parkinson's disease.

This project is suitable for PhD students.

BACKGROUND

Parkinson's disease (PD) is a progressive neurodegenerative disorder characterised by the loss of dopaminergic neurons in the substantia nigra and the accumulation of misfolded α-synuclein into Lewy bodies and neurites. Increasing evidence indicates that neuroglia (microglia, astrocytes, and oligodendrocytes) actively contribute to PD pathogenesis via neuroinflammation, proteostasis failure, and α-synuclein propagation. Genome-wide association studies (GWAS) have identified >140 PD risk loci, but the cell types, regulatory programs, and mechanisms through which many of these loci act remain poorly understood. Tools such as gsMap can integrate GWAS summary statistics with cell-type-specific epigenomic and transcriptomic data to assign

risk variants to likely effector cell types, including specific glial subpopulations.

Human iPSC-derived microglia cultures and midbrain organoids offer physiologically relevant systems to model glial–neuronal interactions in the context of α-synuclein pathology. Combining computational mapping with single-cell transcriptomics of α-synuclein-exposed glial models enables direct experimental interrogation of genetically informed pathways.

AIM

1. Map PD genetic risk to glial cell subtypes using GWAS summary statistics and integrative functional genomics.
2. Experimentally model α-synuclein–induced glial responses using human iPSC-derived microglia cultures and midbrain organoids.
3. Profile glial transcriptional states at single-cell resolution and integrate with genetic mapping results to identify and prioritise candidate pathogenic pathways.

APPROACH & TIMELINE

Year 1 – Computational mapping and model setup.

- Analyse publicly available PD GWAS data using gsMap, LDSC-SEG, and TWAS to identify glial-enriched risk loci.
- Integrate with public single-cell and epigenomic datasets to prioritise candidate genes/pathways.
- Work with Dr Nayler to establish iPSC-derived microglia and midbrain organoid cultures.

Year 2 – Experimental perturbation and single-cell profiling.

- Expose microglia cultures and organoids to pre-formed α-synuclein fibrils to model extracellular Lewy body pathology.
- Perform single-cell RNA-seq and, where feasible, spatial transcriptomics at early and late exposure timepoints.

Year 3 – Data integration and validation.

- Integrate experimental single-cell data with GWAS mapping to find convergence between genetic risk and α-synuclein-responsive transcriptional programs.
- Functionally validate top candidate pathways (e.g. CRISPR knockdown, small-molecule modulation) in microglia/organoid models, assessing effects on neuronal survival, α-synuclein clearance, and inflammatory signalling.

PROJECT POTENTIAL

This integrative project will link PD genetic architecture to human glial responses in disease-relevant models, uncovering cell-type-specific mechanisms and therapeutic targets that cannot be identified by computational or experimental approaches alone.

OUTCOME

The candidate will gain advanced bioinformatics skills in GWAS integration, single-cell data analysis, and network/pathway modelling, alongside wet-lab expertise in iPSC-derived microglia/organoid culture, α-synuclein pathology modelling, and single-cell genomics.

Genetic Epidemiology

Distinguished Scientist: Professor Nick Martin

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qimrb.edu.au/researchers-and-labs/genetic-epidemiology

The Genetic Epidemiology Laboratory seeks to identify the particular genes involved in complex disease aetiology. It performs longitudinal studies with twins on a wide range of complex traits of medical and behavioural interest. Particular research over recent years has moved to genome wide association studies (GWAS) to locate genes influencing complex traits including anxiety, alcoholism, and dizygotic twinning. Most recently, the laboratory initiated projects to recruit large patient samples for GWAS of anorexia, depression and other psychiatric disorders.

Complex Trait Genomics

Team Head: Dr Brittany Mitchell

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qimrb.edu.au/researchers-and-labs/complex-trait-genomics

The Complex Trait Genomics group investigates the genetic and biological basis of neuropsychiatric disorders. By analysing large-scale genomic, clinical, and epidemiological data, the team seeks to uncover the risk factors and biological pathways that explain why some people are more vulnerable to illness, why symptoms differ between individuals, and why treatment response varies.

