# Centre for eResearch 2022

ANNUAL REPORT



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# WELCOME MESSAGE

The Centre for eResearch (CeR) was first established in the 2009/10 academic year. At the time we had just two full-time employees and some part-time FTE for leadership and management. None of these positions were permanent. These were indeed very humble beginnings. At the start of 2023, our team now numbers over 25 people, most of whom have permanent contracts, all of whom have significant skills and experience supporting research. This growth mirrors the impact of digital tools and methods in the conduct of research, and by now almost all research fields are impacted.

Beginning from January 2023, the Centre for eResearch is now recognised as a University Research Platform meaning that it is recognised as a key facility for the support of research endeavours. Research Platforms typically represent large investments in research infrastructure, such as expensive laboratory instruments, that need significant central support over a long period of time. This change opens up some additional responsibilities and opportunities for us, including more coordinated governance and investment across the University's major research facilities. This change should improve longer-term planning of eResearch services and engagement across the University's research ecosystem.

The report you are reading describes the impact that the Centre for eResearch has had on research productivity and impact, showcasing some of the digital innovations we have achieved in partnership with researchers across the University. Scholarship that is enabled by computational methods takes many forms across the University: from High Performance Computing and Instrument Data Services, to Deep Learning and Augmented Reality Visualisation, from the study of relationships amongst online actors to the creation of interactive research exhibits.

This digital revolution in research began in the hard sciences and engineering, but has slowly worked its way to every corner of the University. In recent years, the pace of this change has increased, as all faculties look to take advantage of emerging computational tools and methods such as advances in Artificial Intelligence and Deep Learning, Immersive Reality and Data Visualisation, Virtual Laboratories and Simulation Modelling. Providing the necessary tools to researchers, along with the training to use them well, is critical in maintaining our research standing and productivity. This report details the part we have played in delivering these capabilities to our researchers.

In 2022 the Centre for eResearch supported around 1,500 research projects and over 3,000 individual researchers with a wide variety of computational services and tools. We also provided training to over 1.500 researchers, on topics ranging from data privacy & security to advanced analytics and data visualisation.

Additionally, we provide a private cloud computing facility for our researchers to use and are managing over 1.3PB of research data across the various Research Data Services we support. In every department in the University, there is some footprint of our activities.

# SUPPORTING RESEARCHERS

### **Research Computing**

Many researchers require computing capability beyond their desktop / laptop computers. For example, they may have different operating systems, require more computational power and/or an interactive workflow; they may need access to the high Performance Computing (HPC) environment for their research etc. Often time, the Centre is the first point of contact for researcher computing support. We discuss requirements with researchers before enabling access to the following platforms for computationally intensive research and, in exceptional cases, researchled teaching. The Centre brokers researcher access to Connect or New Zealand eScience Infrastructure (NeSI) hosted research computing capability.

The research computing platforms in the University require annual evaluation on usage, capacity and performance. Through the IT CAPEX initiatives, we have helped the University to evaluate the priority investments in research virtual machines, Nectar Research Cloud and GPU equipment, and have refreshed some ageing equipment and upgraded to some newer servers in order to keep up with the current and future demand.

### **Research virtual** machine service

In collaboration with Connect, the Centre provides researchers with virtual machines and offers advisory, user-facing configuration and software installation.

### Nectar Research Cloud

This is a part of the Australian Research Data Commons and a federated private cloud dedicated to supporting research. Together with many of the Australian research institutions, the University, through CeR, is a partnering Nectar node. Nectar follows a selfservice model that is similar to public cloud providers and is better suited for international collaboration.

### **High Performance** Computing (HPC)

New Zealand eScience Infrastructure (NeSI) offers a specialised HPC platform, analytics software and a consulting service. For many UoA NeSI users, CeR is the door by which they access this service. NeSI's main systems are Linux-based, ideal for high-performance or high-throughput use cases. For more details about NeSI, see www.nesi.org.nz.

### Machine and deep learning

There is an increasing demand to support data intensive research using machine and deep learning techniques. It is used to automate labour intensive tasks and to develop more accurate predictive models.

We are continuously exploring options to better support machine and deep learning by expanding the capability of GPUs available in the Nectar Research Cloud (investment as mentioned above). In some cases, the Centre's specialists offer more in-depth support in implementing machine learning solutions for their research problems. Our prototyping skills have led to several successful grants applications.

### **Research Data Solutions**

Research is increasingly multidisciplinary, with higher resolution data as collection tools become more sophisticated. This had led to a growing understanding of the variety of research data<sup>1</sup> and artifacts, their visibility and the need to think sustainably about the data or artifacts created.

### Research data has gravity and mana, is valuable, and requires careful management.

Our research data services and training span the research data lifecycle with respect for the different capabilities, practices and tools required at different stages and by different communities involved in research. We continue to focus on developing and expanding Research Data Management training and outreach (detailed in the Digital Skills section); supporting access to appropriate storage and data transfer, maturing our provisioning of research storage; publishing research data and digital artifacts with our Digital Services colleagues; and developing instrument data management tools.

### Data storage, transfer and collaboration

Together with Digital Services, we are working to integrate and support good practices in research data management that align with external requirements from funders and publishers and our strategic goals. We now have more than 556 projects recorded against our managed research drive service and over 1,814 researchers with more than **1.3 PB** of actively managed data, and an additional 950 TB of data in vault/ archived storage (Figure 1 shows the growth of Research Drive storage for the past 4 years). The use of Dropbox as a collaboration tool grows with a subscription renewal for three more years.

### Data publishing and discoverv

Throughout 2022 our research community published 820 items in our institutional Figshare, the University hosted research data repository. This adds to the collection of over 3200 items with 2 million views and 602K downloads

across this service to date. Within this sits one of our special projects - the HVN metadata catalogue (see Case Study #4), one of the 21 group sites which enables specific community groups to showcase their published research data or information about the data they have collected. During 2022 this service subscription was renewed for the 2023-2025 period and will support growth associated with the MBIE Open Research policy released late 2022 and the implementation of the University's Research Data Management policy that comes into effect mid 2023.

### Instrument data

During 2022 we consolidated the functionality and maintainability of the instrument data platform MyTardis, a community driven platform initially developed at Monash. In 2023 as part of the University strategic funding we will expand the use of MyTardis to other instruments, and introduce new instrument data pipelines linking to analysis platforms such as NeSI, and virtual computing platforms running in Nectar (see Research Instrument Data Strategic Project section).

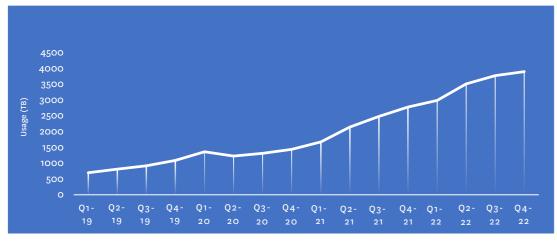


Figure 1. Growth of research drive storage from 2019 to 2022.

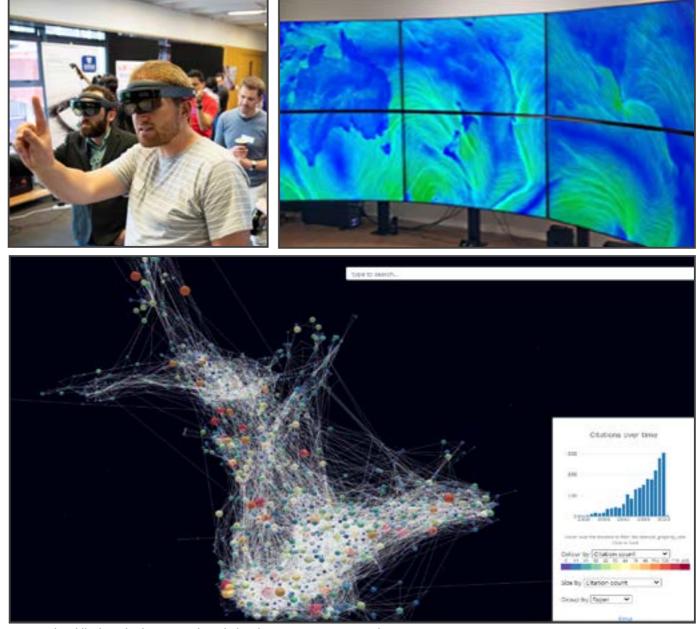
<sup>1</sup> The University defines research data as the evidence that underpins the answer to a research question and can be used to validate findings regardless of its form (e.g., print, digital, or physical).

### **Research Visualisation**

The Centre provides researchers access to advanced visualisation facilities for multi-user collaboration. This includes high-resolution large visualisation displays powered by fast computing nodes and high-end graphics on the City and Grafton campuses.

In addition to these bookable hardware and spaces, we also offer free technical advice and support for using this equipment. The visualisation capability helps researchers to capture and act on complex problems more effectively, especially when dealing with vast volumes of information and helps them bring their data to life.

The equipment and tools can provide a 3D and immersive experience. There



Reserach publication citations network analysis using Microsoft Academic and 3D force graph

are portable set-up options for users to use off-site and in classrooms. These are bookable Augmented and Virtual Reality headsets, including Hololens 1 & 2, Oculus Quest/Rift, HTC Vive, and Gear VR, 4k-3D, 8K displays and a curved tile wall.

### **Special Projects - Research**

Besides providing consultations and access to various storage options, computing platforms and training workshops to upskill researchers' digital competencies, the Centre's specialists also work with researchers by delving into their research projects and offering customised digital solutions. Below are examples of how we supported researchers on special projects in 2022.

