ENVIRONOMICS FUTURE SCIENCE PLATFORM
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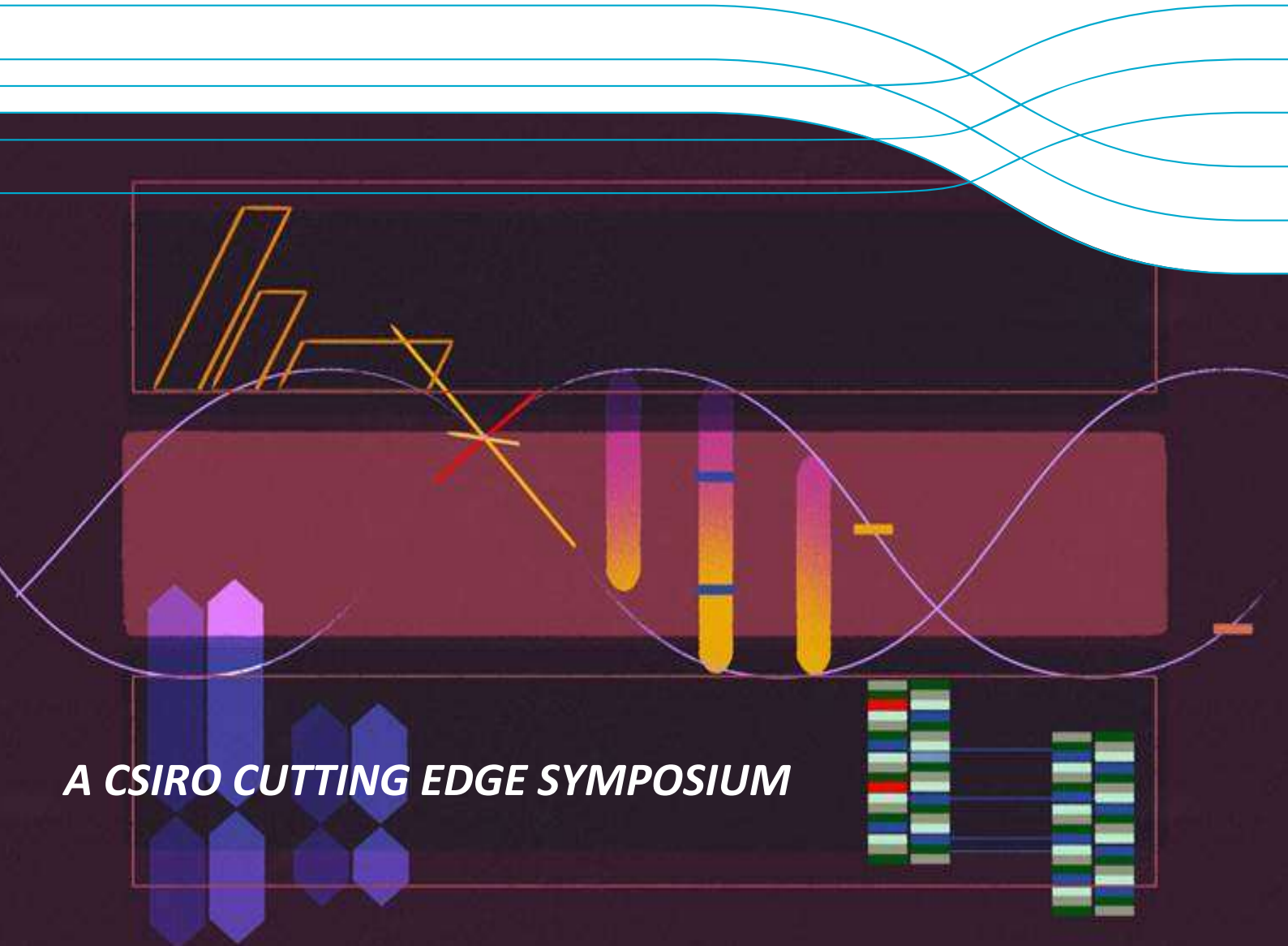
Cancer, whales & robots…

Molecular Sensing of Biological Environments

October 2nd & 3rd, 2018

Hobart, Tasmania

SYMPOSIUM PROGRAM



A CSIRO CUTTING EDGE SYMPOSIUM

Welcome!

You've probably come across the meme that interesting and ground-breaking things happen at the intersection between cultures and disciplines. Frans Johansson called this the "Medici Effect"[1], and one of his favourite case studies was Charles Darwin, whose cross-disciplinary insights changed the world.

Darwin's insights also paved the way for molecular biologists like us to be doing the exciting and impactful work we do. The vastness of today's molecular biology industry illustrates the scale of this impact across social, economic, and environmental dimensions. But, the downside of this success is that it's easy to miss breakthroughs happening just over the hill in neighbouring sub-disciplines like health, environment, biosecurity and forensics. Not to mention how difficult it is to keep up with progress in material science and engineering.

The purpose of this symposium is to create a check-in to see what's happening over the hill, and to test whether we can learn something new and useful from colleagues we ordinarily wouldn't encounter. We have an unusually diverse mix of scientists speaking and in the audience. At a minimum we hope you find the symposium enjoyable and interesting, but even better, we hope it provides inspiration, opportunities for new collaborations, and perhaps a bit of Medici.

Registration desk (and caffeine)

The registration desk will be located in the Freycinet Room, next door to the Auditorium and will be open from 8am-5pm on both days. Please come early on the 2nd to collect your name badge and program. There will also be coffee and tea available from 8am in the Foyer on both days, so come down early to get your caffeine fix and meet other delegates. The symposium will begin at 8.50am sharp on Tuesday, and 9am on Wednesday.

If you have any questions or concerns throughout the symposium, please seek assistance at the registration desk. You can also contact Alex Bouma on 0404 292 982, and Olly Berry on 0400 747 197.

[1] Johansson, F. (2004) The Medici Effect: Breakthrough Insights at the Intersection of Ideas, Concepts, and Cultures. Harvard Business School Press.

What to expect

The Symposium on Molecular Sensing of Biological Environments will explore current and future developments in molecular sensing research and engineering employed by a wide range of scientific disciplines.

This meeting is deliberately unusual in bringing together scientists from diverse fields of molecular biology and engineering. The motivation for this is to break down disciplinary barriers and to expose researchers to new techniques, engineering solutions, ideas and applications.

The two days will comprise of a mix of key-note, short presentations, and lightning talks from global and national research leaders as well as early career researchers representing four main scientific themes: Biomedical, Environment, Biosecurity & Forensics, and Technology & Engineering.

Speakers will present the latest research in their fields, but have also been asked to reflect on what may be on the research horizon, and if they foresee any relevance to other fields. There will be plenty of opportunity for networking during breaks and at the social event on Tuesday evening. We encourage you to take advantage of the opportunity to have conversations with people you might not meet every day.

Enjoy!