Through advanced statistical genetics, computational biology, and large-scale international collaboration, the group investigates the genetic architecture of conditions such as depression, anxiety, and migraine across diverse populations. We leverage genome-wide analyses, polygenic risk prediction, causal inference approaches, and integrative genomic methods to identify biological mechanisms and clarify pathways underlying disease risk. Ultimately, our goal is to translate genomic discovery into meaningful clinical insight by enabling earlier identification of vulnerability, improved risk stratification, and more precise, evidence-based approaches to prevention and treatment.

Investigating sex differences in mental health disorders using genetic data.

Co-supervisor: Dr Jodi Thomas

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Co-supervisor: Professor Nick Martin

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This project is suitable for a PhD or Honours project. Seeking a motivated student with experience in psychology, genetics, epidemiology or statistics for dry lab analysis focused project.

BACKGROUND

Mental health disorders, such as depression and anxiety, exhibit notable sex differences in prevalence, age of onset, and symptomatology. Women are more likely to be diagnosed with depression and anxiety, whereas men have higher rates of certain externalizing disorders. While social and environmental factors contribute to these differences, genetic and biological mechanisms also play a crucial role. Advances in psychiatric genetics have enabled researchers to explore sex-specific genetic influences on mental health, yet many studies continue to overlook these differences.

AIM

This project aims to investigate whether genetic risk factors for depression and anxiety differ between males and females. Specifically, it will:

1. Identify sex-specific genetic variants association with these disorders.
2. Assess whether sex-specific polygenic risk scores (PRS) have differing associations between sexes.
3. Examine potential gene-by-sex interactions that contribute to mental health outcomes.

METHODS

The project will use large-scale genome-wide association study (GWAS) data from studies such as the Psychiatric Genomics Consortium (PGC) and the Australian Genetics of Depression Study (AGDS). This project provides an opportunity to develop skills in genetic data analysis, statistical programming, and genetic epidemiology. The findings may improve our understanding of the biological mechanisms underlying sex differences in mental health disorders and contribute to more personalized treatment approaches.

PROJECT POTENTIAL

This project has the potential to provide valuable insights into the genetic basis of sex differences in mental health traits, such as depression and anxiety, by identifying sex-specific genetic risk factors and exploring how they influence the onset, severity, and treatment response of these disorders. The findings could pave the way for more tailored, sex-specific interventions and improve our understanding of the biological mechanisms driving mental health disparities between men and women.

Decoding the complexity of depression: genetic drivers of heterogeneity and treatment outcomes.

This project is suitable for Honours, Masters, or PhD students. Seeking a motivated student, ideally with a background in psychology, genetics, epidemiology or statistics, to contribute to a dry-lab, analysis focused research project.

BACKGROUND

Depression is a major public health crisis, affecting one in five Australians over their lifetime. The heterogeneous nature of depression complicates both its diagnosis and the advancement of effective therapeutic strategies. Alarmingly, about a third of those diagnosed do not respond to conventional treatments, highlighting an urgent need to better understand the underlying biology of the disorder. While genetics is known to play a role in depression risk, less is understood about how it influences specific phenotypic characteristics (such as symptomatology, age of onset, recurrence, and sex differences) or why some individuals respond well to treatment while others do not.

This project aims to unravel these complexities by investigating the genetic basis of depression characteristics and treatment response, paving the way for more targeted and effective interventions.

AIM

This project will:

- Identify genetic factors that contribute to depression risk and key clinical features, such as age of onset and recurrence.
- Explore the relationship between depression and related traits
- Determine whether treatment response traits, such as medication efficacy, tolerability, and side effects, are influenced by genetic variation.

APPROACH

Leveraging large-scale national and international genetic datasets (N=20,000 and N=500,000), this project will apply cutting-edge statistical genetics approaches, including genome-wide association studies (GWAS) and polygenic risk scoring (PRS), to uncover the genetic architecture of depression-related traits. The student will investigate how genetic risk factors shape treatment response, differ between males and females, and contribute to key phenotypic features such as age of onset, recurrence, and symptom presentation.

PROJECT POTENTIAL

This project has the potential to significantly advance our understanding of the genetic underpinnings of depression, with a particular focus on identifying genetic factors that influence clinical features like age of onset, recurrence, and treatment response. By integrating large-scale genetic datasets with advanced statistical techniques, this research could pave the way for more personalised and effective approaches to depression treatment, particularly for individuals who do not respond to conventional therapies.