- 1. Building and running machines/ deep learning models; developing image processing pipelines; enabling data sharing between different machine learning environments and containerising models for API deployment to improve the implantation of In Vitro Fertilisation (IVF) embryos. (Case study 1)
- 2. Developing the metadata catalogue across multiple organisations with standard operating procedures and tailored data management plans to provide detailed and searchable clinical information as part of the High Value Nutrition National Science Challenge. (Case study 4)
- 3. Tumour Evolution: a Multi-vear project to produce a prototype Augmented Reality (AR) application that facilitates the generation and exploration of different hypotheses of how cancer evolves by combining detailed genomic, pathological, spatial and temporal data from a

single patient with cancer. (Case study 6)

- 4. A study of geospatial data for police responses to mental distress: Analysing data extracted from the NZ Integrated Data Infrastructure (IDI) to better understand the socio-demographic context of people in mental distress who have sought support from the NZ Police (NZP) between 2013 and 2019, using a whole-of-population cohort. We used the spatial scan statistic (SaTScan and ArcGIS) software to explore the feasibility of creating a space-time cube to identify the clustering of police attendance to such events and ultimately help inform policing policies to improve the management of such events. (Case study 7)
- 5. Create the Ahuahu Great Mercury Island artefacts online database by trailing an open source tool -CollectiveAccess - deployment using Nectar Research Cloud to specifically tailor the needs for collaborative records and manage archaeological data. (Case study 11)
- 6. Rongowai: Simulating virtual capabilities of the Science and Payload Operations Centre data infrastructure, using live flight tracking and reflected GPS signals to infer information about the earth's surface. The collaboration between UoA, MBIE, NASA, Air New Zealand, the University of Michigan, Ohio State University and the University of Canterbury

- we develop tools to facilitate data gathering from the receiver, pushing instructions to the receiver and processing the data into a usable product. We also created data visualisation and the generation of data cubes. (Case study 12)

- 7. Calculate the amount of New Zealand developable lands: Looking at a threshold radius of the central business district that is equal to or under a threshold slope based on each functional urban area (FUA).
- 8. The impact of the digital platform on Zoom by mapping internet activities during the Covid-19 lockdown.
- 9. Online study of hate speech: Scripting the automatable API for data collection from publicly available post data from various platforms.
- 10. Creating prototype software, including calibrating and testing a Cellular Automata (CA) model, developing a new fitness measure, and optimising threshold parameters using machine learning algorithms to improve model fitness applied to New Zealand Land Use and Land Cover.

These special projects are run on a cost-recovery basis and are usually funded by external research grants. We welcome the opportunities to partner with research groups for grant applications where our skills and services offer value to researchers.



### **Digital Research Skills**

CeR offers regular digital research skills development opportunities, and runs community events to help empower and equip our researchers. During 2022 most workshops and events were delivered online. These include:

- Research Data Management (RDM) workshops
- Software and Data Carpentries workshops
- Nectar Research Cloud computing workshops
- Research Bazaar (ResBaz) an annual digital skills and community building event
- Hacky Hour weekly community activities and online channel

### **Research data** management

Our Research Data Management educational offerings are available for all staff and postgraduate students, including the generalised overview and bespoke workshops. These workshops increase the University data management maturity by raising awareness of, for example, evolving funder, ethical, legal and institutional requirements, principles of FAIR, CARE and Māori Data Sovereignty, and promotion of the University services and support. Nearly all of the 13 RDM workshops in 2022 were delivered online to 362 attendees from across the University.

### Software and data carpentries

The Carpentries is a global not-forprofit promoting the teaching of foundational research computing skills by hosting community-developed teaching resources. Software Carpentry workshops equip learners with core skills in software programming (such as using a command line to manipulate files), while Data Carpentry workshops offer practical skills for working with data, from collection right through to analyses.

CeR delivered one Software Carpentry and two Data Carpentry events to a total of 111 learners in 2022, split into three cohorts.

### **Research Bazaar**

Research Bazaar (ResBaz) aims to empower researchers, particularly doctoral candidates, to make the most of digital tools and methods to solve problems and improve the research process, regardless of their field. CeR has organised and run an annual ResBaz to encourage the uptake of digital research skills for UoA researchers and research postgraduates for over 5 years. Since 2020, this previously multi-day, inperson cohort event has moved online.

In 2022, CeR hosted ResBaz Aotearoa in collaboration with Victoria University of Wellington, the University of Otago, and the UoA hosted MBIE-funded Data Science Platform: "Beyond Prediction".

2022, our biggest ResBaz to-date, this event offered a total of 46 digital research workshops, a mix of 1 hour taster and 2-3 hour practical sessions, delivered by over 40 contributors. The programme attracted 5,076 session registrations. Our most popular session was 'NVivo for Literature Reviews' which attracted over 300 registrations. A total of 1,486 individual participants registered to attend a session, at least 35% were UoA staff and students. All registrants were provided session slides and recordings to enable selfpaced learning and support off-shore students.



### Hacky Hour

Hacky Hour is an informal online dropin space and community facilitated by the Centre for eResearch. Each week, students and researchers get help and advice with code, data, and software problems relating to their research in a supportive and social environment. Hacky Hour is open and inclusive, so all are invited to join in and make new connections. The growing community of 650+ researchers and support staff is a great place to share skills and knowledge across disciplinary and institutional boundaries.

### University Strategic Projects

### Partnering to inform and co-design initiatives that grow strategic research infrastructure and resources supporting research across the University.

CeR proactively partners with the Office of Research Strategy and Integrity (ORSI), Digital Services, and the School of Graduate Studies to inform and co-design Research & Innovation initiatives. To this end, we are engaged in a variety of Special Projects funded by our University Strategic Projects Office (USPO). These projects are typically University-wide initiatives to grow our maturity in some area of research data and compute capability. Below we outline some of the strategic projects and initiatives we were involved in 2022.

### Research Data Management Programme (RDM)

Following the development of the Waipapa Taumata Rau Research

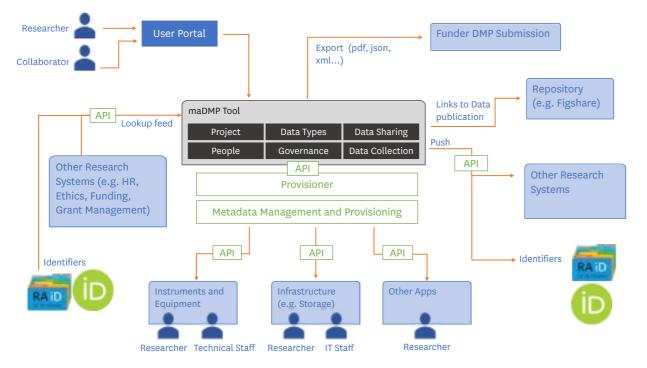
Data Management Capability Maturity Model, CeR is involved in implementing the project's recommendations. This includes team members co-leading the technical implementation, engagement activities and solution development of the following three initiatives for the RDM Programme 2022-2024:

- 1. A Secure Research Environment (SRE) that enables secure storage, analysis, and robust governance of sensitive research data.
- A machine-actionable *Data* Management Planning tool (diagram below) that facilitates connected dynamic data management planning.
   A connected research ecosystem
- using *Persistent Identifiers (PiDs)* at it's heart to enable information flow between the University's systems.

Working in parallel to these three funded initiatives, CeR staff have been part of the a. ORSI-led working group developing the University' first Research Data Management Policy, and b. the inclusion of research data into the updating of the University' Data Classification and Confidentiality Standard .

### Instrument Data Service

The first phase of the Instrument Data service has led to the development, deployment and support of a MyTardis repository for use by our research communities with a solid base of ingestion examples and different patterns of instrument use.



A diagram showing potential for dynamic integrations with a maDMP tool within the University's research ecosystem.

The next two years will see the service mature into a defined university capability aimed at addressing the challenges of modern instrument data storage, access and collaboration, including:

- Expanding the use and operationalisation of the service. This will include those instruments within the existing high-profile facilities (e.g. BIRU, ABI, Mass Spectrometry Centre and Auckland Genomics (SHaRE) and new priority platforms over the next two years.
- 2. Facilitating planning and best practice by aligning transparent data management and retention policies, and facilitating early planning of emerging data and infrastructure needs in Connect Digital Services and the SRI process, particularly within platforms.
- Integration and automation by promoting the use of persistent identifiers, facilitating the development of reporting, and research outputs tracking for facilities and instruments.

### Researcher Skills and Development

In 2022 the Researcher Skills and Development (RSD) Project, an ORSI and Organisation Development jointly-led initiative, funded a composite position within CeR to increase our capacity to deliver digital research skills. Specifically, Carpentries workshops, ResBaz and an increase in research data management training to support RDM improvements (e.g. incoming RDM Policy). See Digital Research Skills section for details. As a member of the RSD Reference Group, CeR contributed to the ongoing effort by RSD providers across the University to coordinate, collaborate and invest in skills and development offerings for the University research community. CeR staff also provided technical development support to enable improved access to RSD 'capabilities' via the Research Hub that will be implemented in 2023. At the end of 2022 CeR successfully bid to the DVC-Research RSD Fund to deliver two machine learning workshops in 2023.



# **OUR TEAM**



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Solutions Co-Lead



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Dr Mike Laverick Snr Solutions Specialist





Klim Belchev



Dr Bincy Jacob



Victor Gambarini Snr Platform & Serv Eng Snr Engagement Specialist Engagement Specialist





Engagement Specialist



# **CASE STUDIES**

- 3. The Effects of Short-Term Tourist Rentals on Local Residents

- Who Are The 1M and 1X? Police Engagement 7. with Citizens in Mental Distress
- 9.