Kimberley reef at low tide

Symposium Organising Committee

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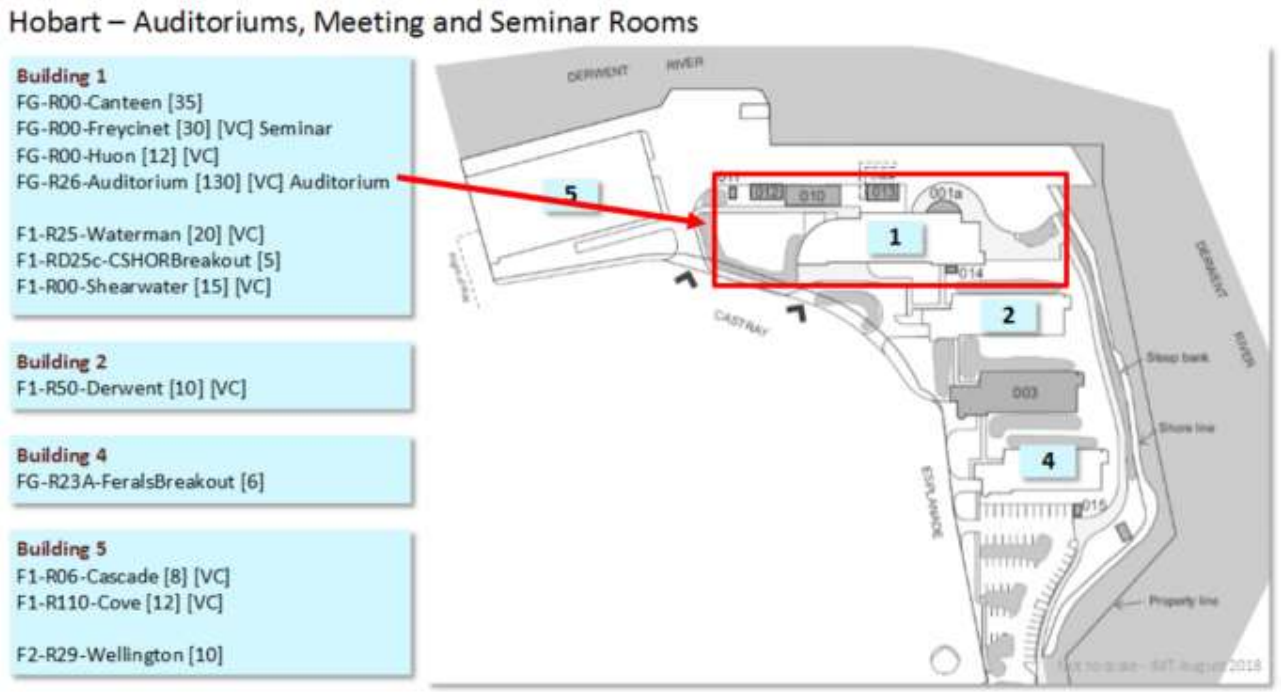
Location & Map

The symposium is being held in the **Auditorium** at the CSIRO Hobart office, located on **Castray Esplanade, Hobart, 7000**. The auditorium is located in Building 1 of the CSIRO complex (see below and overleaf).



Drinks & Conversation – Tuesday Evening

If you indicated at registration that you would be attending the social mixer function, then please join us for drinks and finger food at **Post Street Social from 6.30pm** on the **2nd of October**. The venue is conveniently located at 11-13 Franklin Wharf, less than 10 minutes walk from the symposium venue, along the waterfront (see map below). If you did not register your attendance but would like to join, then please see Alex Bouma at the registration desk.

Where the action happens:

Day 1 Program

Session 1 Morning: Theme 1 - Biomedical

Session Chair: Jason Ross

Time	Session & Speaker	Presentation Title
	Theme 1: Biomedical	
0800-0850	Registration – Freycinet Room	
0850-9000	**Dr OLLY BERRY** (chair, organising committee)	Welcome & housekeeping
0900-1000	*Keynote* **Professor MATT TRAU** *University of Queensland*	*Making Precision Medicine Personal: Translating Genome-Wide & Point of Care Nano-Diagnostics into the Clinic*
1000-1020	*15 minute talk* **Dr MARY BEBAWY** *University of Technology, Sydney*	*A liquid biopsy for precision cancer prognosis and monitoring of drug resistance*
1020-1040	*15 minute talk* **Dr ANTONIO TRICOLI** *Australian National University*	*Miniaturized Sensor Technologies for Wearable and Personalized Medical Diagnostics*
1040-1110	**MORNING TEA**	
1110-1130	*15 minute talk* **Dr PETER MOLLOY** *CSIRO*	*Precise methylcytosine mapping for colorectal cancer diagnostic development*
1130-1135	*Lightning talk* **WARWICK LOCKE** *CSIRO*	*Beyond Cancer: Circulating DNA in Injury and Disease*
1135-1140	*Lightning talk* **JASON WHITFIELD** *University of Queensland*	*Modular allostery in fluorescent proteins – towards a generic sensing platform*
1140-1145	*Lightning talk* **CRAIG LIDDICOAT**	*Biodiversity and microbiota-mediated human health*
1145-1155	*Lightning talk Q&A*	
1155-1215	*15 minute talk* **Dr MAJID WARKIANLI** *University of Technology, Sydney*	*Novel microfluidic systems for single cell analysis, molecular sensing and drug screening*
1215-1320	**LUNCH**	

Day 1 Program Cont.

Session 2 Afternoon: Theme 2 - Environment

Session Chair: Sarah Mathews

Time	Session & Speaker	Presentation Title
	Theme 2: Environment	
1320-1420	*Keynote* **Dr MICHAEL BUNCE** *TrEnD Laboratory, Curtin University*	*From fossils to fish – the many and varied applications of DNA metabarcoding in surveying biological communities*
1420-1455	*30 minute talk* **Dr MICHAEL SCHWARTZ** *National Genomics Center for Wildlife and Fish Conservation (USA)*	*The Next Frontier For Environmental DNA: Scaling Up and Out of the Water*
1455-1515	*15 minute talk* **Dr IDO BAR** *Griffith University*	*Developing nanoparticle-based biosensors for foliar fungal pathogens*
1515-1535	*15 minute talk* **Dr BRUCE DEAGLE** *Australian Antarctic Division*	*Counting with DNA in environmental metabarcoding studies: are sequence counts useful?*
1535-1555	**AFTERNOON TEA**	
1555-1630	*30 minute talk* **Dr MARIA-NEFELI TSALOGLOU** *Diagnostics for All*	*Microfluidic analytical devices for environmental sensing of biomolecules*
1630-1635	*Lightning talk* **KEJAL DODHIA** *Curtin University*	*From sample to result in an hour: towards rapid disease and fungicide resistance detection*
1635-1640	*Lightning talk* **ALYCE HANCOCK** *Antarctic Gateway Partnership*	*Effect of ocean acidification on Antarctic marine bacterial, archaeal and eukaryotic communities*
1640-1645	*Lightning talk* **JULIE MCINNES** *Australian Antarctic Division*	*Using DNA metabarcoding of albatross scats to inform fisheries management*
1645-1650	*Lightning talk* **HAYLEA MILLER** *CSIRO*	*eCells: Developing novel ways to estimate animal abundance*
1650-1700	*Lightning talk Q&A*	