Genetic factors influencing acne and their shared links with other traits.

This project is suitable for Honours, Masters, or PhD students. Seeking a motivated student, ideally with a background in genetics, epidemiology or statistics, to contribute to a dry-lab, analysis focused research project.

BACKGROUND

Acne is a common skin condition that primarily affects the face and varies widely in both severity and treatment response. In its more severe forms, inflamed lesions can lead to permanent scarring, which has been linked to long-term psychosocial consequences. While environmental factors such as diet, hygiene, and skincare contribute to acne risk, genetic influences also play a significant role. Previous genome-wide association studies (GWAS) have identified genetic variants association with acne risk, as well as shared genetic architecture with other conditions, including hormone-related cancers. These findings implicate pathways related to immune function, sebum production, and hormonal regulation in acne pathogenesis. However, further research is needed to understand how genetic risk factors contribute to acne development and severity, and to better characterise potential shared genetic architecture with other conditions.

AIM

This project aims to explore the genetic basis of acne by:

- Identifying genetic variants association with acne risk and severity.
- Investigating whether genetic risk for acne overlaps with other conditions such as depression or metabolic traits.
- Evaluating the predictive power of polygenic risk scores (PRS) for acne.

APPROACH

The project will utilize data from large genetic studies, including the largest GWAS of acne to date. Genetic risk scores will be calculated and compared across different acne severity groups. Genetic correlation analyses will assess shared genetic risk factors between acne and other conditions. Statistical analyses will be conducted using software such as PLINK and R.

PROJECT POTENTIAL

This project offers the opportunity to gain experience in genetic epidemiology, bioinformatics, and statistical genetics, with potential implications for understanding acne pathophysiology and informing personalised treatment strategies.

Exploring the genetic causes of migraine and their overlap with other conditions.

This project is suitable for an Honours or PhD student. Seeking a motivated student, ideally with a background in neurosciences, genetics, epidemiology or statistics, to contribute to a dry-lab, analysis focused research project.

Co-supervisor: Dr Anna Monistrol Mula

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BACKGROUND

Migraine is a highly prevalent neurological disorder characterised by recurrent headaches, often accompanied by nausea, sensitivity to light and sound, and other disabling symptoms. While environmental triggers such as stress and diet contribute to migraine attacks, genetics play a powerful role in determining who develops migraine and why. Recent genome-wide association studies (GWAS) have identified numerous genetic variants association with migraine, implicating pathways related to neuronal signalling, vascular function, and pain processing. Notably, migraine also shares genetic architecture with conditions such as depression, anxiety, and cardiovascular disease, which suggests that migraine might be part of a broader network of interconnected biological mechanisms.

AIM

This project aims to investigate the genetic basis of migraine and its relationships with other traits by:

- Identifying genetic variants association with migraine risk.
- Examining genetic correlations between migraine and other traits and disease.
- Evaluating whether polygenic risk scores (PRS) for migraine can predict risk for related conditions.

APPROACH

The project will utilise GWAS summary statistics from large migraine studies and other relevant datasets. Genetic correlations between migraine and related traits will be assessed using linkage disequilibrium score regression (LDSC). PRS will be calculated and tested for associations with other traits in independent cohorts. Statistical analyses will be performed using R and bioinformatics tools such as PLINK.

PROJECT POTENTIAL

This project provides an opportunity to develop expertise in genetic epidemiology, statistical genetics, and data analysis while contributing to a better understanding of the biological links between migraine and other complex disorders.

Dissecting the genetic architecture of anxiety subtypes.

This project is suitable for an Honours, Masters or PhD student. Seeking a motivated student, ideally with a background in psychology, genetics, epidemiology or statistics, to contribute to a dry-lab, analysis focused research project.

Co-supervisor: Dr Anna Monistrol Mula

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BACKGROUND

Anxiety disorders are common, multifaceted conditions that include subtypes such as generalised anxiety, social anxiety, and panic disorder. Research indicates that anxiety is moderately heritable, and genome wide association studies (GWAS) have identified several genetic variants association with anxiety risk. However, emerging evidence suggests that different anxiety subtypes may be shaped by partly distinct genetic influences. Understanding the balance between shared and subtype specific genetic factors might explain why certain symptoms co-occur, and how these differences might contribute to variation in treatment response.