- 1. Improving In Vitro Fertilisation (IVF) with Machine and Deep Learning
  - Pacific Rheumatic Fever Project
- 4. Metadata Catalogue In High Value Nutrition (National Science Challenge)
  - Assessing Marine Ecosystems to Improve Management
- 6. Representation of Multimodel Data A Challenging Task
- 8. Interpretation of Non-coding Mutations Driving Melanoma Risk and Its Comorbidities
  - Novel Subject-Specific Mothod of Visualising Group Differences from Multiple DTI Metrics without Averaging
- **10.** Travelling Heads Measuring Reproducibility and Repeatability of Magnetic Resonance Imaging in Dementia
- **11.** Automating Data Collection and Generation for The Rongowai Mission
- **12.** Ahuahu Great Mercury Island Online Database
- 13. VRhook: A Data Collection Tool for VR Motion Sickness Research
- 14. Accounting for Errors in Data Improves Divergence Time Estimates in Single-cell **Cancer Evolution**

# **Improving In Vitro Fertilisation** (IVF) with Machine and Deep Learning

Dr Nicholas Knowlton, Senior Research Fellow, Molecular Medicine and Pathology, Faculty of Medical and Health Sciences; Dr Nidhi Gowdra, eResearch Solutions Specialist, Centre for eResearch

By exploring how to improve we hope the knowledge will be embedded in a model and made it widerly available locally and overseas where the investment will generate export value for New Zealand and benefit the needed parents by reducing IVF waiting time and increasing the rate of live births.

The current process of selecting embryos for implantation in IVF is based on little knowledge of the relationship between the parameters for embryo selection and the actual success rates post-implantation. Embryos are selected based on the features in a single image taken at a single time. Some researchers and clinicians are starting to apply artificial intelligence (AI) to a selection of

embryos, thereby considering multiple factors at once that indicate potential successful implantation and live birth more likely.

Unfortunately, most of these schemes try to copy the current, and limited approach of embryologists. We have evaluated the existing schemes and realised that we could do much better, particularly given that none of them appears to improve success rates.

Our team of an embryo quality specialist, a machine learning/AI expert, and a clinical embryologist, a key opinion leader in embryology, will use exclusive access to billions of embryo images alongside their clinical information to develop an AI-based approach to embryo selection. We will use information regarding a wide range of aspects of the embryo at different stages in its development, together with information regarding the parents.

This knowledge will be embedded in a model, which will be made available

widely in New Zealand and overseas by a new company developed for the purpose. This enterprise will create new export returns for NZ through selling access to the model while generating significant social benefits in New Zealand by reducing IVF waiting times and increasing the number of live births from IVF.

The Centre for eResearch is a key partner in this project through their Machine and Deep Learning (MaD) Service. They provide support with data storage, retrieval, organization, integration with third-party tools and direct coding support. By leveraging their expertise with my research group, we can work more efficiently by tapping into a much larger experience base.

While the project is ongoing, we will discuss our progress on automated embryo morphokinetic identification in this project update.

### Problem

With billions of unlabeled images, we needed a way to bootstrap the image labeling process. Directly labeling even a fraction of these images would be time-consuming and use expensive clinical expertise. After considering our options, we went forward with an active learning approach, where a small set of data is labeled to build a base model, and new data is added where the model lacks confidence.

### Lav method description

A random set of ~5,000 images was labeled to start the model-building process. After this, we found that only embryos that progress to blastocyst provide the most cost-effective samples to label, and an additional 10,000 images were labeled using this approach. With model confidence improving, this approach was continued until model accuracy was approaching 90% for all classes. Amazingly this approach required only ~60,000 hand labeled images or 0.0024% of the dataset. With an accurate model, the focus shifted to identifying images the model has low confidence or marginal classification.

### Technical method description

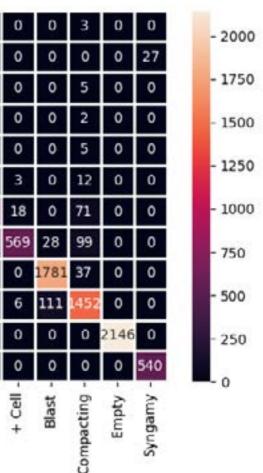
Images are preprocessed and split into training/validation and test sets by 72%/8%/20%. During training, image augmentations are applied, including height and width shifts, horizontal and vertical flips and random image rotations. The augmented images are used to train an EfficientNetv2M from scratch. The model is openly available with the standard Tensorflow and Keras frameworks in Python. Further HyperParameter optimizations were performed to reduce model overfitting and increase classification performance.

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Figure 1. Confusion matrix

### Results

All model training was performed on 2 NVIDIA V100 GPUs, which were made available to us via the Nectar Research Cloud. The classification model of embryo morphokinetic stages was evaluated on unseen randomized images with a top-1 accuracy of 92.79% and a top-2 accuracy of 98.19% for 12 distinct classes (Figure 1. confusion matrix). However, more data is needed to further mature the models for commercial deployment. This project is on track to realize the aim of revolutionizing embryo selection within In Vitro Fertilization (IVF) in NZ and abroad.



### **Pacific Rheumatic Fever Project**

Research team: Research Fellows: Dr Siobhan Tu'akoi', Dr Samuela Ofanoa'. Senior researchers: Dr Malakai Ofanoa', Professor Felicity Goodyear-Smith<sup>2</sup>. Clinical experts: Dr Hinamaha Lutui<sup>3</sup>, Dr Maryann Heather<sup>1,4</sup>. Leader of Pacific People's Health Advisory Group: Rose Lamont.Etu Pasifika Ltd, Auckland, New Zealand.

- 1. Pacific Health Section, School of Population Health, University of Auckland.
- 2. Department of General Practice and Primary Health Care, School of Population Health, University of Auckland.
- 3. Alliance Health Plus, Auckland, New Zealand.
- 4. Etu Pasifika Ltd, Auckland, New Zealand.

The Pacific People's Health Advisory Group (PPHAG) and the Pacific Practice-Based Research Network (PPBRN) are working together to address health inequities faced by Pacific communities in South Auckland. PPHAG is comprised of South Auckland community members from a range of age groups, Pacific ethnicities and professions. It aims to identify where research is most needed for Pacific communities in South Auckland. PPBRN was established through Alliance Health Plus, a Pacific-led Primary Health Organisation; and each general practice designated a staff member to act as a research officer such as a general practitioner, nurse, or manager. Senior researchers from the University of Auckland then collaborated with PPHAG and PPBRN to provide training on different Pacific methodologies and how to ask meaningful research questions. What resulted from this process was a series of priority research questions developed by the community members and practices. The first research priority related to ensuring Pacific people could access and take medication to prevent gout, and this project is underway. The second research priority identified was reducing the inequitable rheumatic fever burden faced by Pacific communities, particularly in South Auckland.

### **Background of** rheumatic fever

Rheumatic fever is an autoimmune condition that occurs in response to an untreated Group A Streptococcus



Figure 1: PPHAG, PPBRN and University of Auckland researchers

throat or skin infection, primarily affecting children aged 4-19 years. Recurrent episodes of rheumatic fever can cause permanent damage to heart valves, heart failure and even death. Māori and Pacific people in Aotearoa New Zealand experience some of the highest rates globally, with Pacific children 80 times more likely to be hospitalised for rheumatic fever and Māori children 36 times more likely than non-Māori, non-Pacific children.

### **Project aims and** objectives

The project aims to co-develop, implement and evaluate an innovative intervention to reduce rates within Pacific communities in South Auckland. The objectives are:

· To determine the burden of GAS

infections, acute rheumatic fever, and rheumatic heart disease in Auckland general practices, comparing Pacific, Māori, and non-Pacific non-Māori groups.

- To co-design a novel approach to prevent GAS infections progressing to rheumatic fever within Pacific communities in South Auckland.
- To evaluate the implementation and effectiveness of the co-designed intervention using an implementation science approach.
- To create an implementation framework that can guide future implementation roll-out within other settings in NZ.

### Fa'afaletui framework

This project utilises the Samoan Fa'afaletui paradigm - a way of facilitating the gathering and critical

validation of different knowledge types. It centres on fa'a, the ways of sharing and validating knowledge from different groups or fale (houses), and tui, weaving these together to reach a consensus. Collective decision-making and mutual respect are key principles both in a traditional fa'afaletui and when applied in a research sense. The method allows researchers and participants to work together towards a shared goal, ensuring that all voices, opinions, and conflicting perspectives on a serious topic are discussed in a respectful manner.

### **Co-design workshops** 2022

A series of co-design workshops with PPHAG and PPBRN are currently underway. Although originally designed as in-person workshops, we shifted to an online zoom format due to COVID-19 restrictions and based on the preferences of our groups. Two

community co-design workshops were held so far in 2022. Workshop One included an interactive session between community members and Pacific health professionals about what rheumatic fever is and how it presents within clinics in South Auckland. To inform the workshops' participants, a scoping review was undertaken to take stock of previous interventions in New Zealand. The research team then led discussions on these interventions and explored the incidence rates in NZ over time. Participants were then split into smaller groups for further discussion and to start brainstorming ideas about what might work in their community. Workshop *Two* built on these ideas and participants started to refine specific interventions including who would deliver it, the costs involved and how it could be evaluated. Group members spoke passionately throughout the workshops of their own experiences with rheumatic



#### Reference

- intervention to prevent rheumatic fever in Pacific People in South Auckland: a study protocol. International Journal for Equity in Health, 21(1), 1-6
- 2. Tu'akoi, S., Ofanoa, M., Ofanoa, S., Lutui, H., Heather, M., Jansen, R. M. & Goodyear-Smith, F. Addressing rheumatic fever inequities in Aotearoa New Zealand: A scoping review of prevention interventions. Journal of Primary Heath Care. 2022 In Press.

CASE STUDIES

fever and the challenges of accessing healthcare. Co-design workshops will continue until a final intervention is reached and can be tested. This will be complemented by discussions with an expert advisory group to ensure that the final intervention is feasible and appropriate. PPHAG and PPBRN will be actively involved in the implementation and evaluation stages, serving as champions. This will help to facilitate intervention uptake and ensure barriers are identified and addressed.

Addressing rheumatic fever will not only improve health outcomes for Pacific families and communities but will also have long-term benefits for reducing hospitalisations and health system related costs in NZ. Community-led approaches such as outlined in this project are needed in each context to ensure interventions are appropriate, relevant, and effective for the local community.