Day 2 Program

Session 1 Morning: Theme 3 - Biosecurity & Forensics

Session Chair: Cameron Stewart

Time	Session & Speaker	Presentation Title
	Theme 3: Biosecurity & Forensics	
	****COFFEE AVAILABLE FROM 8.00AM IN THE FOYER****	
0900-1000	*Keynote* **Dr REBECCA JOHNSON** *Australian Museum Research Institute*	*Putting the 'capital F' in Forensic science Important considerations for future biosecurity & forensics applications*
1000-1020	*15 minute talk* **Dr RYAN FARR** *CSIRO*	*Working towards next-generation diagnostics for viral encephalitis*
1020-1040	*15 minute talk* **Dr RAJESH RAMANATHAN** *RMIT University*	*NanoZyme biosensors*
1040-1110	**MORNING TEA**	
1110-1145	*30 minute talk* **Dr ADRIAN DINSDALE** *Australian Government Department of Agriculture*	*Next-Generation Sequencing: an innovative tool for phytosanitary screening of high-risk plants.*
1145-1150	*Lightning talk* **KATHERINE ZULAK** *Curtin University*	*High-throughput genotyping using digital PCR improves detection and quantification of fungicide resistance in Blumeria graminis f. sp.*
1150-1155	*Lightning talk* **KELLY HILL** *Government of South Australia*	*Molecular Diagnostics for Plant Protection*
1155-1205	*Lightning talk Q&A*	
1205-1240	*30 minute talk* **Dr NICO VOELCKER** *Melbourne Centre for Nanofabrication*	*Porous Silicon Based Optical Biosensors*
1240-1320	**LUNCH**	

Day 2 Program Cont.

Session 2 Afternoon: Theme 4 - Technology & Engineering

Session Chair: Brano Kusy

Time	Session & Speaker	Presentation Title
	Theme 4: Technology & Engineering	
1320-1340	*15 minute talk* **Dr BEATRIZ PRIETO-SIMON** *Monash University*	*Nanostructured electrochemical biosensors as fit-for-purpose analytical devices*
1340-1440	*Keynote* **Dr JAMES BIRCH** *Monterey Bay Aquarium Research Institute*	*Transforming Oceanography—Mobile Ecogenomic Sensors*
1440-1500	*15 minute talk* **Dr ANDREAS MAROUCHOS** *CSIRO*	*Autonomy and the future of ocean observation platforms*
1500-1520	*15 minute talk* **Dr PASCAL CRAW** *CSIRO*	*Remote sampling devices for eDNA and genomic analysis*
1520-1540	**AFTERNOON TEA**	
1540-1640	*Keynote* **Dr ASHITEY TREBI-OLLENNU** *NASA Jet Propulsion Laboratory*	*Planetary Sample Acquisition and Handling Systems Developed at NASA's Jet Propulsion Laboratory*
1640-1645	*Lightning talk* **ANDY BACHLER** *CSIRO*	*Field diagnostics for plants: extracting, amplifying, and detecting nucleic acids using paper microfluidics*
1645-1650	*Lightning talk* **CLAUDIA MORATTI** *University of Sydney*	*Synthetic biology approaches to hydrocarbon biosensors*
1650-1700	*Lightning talk Q&A*	

Abstracts: keynote presentations

Theme 1: Biomedical

Dr Matt Trau
Professor
Centre for Personalised Nanomedicine,
Australian Institute for Bioengineering and Nanotechnology (AIBN)
University of Queensland

Making Precision Medicine Personal:

Translating Genome-Wide & Point of Care Nano-Diagnostics into the Clinic

Modern medicine is currently transitioning to a new paradigm of precision and personalized care, where patients will be comprehensively screened and monitored for the detailed molecular abnormalities that characterise their specific disease. In the past decade, nanotechnology has provided new tools (e.g., next-generation sequencing) with unprecedented power to comprehensively interrogate genetic, transcriptomic and epigenetic information. The Centre for Personalised Nanomedicine at UQ is focused on translating these new technologies into a clinical setting, whilst simultaneously developing the next generation of point-of-care diagnostic technologies to further empower the personalised and precision medicine approach. As part of a major National Collaborative grant funded by the National Breast Cancer Foundation ("Enabling clinical epigenetic diagnostics: The next generation of personalized breast cancer care", CG-12-07), our consortium recently published hundreds of epigenetic regions that area highly informative in cancer. These are now being validated in a real-time clinical setting, where comprehensive DNA, methyl-DNA and RNA information is collected in tandem and analysed. In this talk we will present data on the clinical translation of this approach, highlighting some of the positive impacts that such an approach can make on the "recovery trajectory" of cancer patients. Along with comprehensive DNA/RNA/methylated-DNA sequencing methodologies, several point-of-care nanotechnologies recently developed by our lab will be presented. These include novel technologies for detecting circulating free DNA/RNA/methyl-DNA, circulated tumour cells, exosomes and protein biomarkers. Several of these technologies have been developed collaboratively with US partners via a collaborative NIH grant ("Accelerated Molecular Probe Pipeline", U01AI082186-01).

Theme 2: Environment

Dr Mike Bunce
Trace and Environmental DNA (TrEnD) Laboratory
Curtin University

From fossils to fish – the many and varied applications of DNA metabarcoding in surveying biological communities

DNA isolated and characterised from a variety of substrates including sediments and water is collectively referred to as environmental DNA (eDNA). DNA is shed into the environment from a variety of biological secretory processes leaving genetic footprint that acts lens into species composition. When combined with next generation sequencing (NGS) and metabarcoding, eDNA can provide a wealth of information for studies of biodiversity, food web dynamics, diet analysis, invasive species monitoring and disturbance gradients. Metabarcoding eDNA has become feasible only because it is now possible to simultaneously sequence millions of copies of DNA from complex multi-species environmental samples.

The research in the Trace and Environmental DNA (TrEnD) laboratory has been developing a variety of eDNA workflows to investigate how best to conduct eDNA. This presentation will explore a number of applications of metabarcoding from surveys of marine environments and herbal medicines to reconstructions of past biodiversity using ancient DNA.

Theme 3: Biosecurity & Forensics

Dr Rebecca Johnson
Director
Australia Museum Research Institute

Putting the 'capital F' in Forensic science

Important considerations for future biosecurity & forensics applications

Professor Rebecca Johnson is Director of the Australian Museum Research Institute (AMRI), a Wildlife Forensic Scientist, conservation geneticist and chief investigator of the Koala Genome Consortium. This presentation will describe the breadth of AMRI research and how the museum utilises their natural science collections including in wildlife forensic science applications. These collections are some of Australia's oldest and most valuable research infrastructure collected through the Museum's journey of discovery, exploration and education.

Rebecca will share some case studies from her groups work in the illegal wildlife trade and lessons learned from working with the human and wildlife forensic communities.

Most significantly she will discuss the importance of understanding the critical factors when conducting forensic analyses to ensure practises are standardized and acceptable in a legal context. This especially relevant with the advent and application of next generation sequencing technologies and current legal considerations of what makes 'an expert' in the forensic sciences.