AIM

This project will:

- Identify genetic factors that contribute differently to anxiety subtypes (e.g. panic disorder vs generalised anxiety).
- Explore the relationship between anxiety subtypes, as well as their relationships with other traits.

APPROACH

Using large scale national and international genetic datasets, the project will apply advanced statistical genetics approaches, including GWAS, polygenic risk scoring (PRS), and genetic correlation analyses, to characterize the genetic architecture of anxiety subtypes. The student will investigate how genetic risk influences symptom patterns and potential links with treatment response.

PROJECT POTENTIAL

This project will investigate the genetic underpinnings of anxiety subtypes to better understand why symptom patterns differ between individuals. Using large-scale genomic data and advanced quantitative methods, the research will examine biological pathways contributing to heterogeneity in anxiety disorders. The findings aim to support more refined, biologically informed models of classification and guide the development of targeted treatment strategies. Ultimately, the project seeks to improve outcomes for individuals who do not benefit from current standard therapies while providing rigorous training in complex trait genomics and statistical analysis.

Psychedelic Medicine and Supportive Care

Team Head: Associate Professor Vanessa Beesley

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qimrb.edu.au/researchers-and-labs/psychedelic-medicine-and-supportive-care

The Psychedelic Medicine and Supportive Care Group is dedicated to advancing psychedelic medicine and developing supportive care interventions for cancer and mental health.

Our research aims to maximise quality of life by:

1. Using population and person-centred approaches to assess supportive care needs.
2. Identifying the most promising interventions and models of care.
3. Embracing innovation and using cost-effectiveness and implementation trial designs.
4. Championing equity and inclusivity for culturally safe, responsive and accessible care.
5. Fostering interdisciplinary partnerships with clinicians, consumers and healthcare providers to facilitate translation.

Our current projects target cancer-related supportive care, adjustment disorders, prolonged grief and post-traumatic stress disorder (PTSD) in disaster-affected communities.

Clinical Brain Networks

Group Leader: Associate Professor Luca Cocchi

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With the goal of progressing knowledge on brain disorders and evidence-based psychiatric therapies, the Clinical Brain Networks Group focuses on understanding how the structural and functional wiring of the brain underpin health and pathology.

The laboratory uses a variety of neuroimaging, brain stimulation, and computational techniques and operates one of the first transcranial focussed ultrasound stimulation facilities in Australia.

We work closely with a not-for-profit brain stimulation clinic, the Queensland Neurostimulation Centre to rapidly translate our scientific insights into effective new treatments for refractory mental disorders.

Our research is supported by philanthropic and government bodies including the National Health and Medical Research Council (NHMRC).

Cerebellum & Neurodegeneration

Group Leader: Associate Professor Ian Harding

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qimrb.edu.au/researchers-and-labs/cerebellum-and-neurodegeneration-research-group

The Cerebellum and Neurodegeneration Research Group (CNRG) uses neuroimaging, fluid biomarkers, and digital assessment tools to understand brain and behavioural changes in people with cerebellar diseases, other forms of neurodegeneration, and aging.

We use a range of magnetic resonance imaging (MRI) and positron emission tomography (PET) approaches to investigate and track brain changes in people with neurodegenerative diseases.

Human neuroimaging and blood biomarkers for inherited neurodegenerative diseases.

This project is suitable for PhD students.

BACKGROUND

Can new human brain imaging techniques allow us to better understand, track, and treat neurodegenerative diseases?

Can blood-based proteomics/metabolomics help us to better define and predict heterogeneity in the onset and progression of neurodegeneration?

Can machine learning be applied to complex, multi-domain clinical and biological data to identify disease subtypes?