Figure 2: A zoom workshop with PPHAG and PPBRN

1. Tu'akoi, S., Ofanoa, M., Ofanoa, S., Lutui, H., Heather, M., Jansen, R. M., van der Werf, B. & Goodyear-Smith, F. (2022). Co-designing an

# The Effects of Short-Term Tourist Rentals on Local Residents

Dr William Cheung, Senior Lecturer, Property, University of Auckland Business School; Assoc Professor Edward Yiu, Member of the Faculty Research Committee, University of Auckland Business School.

This Press Release was contributed by (Cheung & Liu 2022) and posted by AUSTRALIA'S SPATIAL INTELLIGENCE NETWORK (AURIN) on 4 Oct., 2022 and has granted the permission to use for this reporting.



Image source: https://aurin.org.au/research-impact-the-effects-of-short-term-tourist-rentals-on-local-residents/

Using APM (Australian Property Monitors) Point Level Data and the Inside Airbnb dataset available through AURIN, researchers at the University of Auckland have assessed the impact of short-term tourism rentals, in particular, those through Airbnb, on rental prices across different suburbs in Melbourne, Australia.

Cheung & Yiu's (2022) study 'Touristification, Airbnb and the tourism-led rent gap: Evidence from a revealed preference approach', addresses critical questions related to these rentals and their impact on local residents. In particular, their work seeks to move away from assessments of these rentals as having only positive or negative effects, contributing to a more nuanced understanding of the costs and opportunities of this accommodation style in different types of neighbourhoods.

### Problem

The rise of home-sharing platforms, such as Airbnb, has driven the process of 'touristiflcation' in major tourism cities. Touristiflcation is a term used to describe tourism-induced gentriflcation, with the process often leading to the transformation of a community into a tourism commodity. For example, services, facilities, and shops may be re-oriented towards the tourists' preferences rather than local residents, impacting the social and economic value of housing in these areas.

These changes have the potential to be positive if the touristification process increases a neighbourhood's appeal and attracts improved amenities. However, if they contribute to a loss of relevant or useful local amenities, residents may seek to move elsewhere, leading to their displacement. While tourism is a leading industry in many

global cities, creating jobs and enhancing the flnancial well-being of destinations, the touristiflcation process led by home-sharing platforms has created rifts between local residents and visitors. This has left governments worldwide to decide how Airbnb-style accommodation should be regulated. For example, Christchurch City Council in New Zealand has recently introduced rules regulating Airbnb-style accommodation, requiring homeowners to obtain council approval in order to rent out their properties as un-hosted visitor accommodation in residential areas. The council can consider impacts on neighbours, including noise and trafflc movements, before deciding whether to grant or decline this approval, which also carries a cost of NZD \$1000. However, questions remain about whether such a 'one-size-flts-all' bed tax is the best way to govern the Airbnb market, as well as how we can best

understand the impact of these rentals on local communities.

### Approach

Most previous studies on the effects of Airbnb-induced touristiflcation have considered the phenomenon either entirely positive or entirely negative. However, this approach does not fully capture the impacts of tourism in transforming urban neighbourhoods and has left unanswered questions regarding the optimal design of relevant policies.

Cheung & Yiu's (2022) study seeks to provide a new perspective on Airbnb's impacts on urban housing markets in relation to residential location preferences – that is, the neighbourhood qualities where people want to live. Their analysis uses a tourism-led rent gap model - identifying how and where short-term rentals impact rents in their geographic area, compared to expected rents if these short-term rentals were not present - to argue that the touristiflcation process in a neighbourhood can result in both positive and negative external effects, as revealed by different magnitudes and directions of rent gaps. In the study, they compare similar properties across different areas of Melbourne, with residential rental rates used to identify the revealed preference of locals about their residential location choices, after considering all factors involved. Using more than 22,000 Airbnb and 200.000 residential rental listings in Melbourne (Figure 1), their findings provide new evidence on how touristiflcation contributes to a tourism-led rent gap in high-density

"With such a granular level of rental data provided by aurin, we can better understand the dynamics between airbnb and residential rental markets. The beauty of having such granular rental property data is that it allows us to have a much more in-depth analysis of the factors that contribute to causing changes in neighbourhoods, pinpointing the source of rental differentials and offering more insights on the effects of Airbnb-induced touristiflcation," Dr Cheung says.

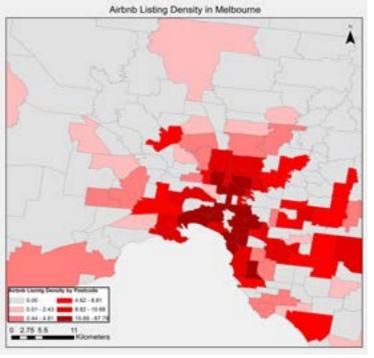


Figure 1. Airbnb listing density in Melbourne by postcode (Source: Cheung &Yiu)

neighbourhoods and a negative rent gap in low-density neighbourhoods.

With these flndings, they note that highdensity neighbourhoods, such as those with a large number of apartments, may experience net positives as a result of touristification, while lower-density neighbourhoods may experience more negative effects.

#### Impact

This study provides an evidence base to help address and inform ongoing tourism policies aimed at managing and regulating short-term rental accommodation. On the basis of their flndings, the researchers propose policies that aim to regulate short-term rentals based on property types. They argue that banning Airbnb in some tourism cities would limit the flexibility of the industry to respond to high tourist demands for accommodation during the peak season and that such blanket bans would require exorbitant enforcement costs.

However, as apartment-type properties are more compatible with Airbnb in high-density areas, designated zoning for Airbnb could provide a city with more flexibility to supply tourism accommodation while avoiding creating severe urban conflicts in low-density areas. Identifying properties and neighbourhoods compatible with Airbnb is essential for strategic tourism development and management, allowing tourism to continue without negatively impacting local communities. Ultimately, this research provides a strong basis for further studies on the more complex impacts of touristiflcation, rather than simply identifying short-term rentals as having only positive or negative effects, and offers possible directions for policymakers to respond more effectively to the needs of residents and tourists.

The research has also had a wide media impact, with coverage in New Zealand in outlets such as *Newsroom* and *Interest*. *co.nz* demonstrating how zoning laws could assist to support sustainable tourism and reduce conflicts between residents and tourists.



# Metadata Catalogue in High Value Nutrition (National Science Challenge)

Rob Carter, Dr Dharani Sontam, Yvette Wharton, Professor Mark Gahegan, Centre for eResearch; Dr Simmon Hofstetter, Operations Manager, Professor Richard Mithen, Liggins Institute; Joanne Todd, Challenge Director, High Value Nutrition, National Science Challenge.

### Nutrition and research data

You'd think that research projects would share methodologies in common with Libraries when it comes to research collections. But in practice it is uncommon to build a Data Catalogue that itemises what research data was created.

CeR's Research Data Management team provides consultancy on processes and structures that support healthy data workflows. Central to this work, we must be able to answer the question: "Where is the data?"

It's important to keep standardised records about the research data that is collected and created. Metadata enables future researchers to discover previous knowledge, because metadata records are publicly searchable. Metadata is what makes services like Google search possible.

Apart from being good for exposure and internet search, a Metadata Catalogue should be flexible enough to make statements about this data in the context of Tikanga Māori. For example. where Māori assert kaitiakitanga over a particular species that is the subject of research.

The Data Catalogue sets out contact information for individuals and organisations who are involved in the guardianship of the data. In this way, it is possible to involve these people in future decisions around the data. We use an industry standard knowledge repository platform to publish these metadata records. Records are regularly syndicated to data.govt.nz (Figure 1) and included in their collection of datasets. Syndication helps to ensure that the data is more likely to continue to be available into the future.

Ko Ngā Kai Whai Painga, High Value Nutrition (HVN) National Science *Challenge*, is a multi-year, multi-study research programme. It asks questions about nutrition and diet from early childhood onwards. It's aim: to grow the science excellence and knowledge Aotearoa New Zealand needs to create and deliver food to the world that people choose to stay healthy and well. CeR provides two staff members, Robert Carter and Dharani Sontam, to develop the Metadata Catalogue from the ground up. The scale and number of studies being conducted, along with the added complexities of COVID. required a flexible, collaborative approach. With many data types spread across multiple organisations, the project has benefited from previous work with CeR on Data Management Plans and Standard Operating Procedures. The Metadata Catalogue links each study with it's Ethics Registry approval records; providing detailed, searchable, clinical information.

### Seeding Through Feeding (SUN): Nourishing the infant microbiome to support immune health

The SUN Study is a double-blind, randomised controlled trial designed to recruit 300 infants from urban and central Auckland, New Zealand. The SUN Study aims to determine the associations, and possible causality between prebiotic feeding, growth of immune health beneficial microbes in the infant gut, with reduced number of respiratory infections and improved vaccination responses in infants 6 to 12 months of age. We are working with the project team to define and include information relating to 19 individual data types resulting from the work.

### He Rourou Whai Painga: An Aotearoa New Zealand diet for metabolic health and whanau wellbeing A national Aotearoa New Zealand

dietary intervention study to evaluate the effect of a 12-week whole-diet intervention incorporating nutritious domestically-produced food and beverage products and dietary change support, compared with habitual diet, on the MetS-Z score in individuals at risk of developing metabolic disease in a randomised controlled trial. In this case, CeR collected details of 11 different data result sets, for inclusion in the Metadata Record.



Figure 1. HVN Metadata recods are regularly sundicated to data.govt.nz

### Future-proofing research data

Δ

With technology changing at such a rapid pace, the phrase 'future proof' might raise alarm bells. Institutional archives have been replaced by Digital Object Stores, filing cabinets with cloud storage, all in the space of one lifetime. How do you make provision for longevity in the digital age?

The tools of Archivists come into play when making calculated guesses about what the future will hold. Metadata must obey some kind of consistent format that is both human and machine readable. Short of inscribing the information on a brass plaque, we try to ensure that only the minimum of technology is required to read and make use of the Metadata Record. The record must carry with it a description of what the fields in the record mean.