As molecular technologies advance there are exciting collaborative opportunities for biosecurity & forensics applications, providing these important factors are considered.

Theme 4: Technology & Engineering

Dr James M. Birch
Director of the Surf Centre
Monterey Bay Aquarium Research Institute, California, United States

Transforming Oceanography—Mobile Ecogenomic Sensors

Researchers are increasingly using autonomous platforms to characterize ocean processes. Conceptually, studying processes that change both spatially and temporally seems relatively straightforward. One needs to sample in many locations synoptically over time, or follow a coherent water mass and sample it repeatedly. However, implementing either approach presents many challenges. For example, acquiring samples over days to weeks far from shore, without human intervention, requires seamless autonomy, navigation and communications.

We are addressing these challenges by developing a new generation of robotic systems that are primarily aimed at studies of microbial-mediated processes. We have taken lessons learned from our second-generation Environmental Sample Processor (2G-ESP), a robotic microbiology "lab-in-a-can" and have re-engineered the system for use on a Tethys-class Long Range AUV (LRAUV). The new instrument is called the third-generation ESP (3G-ESP), and its integration with the LRAUV provides mobility and a persistent presence not seen before in microbial oceanography.

This presentation will focus on results from several deployments of the 3G-ESP/LRAUV system, the challenges encountered in building the ESP and integrating with the LRAUV, and operational capabilities that show the potential of mobile, ecogenomic sensors in the ocean sciences.

Dr Ashitey Trebi-Ollennu
Chief Engineer of Mobility and Robotics Systems
InSight Mars Mission Instrument Deployment System;
Instrument Deployment System Operations Team Chief & Technical Group Supervisor of Robotics Systems Group
NASA Jet Propulsion Laboratory, Caltech

Planetary Sample Acquisition and Handling Systems Developed at NASA's Jet Propulsion Laboratory

Sample acquisition and analysis as part of in-situ exploration and sample return from solar system bodies has high science priority for NASA. The samples can provide information about the evolution of the planetary bodies and potential for harboring past or extant life. Ocean worlds of the outer solar system (Europa, Enceladus, and Titan) with liquid oceans below tens of kilometres thick ice shells are particularly intriguing locations for possibly harboring extant life.

This presentation will describe sample acquisition and handling systems technology developed for planetary exploration at NASA's Jet Propulsion Laboratory for Lunar, Mars, Venus, Comets, Asteroids, and Ocean worlds of the outer solar system.

Abstracts: short presentations (15 & 30 minutes)

Theme 1: Biomedical

Dr Mary Bebawy
Associate Professor, Pharmacy
University of Technology, Sydney

A Personalised Approach to Managing Drug Resistance and Treatment Failure in Myeloma

Purpose of Study: We describe the development of a new blood test- a liquid biopsy- for the diagnosis and management of drug resistance in multiple myeloma (MM).

Description of project: MM is a progressive malignancy of bone-marrow plasma cells which is currently incurable. Treatment typically involves combination chemotherapy, but therapeutic response and patient survival are unpredictable and highly variable – attributed to the evolution of multiple drug resistance (MDR) in response to chemotherapy. Currently, no procedures are available which allow for direct, non-invasive, real-time monitoring of the development of MDR in myeloma. For this test to be clinically viable, it should: (1) directly measure markers of MDR expressed in myeloma cells during routine follow-up; (2) be non-invasive; (3) account for heterogeneous tumours at multiple sites; and (4) allow for simultaneous comparative analysis of tumour burden. This is the unmet medical need that our test addresses, enabling treatment that is personalised for each individual patient and optimised throughout the course of treatment.

Results and conclusions: This test monitors a patient's unique cancer phenotype by analysing biomarker 'signatures' on extracellular vesicles (microparticles (MPs) 0.1 -1 um diameter), isolated from the blood samples of myeloma patients. The biomarker signatures include resistance markers, stem cell markers and phospholipid markers, the configuration of which correspond to disease progression and therapeutic response in individual patients. We describe MP subpopulations in the context of these signautures. We show that patients have higher P-glycoprotein (P-gp^{+}) MPs in the total CD41a^{-} and CD138^{-} MP populations compared to healthy subjects. P-gp^{+} MP levels correspond to poor treatment response and resistance to treatment. We also provide evidence for the presence of a 'dual positive' '*stem cell-like'* subpopulation of CD138^{-}P-gp^{+}CD34^{+} MPs in patients which are elevated in unresponsive disease and an evolving shift in the dominance of vesicle subtypes with disease progression and treatment failure.

In conclusion we provide evidence that MDR in myeloma patients can be detected and monitored serially by analysing MPs in blood samples in the foorm of a 'liquid biopsy'. This test has potential to complement existing biochemical benchmarks used in diagnosis and staging of myeloma.

Dr Antonio Tricoli
Associate Professor
ANU College of Engineering and Computer Science

Miniaturized Sensor Technologies for Wearable and Personalized Medical Diagnostics

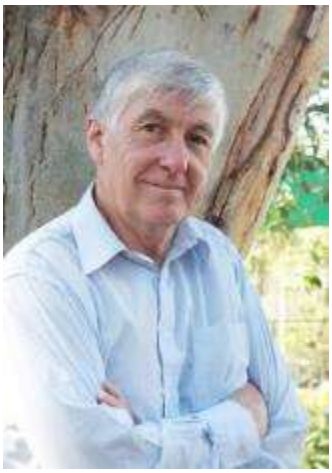
The unprecedented medical achievements of the last century have dramatically improved our quality of life. Today, the convergence of wearable electronics, miniaturized sensor technologies and big data analysis provides novel opportunities to improve the quality of healthcare while decreasing costs by the very early-stage detection and prevention of fatal and chronic diseases. Here, we will discuss some exciting achievements, emerging technologies and standing challenges for the development of non-invasive personalized and preventive medicine devices. The engineering of wire- and power-less ultra-thin sensors on wearable biocompatible materials that can be placed on the skin, pupil and teeth will be reviewed focusing on common solutions and current limitations. The integration and development of sophisticated sensing nanomaterials will be presented with respect to their performance showing exemplary implementations for the detection of ultra-low concentrations of biomarkers in complex mixtures such as the human breath.

Dr Majid Warkiani
Senior Lecturer, School of Biomedical Engineering
University of Technology, Sydney

Novel microfluidic systems for single cell analysis, molecular sensing and drug screening

Microfluidics, a technology characterized by the engineered manipulation of fluids at the micro-scale, has shown considerable promise in point-of-care diagnostics and clinical research. Microfluidic platforms are creating powerful tools for cell biologists to control the complete cellular microenvironment, leading to new questions and new discoveries. By simply miniaturizing macroscopic systems and taking advantage of the possibility of massive parallel processing, some microfluidic chips enable high-throughput biological experiments such as cell sorting, single cell analysis, PCR, ELISA and chromatography. This revolution promises to bring with it better ways to detect cancer and other diseases, as well as a more efficient drug-discovery process. Over the past 7 years, I have developed a number of microfluidic systems which are translated into practice. In this seminar, I will describe our recent efforts in development of new miniaturized systems for micro/nano-particle separation as well as cell/exosome sorting. In addition, I will present some of our new 2D and 3D microfluidics systems for single cell analysis, molecular sensing and drug screening.