These are some of the burning questions that are at the forefront of research in our lab. Hereditary cerebellar ataxias (HCAs) are inherited neurodegenerative diseases that are association with motor, cognitive, and neuropsychiatric impairments. These diseases result in profound disability and mortality. There are currently no cures, but the field is on the precipice of gene therapies, stem cell interventions, and targeted pharmaceuticals. Next-generation magnetic resonance imaging (MRI) and proteomics/metabolomics approaches offer powerful new methods to characterise the onset and progression of disease, to define disease subtypes, and to optimise clinical trial design by improving patient selection (stratification) and outcome monitoring (sensitive endpoints).

AIM

Multiple projects are available to undertake one or more of the following in cohorts of individuals with hereditary cerebellar ataxias:

1. Application of novel quantitative MRI approaches to assess changes in myelination, iron metabolism, inflammation, and tissue microstructure.
2. Determine the proteomic and metabolomic profile of disease expression and progression.
3. Machine learning approaches to define disease clusters (subgroups) and predictive models of disease progression using clinical, imaging, and biological data.

PROJECT POTENTIAL

These projects will improve biological understanding, treatment targeting, and outcome monitoring for debilitating, fatal, and currently intractable neurodegenerative diseases.

Neuroimaging big data in rare neurodegenerative diseases: An international collaboration.

This project is suitable for an Honours, Masters, MD, or PhD student.

BACKGROUND

Hereditary Cerebellar Ataxias (HCAs) are rare neurodegenerative diseases that are association with profound and extensive motor control impairments, predominantly affecting the cerebellum and brainstem. Neuroimaging provides a powerful tool to investigate the functional and structural alterations occurring in HCAs, and ultimately advance our understanding of these diseases. However, current studies of these diseases usually rely on small samples and are therefore limited in there scientific and clinical significance.

Our lab has teamed up with clinicians and researchers from around the world to overcome these barriers by establishing international consortia (such as the ENIGMA-Ataxia working group) and multisite research studies (including TRACK-FA and the RFC1 Natural History Study). Combined with new tools for multi-site image harmonisation (COMBAT, SynthSeg), these initiatives provide unprecedented power to define the profile, evolution, and heterogeneity of rare neurological diseases.

AIM

This study will undertake the large-scale analyses of structural and connectivity changes in HCAs using data from international consortia of clinical research sites. This work will include functional and structural MRI methods including resting state fMRI and diffusion tensor imaging (DTI) to examine cerebellar anatomical, microstructural, and connectomic changes in these diseases.

PROJECT POTENTIAL

This project will define the profile of anatomical, functional, and connectivity changes that occur in the brain and spinal cord of individuals with hereditary cerebellar ataxias, improving efforts to define sensitive markers of disease progression (biomarkers) and characterise inter-individual variability in disease expression.

Human neuroimaging of neurodegenerative diseases.

This project is suitable for a PhD student.

BACKGROUND

Are you passionate about neuroimaging, bioinformatics, and the quest to better understand neurodegenerative diseases?

This exciting PhD opportunity focuses on utilizing advanced brain imaging techniques to explore hereditary cerebellar ataxias (HCAs), an inherited group of neurodegenerative diseases that cause significant motor, cognitive, and neuropsychiatric impairments. HCAs led to severe disability and mortality, with no existing cures.

Our Cerebellum & Neurodegeneration Research Group (CNRG) is at the cutting edge of these developments, employing state-of-the-art magnetic resonance imaging (MRI) and advanced blood and digital biomarkers to better understand the onset and progression of HCAs. This project aims to improve patient characterization and biomarker validation, leveraging novel data analysis approaches, including advanced statistics and machine learning to analyze complex clinical and biological data.

AIM

PhD students will have the opportunity to work on one or more of the following research areas within a cohort of individuals diagnosed with hereditary cerebellar ataxias:

- Neuroimaging: Apply cutting-edge quantitative MRI techniques to assess changes in myelination, iron metabolism, inflammation, and tissue microstructure.
- Profiling disease expression and progression using bloodbased biomarkers.
- Statistical Modelling & machine learning: Develop machine learning models to identify disease subgroups and predict disease progression using clinical, imaging, and biological data.

Research Questions

- Can sophisticated neuroimaging techniques enhance our understanding and treatment of neurodegenerative diseases?
- Can blood-based proteomics and metabolomics add additional insights into the variability in disease onset and progression?
- Can advanced statistics and machine learning models help define disease subtypes and predict clinical outcomes?

Notes

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