To this end, three items of data are collected for each field in the record: the field name, a description of the data the field contains, and the data itself. The intension is to make the Metadata self-descriptive, rather than relying on some external pre-existing schema. Over time data formats change, and where possible, text is probably the most accessible format to use. On top of this, the project employs JSON as it's baseline machine readable format.

### Where to from here?

As the team continues to build the Metadata Catalogue, we measure what we have done in terms of the number of studies covered by the work, and in terms of the discoverability of the research.

While it sometimes seems that digital data has begin to take on an ephemeral quality, the HVN Metadata Catalogue provides visibility of research data to a standard that supports researchers in the years to come.

# Assessing Marine Ecosystems to Improve Management

Project team: Dr Jenny Hillman, Lecturer, Institute of Marine Science; Professor Simon Thrush, Director of the Institute of Marine Science; Professor Conrad Pilditch, University of Waikato; Eliana Ferretti, Lucy van Oosterom, Maria Martin, Research Assistants, Institute of Marine Science; Data visualisation support: Nick Young, Centre for eResearch, Rakshan Roohi, Institute of Marine Science

### Background

This project investigates the ecological effects of fishing and sediment runoff from land in Queen Charlotte Sound, whilst be suitable for restoration in the future. Marine health data gathered will support more integrated management of the ecosystem. The team of researchers from the University of Auckland, University of Canterbury, University of Waikato and NIWA worked with the local community, including local iwi and schools, to help focus on shared goals and engage with management of the Sound.

This project is part of the Sustainable Seas National Science responses to cumulative effects. It addresses the cumulative effects (CE) of multiple stressors on soft-sediment and rocky reef biodiversity and ecosystem function. This knowledge i necessary to underpin models, decision-making processes and to implement Ecosystem-Based Management (EBM). This research will allow us to develop frameworks across the Challenge that improve the way we make decisions about the risks posed by different activities in the marine environment, and the opportunities we have to improve the ecological health and mauri of our coasts and estuaries.

### Approach

The team spent eight days in the Sounds in 2018 sampling at more than 200 sites, with follow-up experiments on ecosystem functioning carried out in 2021. To assess the status of the marine environments at each site transects were run from the shore outwards at each site around the coastline of Queen Charlotte Sound and around islands within the Sound. Drop cameras (Figure 2) were either towed behind boats videoing continuously along each transect or dropped at multiple locations along each transect and still images taken. Each video and image were assessed live on the boat and notes taken, and post-assessment was also undertaken at NIWA Hamilton and the Leigh Marine laboratory of the video and images to further assess the animals and plants seen and the type of habitat. This process selected

representative video clips and/or images for each of the surveyed sites which were then mapped to show what each site looks like underwater in terms of the dominant habitat(s)(Figure 1).

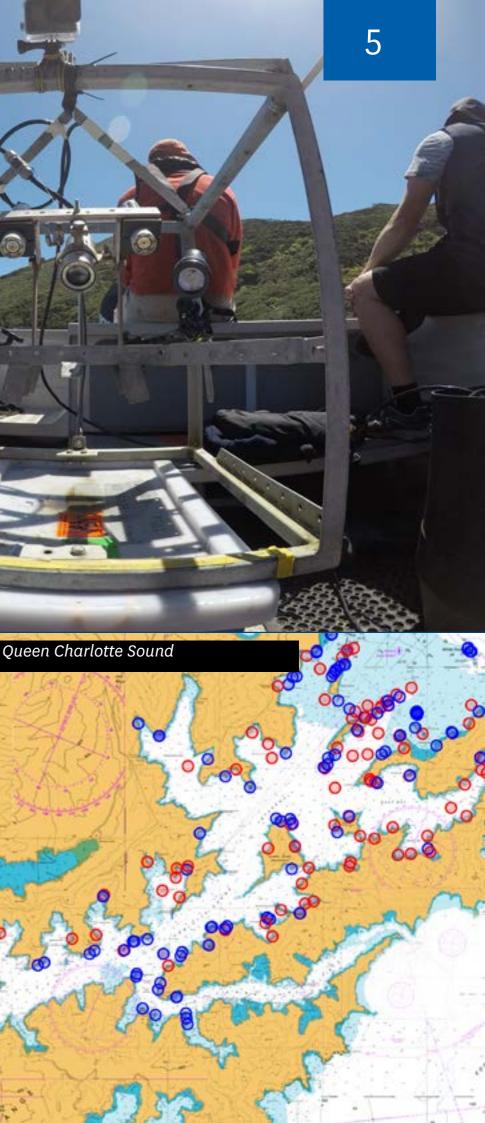
### Data visualisation

An important aspect of this work was to make it accessible to the general public, including the local community that live and work around Queen Charlotte Sound. Nick Young from the Centre for eResearch set up a webbased interface to browse a map of the Sound (Figure 3) with clickable links that open up either video clips or still images with text explaining the habitat at that site.

Figure 1. An example of a still image showing the habitat at one of the sites. Figure 2. One of the drop cameras used to assess marine health (Photo: Drew Lohrer)



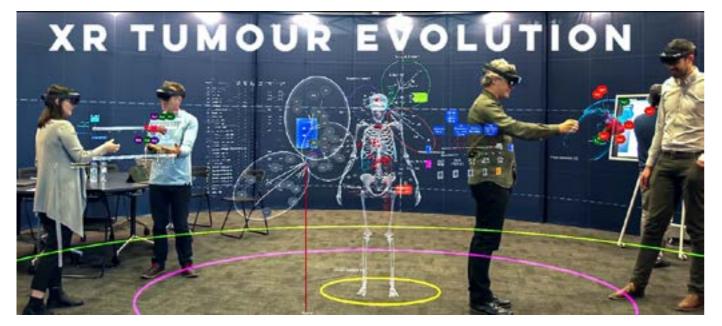
Figure 3. The online map showing all of the surveyed sites in Queen Charlotte Sound.



# **Representation of Multimodel Data** - A Challenging Task

Dr Ben Lawrence, Dr Tamsin Robb, Braden Woodhouse, Faculty of Medical and Health Sciences, Dr Mike Davis, Assoc Professor Uwe Rieger, Yinan Liu, School of Architecture and Planning; Rose McColl, Sina Masound-Ansari, Nick Young, Centre for eResearch.

The Tumour Evolution project (XRTEP) has received a bronze for the NZ Best Awards in the value of Design category. https://bestawards.co.nz/value-of-design-award/university-of-auckland-school-of-architecture-1/xr-tumour-evolution-project/



The project began with a patient's decision to donate her inoperable cancer tissue for research. Over the years, medical monitoring has enabled scientists to gather a large amount of information on the growth of cancer as well as its distribution in the patient's body. The documentation began with the discovery of a tumour in the lung. At the time of death, there were eventually 89 different tumours, all of which the research team sequenced. This extent, as the data increases with distance from well as the complexity of the information obtained, created new challenges for the presentation of the data.

### The product of an interdisciplinary collaboration

An interdisciplinary team from the arc/ sec Lab at the School of Architecture and Planning, *NETwork!* at the Faculty of Medical and Health Sciences and the

Centre for eResearch at the University of Auckland took up the challenge. As a result, an immersive arena has been created in close collaboration with medical professionals. At its center is an interactive, holographic model of the patient's skeleton, organs and tumours. The associated data are arranged around the model in three concentric layers. In each case, the disciplinary specificity of the model. This allows for moments of intra- and inter-disciplinary focus at different points in space. Through the use of HoloLens, users of the application are immersed in this virtual augmented reality and interact with the model at the same time.

Immersive technology human interaction focus To realize the project, the Auckland team used the latest and most complex immersive technology: extended reality. It allows an extension of the real environment with virtual objects and links them to a new reality. Users can also interact with the digital world. They can grab organs from the skeleton to get a closer look at the tumours inside. By sliding a time scale, users can see how tumours grow, shrink or spread over time. Thus, immersive technologies not only offer the possibility of an extremely realistic representation of objects and data in virtual space, rather, they enable users to enter a virtual environment and become part of it. From the users' perspective and experience, this is probably even more important than the highly realistic representation of content. This feeling of being fully absorbed by an environment is referred

to as immersion. It can be very effective in encouraging engagement with scientific content by creating a sense of awe and fascination.

However, the basic requirements for exploiting the full potential of immersion and binding users to the content are fluid interaction with the medium and a high level of usability. In other words, a high quality of user experience. This is also what KielSCN\* aims at. We want to understand how emotions and usability are related in the user experience. For this purpose, we investigate in-situ processes that reveal in which way and how successfully individuals use visualizations when exploring scientific information.

### Usage currently still limited to education and training in the medical field

Currently, the immediate use of this research project lies in the education and training of medical professionals. However, KielSCN also sees promising potential in the use of XRTEP, or similar projects, in non-scientific target groups. This, however, requires the further development of the design features as well as the usability. In addition, a stronger guidance of the user during the exploration seems promising to expand the circle of users to a broader target group. This could be achieved, for example, by embedding it in a narrative or storytelling.

### **XRTEP** facilitates access to cancer research and abstract data

Fundamentally, the XRTEP represents an exemplary implementation. It offers a novel and unique experience to engage with cancer research data. Not only do the developers generate attention, they also facilitate access to abstract genomic data and the contexts of an oppressive topic.





To learn more about the XR Tumour Evolution Project detailed background information is available on the project website.

### Acknowledgement:

All images in this case study are credited to the team of Mike Davis, Uwe Rieger, Yinan Liu, School of Archotecture & Planning.

The article was featured in the Kiel Science Communication Network (KielSCN).