Dr Peter Molloy
Senior Principal Research Scientist
CSIRO Health and Biosecurity, Sydney



Precise methylcytosine mapping for colorectal cancer diagnostic development

Site-specific methylation of DNA at the 5' position of cytosine (5meC) is a core component of the epigenetic processes that regulate which genes are expressed in different cell types in the body. Aberrant gene regulation associated with the development of cancer is accompanied by extensive changes in the DNA methylome. Characteristic changes in methylation of particular genes can be more common than oncogenic mutations or genome rearrangements, and thus provide targets for potentially more sensitive diagnostic assays. The identification of "hotspots" of DNA methylation in the genomes of colorectal cancer patients has led to the development of a two gene test for the presence of cancer-derived DNA (ctDNA) in the plasma of colorectal cancer patients. I will describe how we progressed from initial genome-wide scans profiling DNA methylation to targeted deep sequencing of 5meC at single base resolution to guide development of PCR-assays for highly sensitive detection of aberrantly methylated ctDNA. This assay, Colvera®, is currently being used for monitoring of cancer recurrence following surgery to remove the primary tumour.

Theme 2: Environment

Dr Michael Schwartz
Director
National Genomics Center for Wildlife and Fish Conservation, USA

The Next Frontier for Environmental DNA: Scaling Up and Out of the Water

Environmental DNA (eDNA) sampling, the sampling to infer species presence from genetic material in the environment, has revolutionized aquatic biology over the past 5 years in the United States. However, most uses are either pilot studies to assess if the sampling and benchwork products can detect a particular species in a particular water system, or are small scale studies to detect single species in relatively small ecological systems. In this talk, we discuss what is next for environmental DNA, which is (1) increasing the scale of studies, (2) using information for more than detection, range, or occupancy research, and (3) moving out of the aquatic environment into terrestrial ecosystems. We start with describing how we have scaled up an eDNA sampling effort to provide a fine scale species distribution model for a Threatened fish, the bull trout (Salvelinus confluentus). Specifically we present information on how we used crowd-sourced environmental DNA sampling and high-resolution habitat covariates across 630 sites over an area of nearly 10,000 km2 to build an accurate species distribution model for bull trout in cold water habitats that incorporates fine-scale, context-dependent interactions with invasive brook trout. We next describe our efforts to use environmental DNA with snowtracks of rare carnivores across the landscape. Finally, we discuss our the challenges we have faced with pushing the cutting edge of multispecies detections in both aquatic and terrestrial systems.

Dr Bruce Deagle
Research Scientist
Australian Antarctic Division

Counting with DNA in environmental metabarcoding studies: are sequence counts useful?

Many biodiversity studies make use of metabarcoding, an approach which combines high-throughput sequencing (HTS) with DNA barcoding to characterise organisms in complex mixtures (e.g. in eDNA or bulk samples). The approach is also used to study animal diet by analysing food DNA in faecal samples. One features of HTS is that it provides counts of DNA sequences and therefore has the potential to provide not only a qualitative list, but also a quantitative assessment of what DNA is present in each sample. But what do these counts mean and do they reflect biomass of metazoans? Is it reasonable to use read proportions to retrieve semi-quantitative information, or should we work strictly with presence/absence datasets? Here, we explore how sequence counts are used in metabarcoding studies and discuss results from our research on animal diet (seals and seabirds) and zooplankton communities. We point out that summaries based on frequency of occurrence data have their own biases and argue that in some situations the quantitative interpretation of count data can be justified. We also outline our use of correction factors to account for taxa-specific recovery biases and the inclusion of internal standards to enable quantitative comparisons between samples.

Dr Maria-Nefeli Tsaloglou
Scientific Director
Diagnostics for All & Harvard University, USA

Microfluidic analytical devices for environmental sensing of biomolecules

Detection and analyses of biomolecules−metabolites, proteins and nucleic acids−are essential for a range of important applications in life sciences and environmental sensing. These applications include speciation of pathogens in food and water samples, pre-symptomatic detection of infectious diseases, management of chronic disorders, as well as perinatal genetics and inherent genetic disorders. Microfluidic analytical devices make for excellent candidates to address the need for portable, rapid and cloud-connected alternatives to existing instrumentation for biological environmental sensing.

In this talk, we will: (1) provide with a short background on microfluidics; (2) review the state-of-the art of commercially-available microfluidic devices for molecular sensing, and (3) present case studies of fieldable low-cost devices.

Dr Ido Bar
Research Fellow
Environmental Futures Research Institute, Griffith University

Developing nanoparticle-based biosensors for foliar fungal pathogens

Botrytis grey mould (BGM) and Ascochyta blight, caused by pathogen fungi of the Botrytis and Ascochyta spp., respectively, cause serious yield losses in legumes during conducive seasons in Australia and worldwide. A greater success in Integrated Disease Management (IDM) approaches to prevent this loss would result from fast, accurate and cost-effective diagnosis and quantification of the causal pathogen(s). Tools to enable this would provide a large opportunity to save on targeted fungicide chemistries input costs and enable the faster application of other management options. The existing immunogenic and molecular probe type diagnostic methods, based on whole genome sequencing, PCR amplification or antibodies, are time consuming and offer varying levels of specificity and/or sensitivity. As an alternative, we are developing species-specific molecular biosensors for fast, accurate and sensitive detection and quantification of the mycelium and spore derived nucleic acid of both target pathogens. To achieve this, sets of species-specific qPCR compatible primers were designed and tested to determine their sensitivity (minimum copy number detection). Simultaneously a specific and sensitive assay for the electro catalytic detection of the target pure fungal DNA using functionalised magnetic nanoparticles has been assessed and shown to have 100 times better sensitivity than the qPCR assay for Botrytis.

Theme 3: Biosecurity & Forensics

Dr Ryan Farr
Postdoctoral Fellow – Science, Pathology & Pathogen Biology
CSIRO

Working towards next-generation diagnostics for viral encephalitis

Viral encephalitis (VE) is a serious and debilitating disease, with high rates of mortality and long-term sequelae. The efficacy of medical intervention on VE is often dependant on the stage of infection; once a patient is symptomatic, treatment options are often limited. Despite the clear need to identify infected individuals prior to clinical onset, developing a diagnostic tool is problematic, due to ethical and practical limitations of experimental models.

To circumvent these limitations, we have established and characterised a human stem cell derived neuronal model to investigate the host response to viral infection. Using next-generation sequencing, we have identified microRNAs that are differentially expressed when neurons are infected with several strains of Rabies virus. MicroRNAs are small non-coding RNAs that show promise as biomarkers of a range of diseases, including cancer and diabetes. Along with parallel in vivo studies, these results will form a biomarker signature of VE. Establishing this model and interrogating the response to infection required expertise from stem cell biology, virology, and bioinformatics, and the potential translation of this research into a diagnostic platform has necessitated engineering input.

This cross-disciplinary project is the first step in developing next-generation diagnostics for the prompt detection of VE, allowing early, effective intervention.

Dr Rajesh Ramanathan
Senior Research Fellow
RMIT University

NanoZyme biosensors

The catalytic behaviour of nanoparticles mimicking the activity of natural enzymes, commonly known as 'NanoZymes', has seen its widespread interest. The unique properties of nanozymes has seen its diverse applicability ranging from sensing, imaging, therapeutics, pollutant removal, water treatment etc. Our group has established the NanoZyme activity of different nanomaterials with the ability to tailor its activity through nanoparticle surface modification, morphological control, and external triggers. A primary focus for our group is in the area of biosensing where we combine the NanoZyme activity with molecular recognition elements (MREs) such as aptamers. By modulating the dynamic interaction between the NanoZyme, aptamer and the target, we have created new highly sensitive and selective colorimetric biosensing platform for the detection of a range of analytes of biological importance. Further, by generating sensor arrays, we create a sensor system that mimics the senses of smell and taste. The sensor array generates a unique colorimetric fingerprint that can be analysed using multivariate pattern recognition algorithms. Using this strategy, we have created sensing systems for the detection of pathogenic bacteria with sup-species level specificity, cancer cells and cell receptor expression profiles. This talk will outline some of the recent developments made by our group in this area.

Dr Adrian Dinsdale
Assistant Director
Australian Government Department of Agriculture

Next-Generation Sequencing: an innovative tool for phytosanitary screening of high-risk plants

Imported high-risk plants spend up to 2.5 years in Post Entry Quarantine (PEQ) facilities prior to their release to plant industries. During their time in PEQ, imported plants are screened for exotic pests including viruses, viroids, bacteria, fungi and nematodes. Existing post entry quarantine protocols to screen for viruses and viroids rely on resource intensive molecular and serological tests and time-consuming biological indicators. The prolonged PEQ screening schedule impacts plant industries' capability to access new national and international market opportunities. The use of next-generation sequencing (NGS) and suitable bioinformatics pipelines to sequence and analyse small RNAs arising from the natural plant antiviral response system can accelerate the screening process of plants in quarantine. This strategy offers a number of advantages over existing PEQ protocols, namely improved accuracy, scalability, reduction in PEQ costs and screening times facilitating more rapid release of new genetic stocks. The workflow for this technique includes extraction of small RNA enriched fractions, library preparation and deep sequencing by external provider, and analysis of sequence through an automated viral surveillance and diagnosis (VSD) toolkit. This

technique is currently in use at PEQ for imported clonal grasses. Side-by-side trials are in progress for other commodities.

Dr Nico Voelcker
Scientific Director
Melbourne Centre for Nanofabrication

Porous Silicon Based Optical Biosensors

Biosensors fabricated on the nanoscale offer exciting new avenues in the quest to better understand, treat and manage diseases. Thin films of porous silicon are ideally suited for the construction of optical sensor matrices since they can be easily functionalized with biomolecular probes and displays strong optical interferences and 1D photonic effects. We describe the preparation of porous silicon based optical biosensors and their performance in the detection of analytical targets ranging from proteins, enzymes, small molecules and nucleic acids.

Over the last decade, porous silicon has received significant attention in studies aiming at the design of chemo- and biosensors. This is not surprising since nanocrystalline porous silicon films are ideal hosts for the detection of chemicals, mainly due to their large internal surface area and unique optical properties. Most remarkably, porous silicon acts as both matrix and transducer in biosensor devices. Changes in luminescence, interferometric reflectance and photonic resonances have been used to detect binding of diverse chemicals and biomolecules. Most of these sensors however yield linear signal-response curves limiting the achievable sensitivity.

Here, described the fabrication and functionalisation of porous silicon films, the conjugation of biomolecules to these films and their application as interferometric and photonic biosensors operating via in-situ signal amplification. We demonstrate that these biosensors can monitor various biochemical interactions with high sensitivity. The amplification of the signal from the initial ligand binding event is achieved by catalyzed porous silicon degradation induced by DNA duplexes, transition metal complexes, by common redox enzymes or via light enhancement in microcavities.

Theme 4: Technology & Engineering

Dr Beatriz Prieto-Simon
Senior Research Fellow, Drug Delivery Deposition & Dynamics
Monash University

Nanostructured electrochemical biosensors as fit-for-purpose analytical devices

Our research focuses on the development of novel fit-for-purpose electrochemical sensing tools, which exploit the use of chemically and mechanically stable synthetic materials to design nanostructured biosensors. Materials that can easily tailor their electrochemical properties and morphological features, are highly desired. Our recent research has led to the creation of the next generation of highly versatile electrochemical biosensing platforms by

harnessing silicon fabrication and modification methods. These novel structures feature major advantages for electrochemical analysis, such as high surface-to-volume ratio, unique charge transport properties, control over morphological features, even in multilayered configurations, and ease of surface modification and control of the electric properties. We have produced arrays of nanoneedles intended to be used as wearable sensors, and porous membrane-based electrochemical biosensors that have been successfully used for the label-free detection of DNA, toxins and even whole viruses. This new set of pSi-based nanostructures is designed to unlock new sensing paradigms and potentially achieve greater sensitivities and shorter analysis times, providing solutions for environmental, biosecurity and healthcare issues.

Dr Pascal Craw
Research Scientist
CSIRO

Remote sampling devices for eDNA and Genomic analysis

In recent years novel genomic techniques such as qPCR, metagenomics and eDNA analysis have shown their utility as powerful tools for understanding the marine environment using filtered water samples. Unfortunately there is a considerable cost obtaining water samples from remote locations. In recent years CSIRO Oceans & Atmosphere has been working on the development of automated samplers for in-situ filtration and preservation of marine water samples. We hope this technology will allow much broader scale temporal and spatial coverage in genomic studies without adding significantly to the cost of these projects. The sampling instruments currently being developed also hold promise for performing DNA based studies in hostile environments which includes sampling in polar regions during periods where the environmental conditions may make manual sampling prohibitively difficult

Mr Andreas Marouchos
Principal Research Engineer
CSIRO

Autonomy and the future of ocean observation platforms

Autonomy is increasingly becoming a key enabling technology in the collection of marine observations. As new sensors are developed and trialed outside of the lab, careful thought needs to be given on how the sensors will work with these systems, and integrate with existing sensor suites. In particular, it is necessary to identify and address challenges faced by deployments in autonomous systems. This talk with provide an overview of the state-of-the art in autonomous marine observing and outline key paths in the development of future science platforms.

Lightning presentations (5 minutes)

Theme 1: Biomedical

Jason Whitfield

Modular allostery in fluorescent proteins – towards a generic sensing platform

The study of biological systems is often subject to the availability of a suitable biosensor, with the resultant sensors often bespoke for the specific analyte of interest. While this has proven successful for a range of applications including protein-protein interactions and the dynamics of selected small molecules, a more general method that can be easily adapted to a system of interest remains elusive.