### Who Are The 1M and 1X? Police **Engagement with Citizens in Mental Distress**

Assoc Professor Daniel Exeter, School of Population Health, Faculty of Medicine and Health Sciences; Nick Young, Centre for eResearch

### Introduction

While much is known about the prevalence and incidence of mental health based on national survey or routine health databases, little is known about citizens in mental distress that the New Zealand (NZ) Police attend, in response to calls from the general public. The 1M/1X population referred to in this project represent the coding used by NZ Police to categorise citizens being in mental distress (1M) or threats of suicide and/or suicidal behaviours (1X). Unlike centrally funded health services that use the National Health Index (NHI) to follow a patient's journey through the health system, the NZ Police typically have no prior information about the citizens for whom they are called to provide assistance. We proposed that using Statistics New Zealand's Integrated Data Infrastructure (IDI) would enable linkage between NZ Police, health and social sector data, to better understand citizens in mental distress. Initially, we proposed to restrict our research to the Auckland region, but the IDI enabled an assessment of events across Aotearoa.

### What we did

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Using the IDI, we created a wholeof-population cohort based on deidentified, individual-level data from the 2013 Census as our population denominator that was used to 'follow' individuals for up to 5 years following the Census. We did not use the 2018 Census data in part due to data quality issues that Census experienced, and also because we would not have had as much follow-up time to explore our research questions. Next, we linked

data from the New Zealand Police to the 2013 Census population to investigate the socio-demographic characteristics of citizens in mental distress. Further linkage in the IDI to data from the Ministry of Health enabled us to determine the extent to which citizens in mental distress attended to by NZ Police call outs were current mental health service users, or to determine how soon a citizen would have engaged with the publicly funded mental health system, if the 1M/1X event was their first presentation of mental distress.

### How we did it

Although we had local expertise on hand to apply the conventional epidemiological methods required for this project, the geospatial expertise we needed was more challenging to obtain, in part due to COVID-19 restrictions and staff changes.

We therefore sought out the geospatial expertise of the Centre for eResearch (CeR) team, to explore the spatial and spatio-temporal variations in 1M/1X events. Having previously worked with Nick Young from the CeR team on other geospatial projects, I was confident that the team could adapt to the challenges of the IDI environment while also providing the expertise to perform the analyses required.

To explore the spatio-temporal patterns of the 1M/1X events, Nick used the spatial scan statistic to investigate

geographical clusters (hotspots) of 1M or 1X events. Separate analyses were conducted to account for factors that may also explain the presence of any hotspots, such as age, sex, ethnicity and deprivation.

#### Outcomes

The CeR's GitHub repository has made the results available for the research team as an interactive map, which is available *here*. Typically, the output from SaTScan would enable users to show the geographic extent of clusters using administrative boundaries such as Census Meshblocks, SA1s or Data Zones. However, we were restricted in the details we could release from the IDI. due to the risk of potential identification of individuals. To conform with Statistics NZ's confidentiality constraints, we presented the results as circles. This has meant that some of the clusters appear to overlap which hides the true extent of clustering. The circles in the interactive map represent the geographic extent of 1M/1X clusters, with different colours representing more complex models (red = unadjusted, green = adjusting for age + sex + ethnicity, blue = age + sex + deprivation).

Focussing on Auckland (Figures 1-3), we found ten clusters without controlling for any covariates. These clusters vary by both the geographic extent (size of circles) and the number of 1M/1X events. Adding the green layer reveals that that some of the red clusters have

disappeared or reduced in size. This is the effect that adding these sociodemographic factors to the model has in explaining why the clusters exist. The addition of the green layer identified clusters in Hibiscus Coast and Northcote where the number of 1M/1X events is greater than would be expected. It should be noted that explaining why the addition of sociodemographic factors affects a model, it should never be seen as a justification for a variance. When we add controlling for deprivation into the analysis, in addition to the other co-variates, we can see more localised 'pockets' of 1M/1X cases in the Auckland Region.

"Once again, I am immensely grateful for the incredible amount of work that the Centre for eResearch has done to help me achieve the 1M/1X project milestones! Its expertise in geospatial methods, and the ability to learn new methods, and indeed research environments, at speed and under COVID-19 imposed challenges is amazing and I look forward to future collaborations as this research continues." - Daniel Exeter

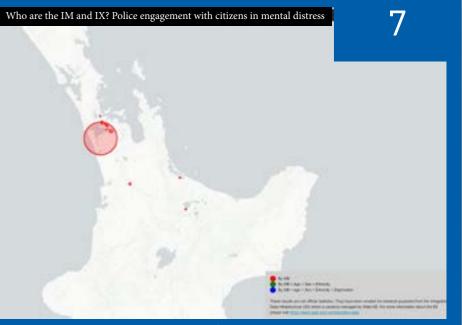


Figure 1 – Unadjusted spatial clusters of 1M/1X responses by NZ Police, in the



Figure 2 – Clusters of 1M/1X responses by NZ Police, adjusting for age, sex and ethnicity, in the Auckland Region.

Who are the IM and IX? Police engagement with citizens in mental distress Figure 3 – Clusters of 1M/1X responses by NZ Police, adjusting for age, sex, ethnicity, and deprivation, in the Auckland Region.

# Interpretation of Non-coding Mutations Driving Melanoma Risk and Its Comorbidities

Michael Pudjihartono, PhD Candidate, Dr. William Schierding, Senior Research Fellow, Prof Justin O'Sullivan, Liggins Institute

### Background

Melanoma is the deadliest form of skin cancer with increasing worldwide incidence. Understanding the underlying mechanisms driving melanoma is crucial for better treatment and prevention. Over the past two decades, the field of genomics has entered a new golden age due to advancements in genetic sequencing and genotyping technologies, which have made genome-wide assessment of genetic mutations that associate with disease risk (i.e. Genome-wide Association Studies; GWAS) possible. However, the interpretation of GWAS remains a challenge because most Single Nucleotide Polymorphisms (SNPs) found to be associated with diseases, including melanoma, lie in the non-coding regions of the genome. These are regions of the genome which lie outside of genes and thus do not code for any proteins. Rather than affecting protein structure, it is hypothesized that modifying the expression level of distal target genes

is one mode of possible mechanism by which these non-coding SNPs affect disease risk. In this study, we integrated publicly available data from melanoma GWAS with tissue-specific markers of the 3D DNA structure (Hi-C) and gene expression data (eQTLs) to identify the genes dysregulated by noncoding risk SNPs in three melanomarelevant tissues: melanocytes, sunexposed skin, and not sun-exposed skin. This approach essentially finds the connection from non-coding SNPs to genes, which help to paint a clearer picture on how non-coding SNPs can potentially contribute to the development of melanoma and its comorbidities.

### Methods

GWAS data for melanoma was downloaded from the GWAS Catalog<sup>1.</sup> Data on 3D genome organization (Hi-C) was downloaded from ENCODE<sup>2</sup>. Expression quantitative trait loci (eQTL) data from melanocyte, sun-

exposed skin and not sun-exposed skin was downloaded from GTEx<sup>3</sup> and a previous study<sup>4</sup>. These data were then loaded into the CoDeS3D pipeline<sup>5</sup>. The CoDeS3D pipeline takes the GWAS SNPs as input and identify regulatory associations between each SNP and specific target genes that are supported by both physical interaction data (Hi-C) and expression data (eQTL) [Figure 1a]. These identified the final set of melanoma target genes. To identify other comorbid traits associated with melanoma, the melanoma target genes were used as input to identify every other SNPs in the genome that associate with the same set of target genes as melanoma [Figure 1b]. Hypergeometric tests (FDR≤0.05) and bootstrapping (n = 350) were then performed to identify enrichment of the SNPs within GWAS Catalog. This process was repeated separately using expression data from melanocyte, sunexposed skin and not sun-exposed skin.

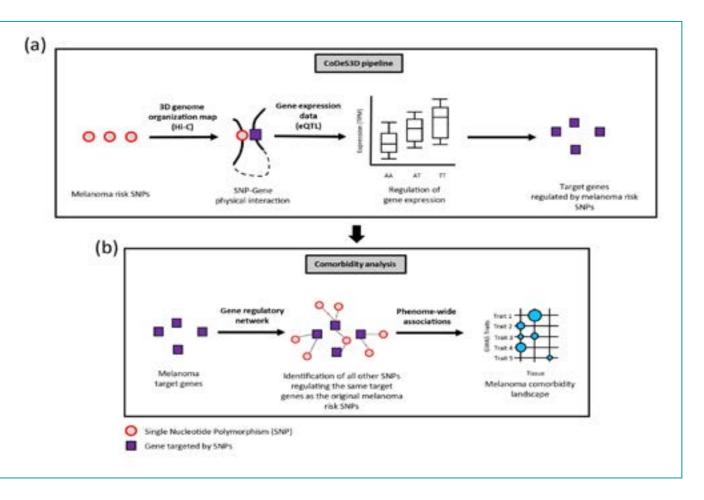


Figure 1. Overview of the computational pipeline used in this study. (a) The CoDeS3D pipeline takes GWAS risk SNPs as input and integrates information on the 3D genome organization to identify physical interactions between GWAS SNPs and genes. For each SNP-gene pair, expression quantitative trait loci (eQTL) data was used to assess whether the SNP also associate with changes in the expression level of the interacting gene. (b) The comorbidity analysis uses the final set of target genes as input and consisted of two parts. (1) Tissue-specific gene-regulatory networks (GRN) was generated by identifying every SNP-gene associations in the whole genome using CoDes3D. The GRN was then queried to identify all SNPs targeting the same genes as the melanoma target genes set. Hypergeometric tests (FDR  $\leq$  0.05) and bootstrapping (n = 350) were then performed to identify traits in the GWAS Catalog whose SNPs are enriched to target the same target genes as melanoma.