In an effort to address this, we sought to employ one of the key tenets of Synthetic Biology where a system is divided into clearly defined modules that can be easily interchanged, allowing for a more broad application of a biosensor architecture. By exploiting the intrinsic large conformational changes of the peptide binding protein Calmodulin and the environmental sensitivity of the fluorescent protein family we have designed a series of fluorescent switches with varying dynamic ranges. These are capable of integration into higher order multi-component sensing systems enabling detection of small molecule and large protein analytes.

Craig Liddicoat

Biodiversity and microbiota-mediated human health

Microbial diversity and key microbial species from biodiverse environments are believed to provide critical inputs to help develop and maintain our immune fitness. Environmental microbiota supplement the protective human (e.g. skin, airway, gut) microbiota, participate in normal healthy immune signalling, and help build immune memory. These immune-boosting interactions may underpin many aspects of our health, and can help regulate both infectious and non-infectious disease. However these connections—between environments, their microbiota, human microbiota, immunomodulatory effects, and ultimate health outcomes—remain understudied due to their multidisciplinary nature. In Australia-wide studies we have found support for the idea that exposure to environmental microbial diversity is linked to immune fitness at the population level. Specifically, we have shown that landscape biodiversity correlates with respiratory health, and populations with ambient exposure to soils of high cation exchange capacity (typically high microbial diversity) have reduced rates of infectious and parasitic disease. In current work we are using 16S bacterial marker gene survey data to identify genus-level microbial indicators of ecosystem restoration (which may point to previously unknown candidate beneficial immunomodulatory taxa), and are testing for impacts to the gut microbiome from biodiverse soil exposures in an environmentally-controlled mouse model system.

Theme 2: Environment

Haylea Miller

eCells: Developing novel ways to estimate animal abundance

Animal abundance is a fundamental aspect of population biology relevant to many fields of research, from wildlife conservation to fisheries management. Yet, abundance is often difficult to estimate accurately via direct observation or tagging, and often requires physical interaction with animals, which can impact their behaviour. Genetic tools can be used to estimate population size and these have recently proven very effective when tissue samples can be taken from many individuals. However, it is not always possible, or ethical to collect these samples.

The purpose of this study is to develop an alternative non-invasive methodology to estimate animal abundance based on the capture of whole cells shed by the animals naturally into the water (termed environmental cells or "eCells"), eliminating the need to directly sample and impact the animals. This project aims to develop a combination of fluorescence-activated cell sorting, followed by whole genome amplification and the identification of individual animals through a DNA fingerprinting analysis to generate genotypes of the animals present in an area. If successful, this method could replace conventional invasive techniques widely used in both biodiversity and fisheries management.

Julie McInnes

Using DNA metabarcoding of albatross scats to inform fisheries management

Almost all of the world's fisheries overlap spatially and temporally with foraging seabirds, with impacts that range from food supplementation (through scavenging behind vessels), to resource competition and incidental mortality. The nature and extent of interactions between seabirds and fisheries vary, as does the level and efficacy of management and mitigation. The spatial and temporal variability of fishery resources in the diet of black-browed albatross was examined using DNA metabarcoding of scats collected over two seasons across their breeding range. We found several fish species that are not easily accessible to albatross, but are commercially harvested or by-caught, were detected in the albatross diet during the breeding season. This was particularly evident at the Falkland Islands and Iles Kerguelen where higher fishery catch amounts (or discard amounts where known) corresponded to higher occurrence of these species in diet samples. This study indicates ongoing interactions with fisheries through consumption of fishery discards, increasing the risk of seabird mortality. DNA metabarcoding provides a valuable non-invasive tool for assessing the fish prey of seabirds across broad geographic ranges. This provides an avenue for fishery resource managers to assess compliance of fisheries with discard policies and the level of interaction with scavenging seabirds.

Kejal Dodhia

From sample to result in an hour: towards rapid disease and fungicide resistance detection

The fungicide resistance epidemic in agriculture is akin to antibiotic resistance in humans. Rapid diagnosis of resistance can help towards making more informed decisions around integrated disease management. From the field to lab, the detection of fungicide resistance can take up to two weeks using conventional methods such as culturing or Sanger sequencing. Laboratory based molecular methods can bring this down

to three days. The window for spraying can be lost by then hence the need for an infield diagnostic test. We have designed assays to detect prevalent phytopathogenic fungi causing yellow spot and septoria blotch of wheat, net blotches of barley, bunch rot of grapes and stem rot of canola, among others. In addition, we have developed assays to detect the genetic changes which result in fungicide resistance. The tests are based on isothermal DNA amplification and conducted on battery operated equipment and coupled with a quick DNA extraction technique detect these organisms, in situ, within 1h of sample collection. In the farm setting, ideally, this would lower operation costs, increase yield, lower selection pressure for resistant strains and increase fungicide lifespan.

Alyce Hancock

Effect of ocean acidification on Antarctic marine bacterial, archaeal and eukaryotic communities

Near-shore Antarctic microbes are the drivers of productivity, elemental cycling and effect ocean biogeochemistry yet little is known about their response to ocean acidification, despite Antarctic waters being amongst the most vulnerable to increased CO2 levels in the world. A six-level ocean acidification experiment was conducted on a natural microbial community at Prydz Bay, East Antarctica using minicosm techniques. The MiSeq Illumina platform was used to investigate the effect of ocean acidification on the bacteria, archaea and eukaryotes within minicosm communities. No significant effect of CO2-driven ocean acidification was seen on the bacterial and archaeal community despite having overall higher abundances in the higher CO2 treatments. This suggests that ocean acidification may indirectly affect bacteria and archaea through their interactions with other microbes within the community. The eukaryotic community, however, showed a shift in community composition, with high CO2 levels favouring small cells. This suggests that in the future, ocean acidification will alter the eukaryotic community composition and microbial interactions, and therefore impacting the ecosystem services these communities provide. The flow on effects of such changes could have significant consequences for the near-shore Antarctic food web and elemental cycling if anthropogenic CO2 release continues unabated.

Theme 3: Biosecurity & Forensics

Katherine Zulak

High-throughput genotyping using digital PCR improves detection and quantification of fungicide resistance in *Blumeria graminis f. sp. hordei*

The management of fungicide resistance in agriculture is a major global issue. This is particularly problematic for the triazole fungicides commonly used to treat human and plant fungal diseases. In Australia, increased occurrence of triazole resistant strains of barley powdery mildew (Bpm; Blumeria graminis f. sp. hordei) has led to important yield loses due to field control failure. Resistance is primarily caused by two point mutations in the target Cyp51 gene that result in amino acid changes Y136F and S509T. Early detection and accurate quantification of fungicide resistant populations in the field is critical so that spray regimes can be adjusted before resistance becomes wide spread. To address this, we have developed a digital PCR assay for the detection and quantification of these mutations in field samples of Bpm-infected barley leaves across Australia. We quantified mutation levels as low as 0.2% in both genomic DNA and field samples. We also detected the T509 mutation for the first time in the Eastern states of Australia using a network of baiting trails and digital PCR. The combination of digital PCR and baiting trails has proven to be a powerful early warning system in the battle against fungicide resistance in Australia.

Kelly Hill

Molecular Diagnostics for Plant Protection

Plant pest and pathogen detection, identification and surveillance in agriculture are integral to production economics and food security. Quantitative assessment of these organisms is important to make management decisions and currently, established molecular methods such as qPCR are ideally suited for this application. SARDI Molecular Diagnostic Centre (MDC) is tailor-made as an automated, high-throughput diagnostic service that delivers specific and quantitative monitoring for over 140 pests and pathogens of relevance to primary industries. While the application driven services and research activities primarily revolve around the reliable and established qPCR technology, the MDC now utilises massively parallel sequencing techniques to support current testing activities as well as research projects arising through closely integrated field pathologists and entomologists. Further research into new and emerging sensing and sequencing technologies are in progress to identify the MDC's next diagnostic platform.

Theme 4: Technology & Engineering

Andy Bachler

Field diagnostics for plants: extracting, amplifying, and detecting nucleic acids using paper microfluidics

Plants have complex and fine-tuned responses to stressors; current methods of rapidly detecting plant stress cannot differentiate among potential sources of stress e.g. drought, temperature, salinity. Management of plants in both agricultural and land management settings would be greatly improved if the source of stress could be rapidly identified in the field.

Most stress responses are underpinned by genetic mechanisms e.g. changes in transcription or translation. Our aim is to detect these genetic responses through identification of target DNA, RNA or miRNA sequences in the field using paper microfluidics. In this talk we will outline some of our efforts to extract, amplify, and quantify nucleic acids on paper. More specifically, we will discuss: paper-dipstick DNA and RNA extraction; isothermal amplification on paper; and, quantifying nucleic acids on paper using intercalating dyes.

Early diagnosis of the cause of plant stress using a cheap, portable device will provide key information to assist farmers and land managers to optimise their decisions.

Claudia Moratti

Synthetic biology approaches to hydrocarbon biosensors

According to Avocados Australia, the majority of damage to avocados occurs at the store level from people squeezing the fruit to test for ripeness. This sort of damage is not limited to just avocados and is a major contributor to the extreme levels of fresh produce wastage that occurs in Australia every year. In the face of the difficulties being experienced by farmers across the country, along with the high demand for seasonal fruits, we need a method to confidently predict the ripeness of fruit at all stages of the supply chain to minimise produce wastage even after long storage and transportation times. Current methods are expensive, labour intensive, and non-portable. As the major ripening hormone of plants, ethylene provides a promising target for the quantification of fruit ripeness. A cell-based ethylene biosensor sticker, comprised of two engineered Mycobacterium NBB4 proteins attached to a chromoprotein, will allow for a

quick, reliable, and easy measurement with a user-friendly readout. This project began as the focus of the University of Sydney International Genetically Engineered Machine (iGEM) team in 2016.

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Partners & acknowledgments

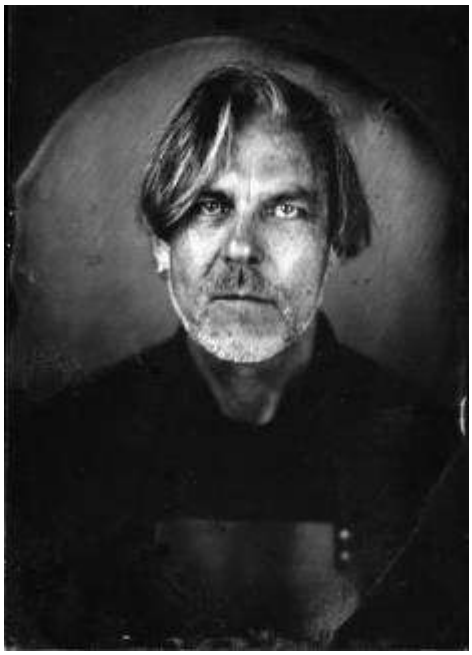
CSIRO acknowledges the Muwinina and Palawa people as the traditional owners and custodians of the land upon which we are meeting. We also recognise the deep history and culture of Tasmania's Aboriginal people and pay our respects to Elders past, present and future.

CSIRO and the symposium organisers would like to thank the following partners:

- CSIRO National Collections and Marine Infrastructure
- CSIRO Oceans and Atmosphere
- CSIRO Health and Biosecurity
- CSIRO Environomics Future Science Platform
- CSIRO Probing Biosystems Future Science Platform
- CSIRO Active Integrated Matter Future Science Platform
- CSIRO Research Office

Our Artist in Residence: Phillip England

Selected works on display in the Canteen during breaks



My photographs show you how I see the world.

I have been making photographic art all my life but four years ago finished a successful professional career as a research scientist to concentrate fully on art.

My practice embraces film, digital and alternative photographic processes. My current practice employs the collodion tintype process, from the dawn of photography, to produce unique, hand crafted image objects that explore the unique materiality and aura of tintype portraiture, still life and landscape.

I live with my family in a straw bale house, off grid in the Tasmanian bush & I am a professional member of the National Association for the Visual Arts.

I am represented by Nolan Gallery, Salamanca Place, Hobart Tasmania

You can buy my digital photographs at any size as archival inkjet prints on cotton rag paper. Or visit Tasmanian Tintype to learn about my collodion tintype practice. http://www.tasmaniantintype.com/

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Arts Grants, Funding & Residencies

- Cradle Mountain Wilderness Gallery artist residency Feb 2017.
- Arts Tasmania Crowbar crowdfunding subsidy April 2017 $500
- Pozible crowdfunding campaign Window to the Soul for June 2017 tintype portrait exhibition. $5500
- CSIRO Australian National Fish Collection tintype photographic project 2016

Selected Exhibitions

- Window to the Soul 2017 Tintype portraits. Studio Gallery Salamanca Arts Centre. With 50 page catalogue.
- Tarkine in Motion 2017 Group exhibition at The Long Gallery, Salamanca Arts Centre
- In Praise of Photography 2017 Group exhibition at TopSpace Gallery, Hobart
- The Medium is the Message 2017 Group exhibition at Entrepot Gallery, Hobart January
- Air, Water, Earth 2016 Sidespace Gallery, Salamanca Arts Centre

Things to see and do in Hobart

If you have some spare time in Hobart before or after the symposium and feel like doing some exploring; here is a brief list of some of the most popular things to see and do in the area!

- MONA (Museum of Old and New Art)

- Kunanyi / Mount Wellington

- Salamanca Market (Saturdays only) / Salamanca Place
    - Salamanca Arts Centre
    - Art Mob – Aboriginal Art Gallery
- Tasmanian Museum and Art Gallery
    - Check out the Thylacine exhibition!

- If whiskey is your thing, check out these distilleries:
    - Lark Distillery
    - Heartwood
    - Overeem
    - Sullivan's Cove
- If you are looking to go further afield and have more time then there are half and full day boat tours that leave from various locations along the harbour, visiting the following places (among others):
    - Bruny Island
    - Tasman Peninsula
    - Port Arthur

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