### Results

Across the three melanoma relevant tissues, a total of 151 genes were identified as being regulated by melanoma GWAS risk SNPs [Figure 2a]. Functional profiling of the 151 target genes showed an enrichment of genes important for various biological processes including developmental processes, apoptosis, and pigmentation. These are consistent with the role of normal cell development, regulation of cell death, and UV damage in the risk of developing melanoma. The comorbidity landscape of melanoma includes a total of 64 significant traits across the three tissues [Figure 2b]. These include 1) Traits with obvious relevance to melanoma (e.g traits relating to cancer, nevus count, pigmentation and telomere length). 2) Traits that are supported by clinical and/or epidemiological observations (e.g increased intraocular pressure in patients with iris melanoma<sup>6</sup>, increased melanoma risk for patients with actinic keratosis<sup>7</sup>). And 3) traits that have not been (or weakly) associated with melanoma (e.g. uterine fibroids and spontaneous coronary artery dissection). Notably, the comorbidity landscape of melanoma is facilitated by target genes that are tissue specific, with 98 genes (65% of target genes) specific to only one of the three tissue types [Figure 2a]. Nonetheless, the comorbid traits found in all three tissues largely agree with each other (e.g traits relating to cancer, pigmentation traits, telomere length, and nevus) [Figure 2b], suggesting a higher-level convergence at the phenotype and pathway level. This study provides novel insights into the biological implications of non-coding SNPs associated with melanoma risk and provide a starting point for further experimental validation of functional variants and disease-related genes.

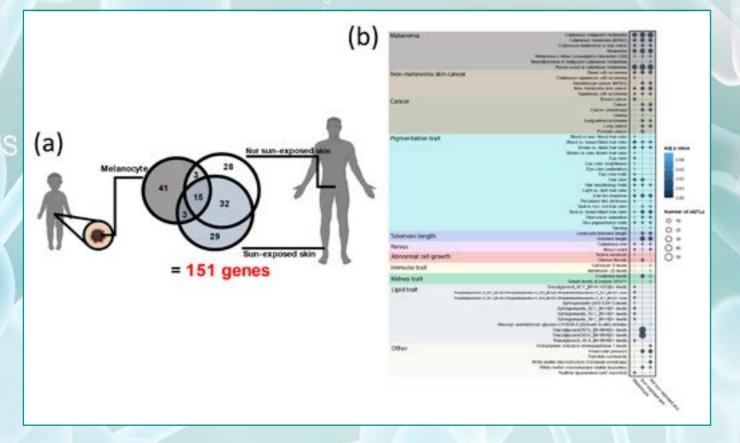


Figure 2. (a) Overlap of the target genes of melanoma risk SNPs found in each of the three tissues. (b) Melanoma comorbidity landscape found in each of the three tissues.

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# Novel Subject-Specific Method of **Visualising Group Differences from Multiple DTI Metrics without Averaging**

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#### Synopsis

Averaging is commonly used for data reduction/aggregation to summarise such high-dimensional data, resulting in information loss. However, individual variability makes group-wise comparisons difficult without data reduction/aggregation. To address these issues, we developed a novel technique that integrates diffusion tensor (DTI) metrics along the whole volumes of the Fibre bundle using a mesh-fitting technique. Using the right Corticospinal Tract (rCST) as an example, we demonstrate the utility of the method in detecting differences in DTI metrics of contact-sports and noncontact-sports athletes.

### Introduction

Diffusion tensor MRI (DTI) generates four metrics (fractional anisotropy [FA], axial diffusivity [AD], radial diffusivity [RD], and mean diffusivity [MD]) per voxel, providing microstructural information about tissue. Averaging is commonly used for data reduction/ aggregation to summarise such high-dimensional data, resulting in information loss. However, individual variability makes group-wise comparisons difficult without data reduction/aggregation. To address these issues, we developed a novel technique that integrates diffusion metrics along the whole volumes of

the fibre bundle using a mesh-fitting technique. Since the right Corticospinal Tract (rCST) is known to be sensitive to brain injury <sup>(1)</sup>, the utility of the method in detecting the differences in DTI metrics of contact-sports and non-contact-sports athletes is demonstrated using rCST.

### Method

Participant information: Under ethics approval, a cohort of contact-sports players (case, n=18) was imaged at 2 timepoints: preseason and postseason. Healthy non-contact-sports athletes from a matching demographic were imaged (control, n=9). Both cohorts were between 16-18 years old. Those with a history of severe brain injury or other neurological conditions were excluded.

#### Image Acquisition:

T1-weighted and DTI images (Table 1) were acquired on a 3T MRI scanner (SIGNA Premier; General Electric Healthcare, Milwaukee, WI; AIR™ 48-channel head coil).

### DTI processing:

using FSL (FMRIB software library) (http://fsl.fmrib.ox.ac.uk/fsl/, version 6.0) <sup>(2, 3, 4)</sup>. Diffusion images were

9

Image processing steps were performed

processed using FDT <sup>(5)</sup>. An output with susceptibility-induced off-resonance field measure <sup>(3, 6)</sup>, was passed onto the eddy tool, which corrects eddycurrent induced distortions and subject movements <sup>(7)</sup>. DTIFIT was used to generate the FA, MD, AD, and RD. To segment the rCST, linear registration (using FLIRT tool and MNI152\_ T1\_1mm\_brain atlas image (8) followed by a nonlinear registration (FNIRT) <sup>(9)</sup> was performed on T1-weighted images. Using the JHU ICBM-DTI-81 white-matter labels atlas (10-12), the rCST from the template space was wrapped back into T1-weighted native space. The diffusion metrics were extracted through rigid registration of the segmented rCST on the 3D tensor maps.

#### Embedding diffusion metrics in a 3D mesh via nonlinear morphina:

A high-fidelity 3D mesh template of the rCST comprising of hexahedral elements was developed from T1weighted MRI. This template mesh was used to generate subjectspecific meshes of rCST via Freeform deformation (FFD) of the template mesh onto the subject geometry. For each subject, the nodes on the external surfaces of the rCST template mesh were fitted to the geometry data points

from the MRI segmentation while the internal nodes were transformed using the same deformation as the external nodes, preserving the relative nodal positions within the mesh (Figure 1). This fitting method has been extensively used in subject-specific finite element model generation for the brain <sup>(13, 14)</sup>, knee, hip, and ankle joints <sup>(15-17)</sup>. After the fitting, the nearest voxel in the MRI space to each element was located using the nearest neighbour search algorithm in Python (Scipy cKDTree) <sup>(13, 14)</sup>. The average diffusion metrics value from the 9 nearest voxels were stored as field information for each node. Due to the use of common template mesh, the dimensionality of the DTI metric information is matched for all subjects, which is essential in performing the principal component analysis (PCA) step below.

#### Principal Component Analysis (PCA):

The pcaMethods library from R statistical software (version 4.1.2) was used to perform PCA. The normalised and scaled values of FA, MD, AD, and RD from each element (total n=20,480) of the fitted mesh were used to generate independent, linear combinations for each individual. Plots of PCA components 1 and 2 were then used to visualise clustering of cases

vs. controls, based on the individual variance in the rCST.

### Results

As shown in Figure 2, the diffusion values of each cohort could be statistically summarised to show the variation between ±2 standard deviations for the entire rCST due to the matched dimensionality. Figure 3 shows clustering PCA dimensions PC1 and PC2 (accounting from 33% (FA) to 47% (RD) of the data variation) which allowed for the discrimination between case vs. controls based on the major variance in the DTI measurements from each element of the rCST model.

### Discussion

A novel approach is introduced for investigating the brain's white matter tracts by combining different techniques from different disciplines - that is, DTI analysis from MRI; mesh fitting from computer graphics; and PCA from statistical data analysis. By generating the 3D template mesh model of the right corticospinal tract (known to be sensitive to brain injury <sup>(1)</sup> and morphing it into each subject's native space, we made a subject-specific model for the tract that matched both the geometry

and diffusion metrics distribution. The method extracts the diffusion metrics corresponding to regions with minimal information loss. The common dimension of the 20,480 diffusion metrics allowed further data aggregation using PCA to cluster the case and control groups.

### Conclusion

The work presents a novel method that accounts for the individual subject's geometric variation, to visualise group differences in quantitative MR data. By embedding tensor-based data from DTI scans to 3D subject-specific mesh, we showed the ability of our model to separate alterations in imagebased metrics acquired from contact sports players and non-contactsports athletes. Future prediction models based on other quantitative MRI methods may benefit from this approach.

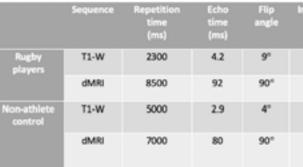


Table 1: Acquisition parameters for the T1- weighted and diffusion tensor (DTI) sequence.

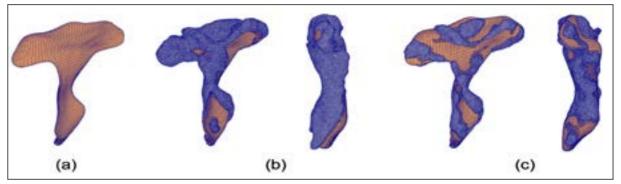
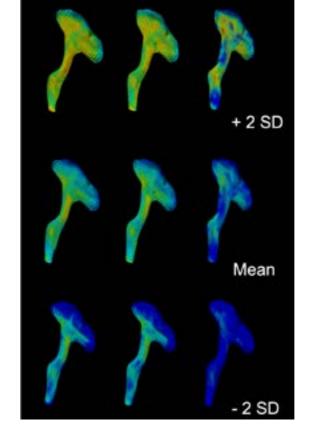


Figure 1: How subject-specific mesh fitting is performed. Free form deformation process that morphs a template mesh to a new subject's geometry. (a) Template mesh created from a subject to roughly resemble the generic shape of the rCST. (b) 20,480 squares are overlaid on each specific subject's geometry. Since the match is not optimized for each subject, the template mesh is deformed to minimize the rms error. (c) The optimized subject-specific fitted mesh. Both coronal and sagittal view are shown for (b) and (c).



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nversion time (ms)	Matrix size	Voxel size (mm)	Number of slices	B value (number of diffusion gradients)
900	170 × 200	$1 \times 1 \times 1$	180	-
•	128 × 84	2.7 × 2.7 × 2.7	58	0, 1000 (5, 64)
700	176×240	1×1×1	256	•
-	128 × 128	1.7×1.7×1.7	88	0, 1000 (7, 60)

Figure 2: How group average values can be visualized based on the subject-specific mesh fitting result. rCST tract FA value visualisation showing different group mean and ±2 standard deviations of the preseason (left), postseason (middle), and control (right) cohorts

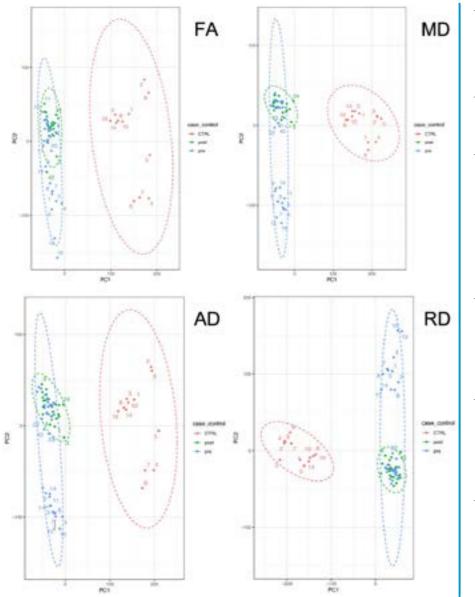


Figure 3: Principal components 1 and 2 shows the clustering of the case and control for each diffusion variable FA (Fractional anisotropy), MD (Mean diffusivity), AD (Axial Diffusivity), RD (Radial Diffusivity).

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# Travelling Heads – Measuring Reproducibility and Repeatability of Magnetic Resonance Imaging in Dementia

Catherine Morgan, Reece Roberts, Lynette Tippett and the Dementia Prevention Research Clinic Staff and Research Group School of Psychology and Centre for Brain Research, The University of Auckland

### Cognitive decline in ageing

Some cognitive decline is normal as we age, but people with mild cognitive impairment (MCI) show an age-related decline that is greater than that of their age-matched peers. Dementia is a significant cognitive loss which impacts daily functioning. Approximately 50 million people are living with dementia worldwide, and in New Zealand, 1.4% of the population have Alzheimer's disease or related dementia. With an ageing population, the prevalence is predicted to double by 2050 [1]. Although MCI can be a precursor, not all people with MCI go on to develop dementia. Biomarkers that accurately track cognitive decline may also hold the potential to predict which individuals will progress to dementia.

### The Dementia Prevention Research Clinics (DPRCs)

The reasons why some individuals with MCI progress to dementia and others do not is unresolved and is the focus of the Dementia Prevention Research Clinics (DPRCs) [2], a national New Zealand study with clinics in Auckland, Christchurch and Dunedin. Participants in the DPRC undergo clinical and neuropsychological evaluation and provide blood samples for studies of protein, gene and metabolic biomarkers. Participants also have 18F-florbetaben Positron Emission Tomography (FBB-PET) and Magnetic Resonance Imaging (MRI) scans to evaluate imaging biomarkers. The study is ongoing, and so far data has been collected on over 250 participants, with a large proportion having longitudinal follow up.

# Studying dementia with magnetic resonance imaging

MRI biomarkers that are of interest in dementia studies include grey matter brain volumes derived from T1-weighted (T1w) imaging for tissue atrophy (shrinkage), arterial spin labelling (ASL) metrics for cerebral blood flow (hypo-perfusion/hypo-metabolism), diffusion-weighted imaging (DWI) measures for white matter structure, resting state functional MRI (rsfMRI) for functional connectivity and T2w fluid attenuation inversion recovery (FLAIR) derived estimates of white matter hyperintensity (WMH) volume for small vessel disease. Additional, more clinically focused scans in a dementia protocol often include T2-weighted (T2w) and susceptibility-weighted imaging (SWI) to assess vascular health and other pathologies.

### The need to standardise MRI in multicentre studies

Multicentre studies, such as the DPRCs allow for larger, and more representative cohorts to be recruited for research trials. However, intersite measurement variability needs to be quantifiable to interpret the pooled data. For imaging markers to be adopted widely and incorporated into clinical practice, inter-site measurement reliability needs to be established to determine confidence in diagnostic metrics. Reproducibility can be defined as variability due to measurements being collected under different conditions, e.g., at different sites with different hardware or processed with different software.

In addition, knowledge of imaging biomarker variability over time due to measurement uncertainty is essential when monitoring longitudinal cognitive changes as a function of normal ageing, disease, or treatment. Without this crucial information, it cannot be determined whether subsequent changes in the imaging markers are due to underlying physiological changes, or simply measurement variability. Repeatability refers to variability in a measurement collected under the same conditions multiple times.

### Method

We assessed reproducibility and repeatability in a suite of imaging parameters used in the DPRC MRI protocol to study cognitive decline. We recruited six "travelling heads" (THs), the same participants who travelled to the three imaging centres in the DPRCs, Auckland, Christchurch, and Dunedin. They were scanned at repeated timepoints with the same DPRC MRI scans as used for clinic participants, enabling assessment of the reproducibility and repeatability of quantitative MRI (gMRI) markers for dementia. Images were processed centrally, with the same software used for all data.

### Results

MRI images from a person scanned at the three different sites within seven days are shown in Figure 1, images collected at the different sites show excellent visual agreement with similar signal distribution, contrast, and lack of obvious artefacts. As seen in Figure 2, group means for most metrics appear to be in good agreement between sites, overall group means are reproducible. As one example, group mean hippocampal (HC) volumes were 4.40, 4.38 and 4.44cm<sup>3</sup> for Auckland, Christchurch, and Dunedin respectively. Considering individual participant data, inter-site variability would be low compared to intersubject variation if lines connecting the same participants data at each site do not cross, which appears to be the case for grey matter (GM), white matter (WM), and HC volume. Conversely, the resting state functional MRI (rsfMRI) metrics, (Q, DMN, and DAN connectivity) and ASL metrics (grey and white matter perfusion) have crossing lines, suggesting inter-site variability is greater than inter-subject variability. Repeated scan metrics are plotted relative to baseline values in Figure 3. Volumetric measures derived from T1w images are highly repeatable (top row), as indicated by the flat regression lines and very narrow confidence intervals. Much larger confidence intervals are seen for the functional rsfMRI metrics.

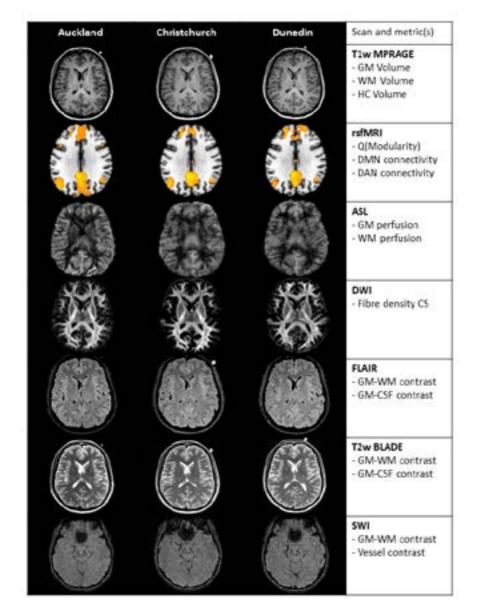


Figure 1. Representative data for a single participant collected at three different sites within seven days (columns 1 to 3) and a list of the 15 derived metrics (column 4). From the top, row 1 shows the acquired T1w MPRAGE scan in participant's native space, row 2 shows DMN connectivity maps (precuneus seed) processed in from resting state functional MRI data, row 3 shows calculated CBF maps, row 4 shows white matter FOD images, row 5 shows acquired FLAIR images, row 6 shows the acquired T2w images, and row 7 the SWI images. An oil capsule affixed to the left side of the head is seen in some images as an hyperintense circle on the right side of the head (images are presented in radiological orientation). Abbreviations: ASL - arterial spin labelling, CS - cross section, CBF - cerebral blood flow, CSF - cerebrospinal fluid, DAN - dorsal attention network, DMN - default mode network, DWI - diffusion weighted imaging, FLAIR - fluid attenuation inversion recovery, FOD - fibre orientation density, GM – grey matter, HC – hippocampal, MNI - Montreal Neurological Institute, rsfMRI - resting state functional magnetic resonance imaging, SWI - susceptibility weighted imaging, T1w - T1-weighted, T2w - T2-weighted, WM - white matter.

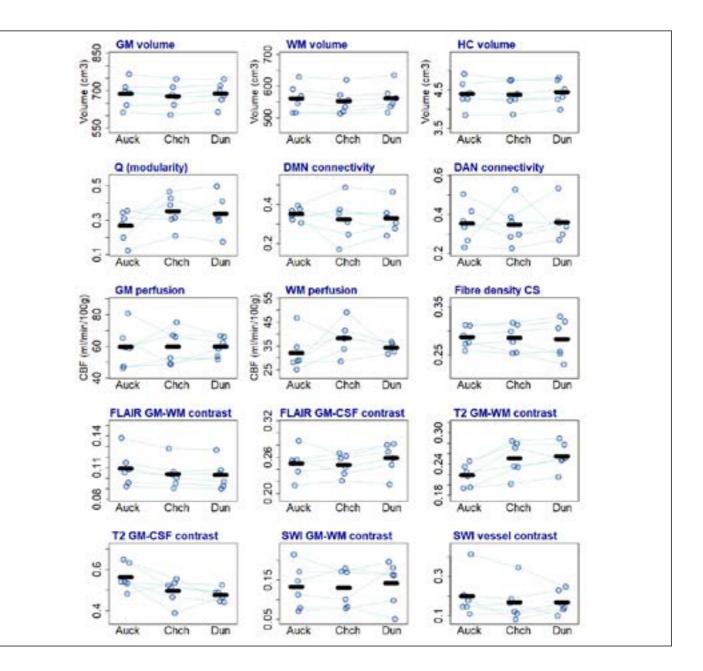


Figure 2. Reproducibility of metrics of interest measured at three different sites. Blue circles represent values measured in individual Travelling Heads at each site and lines connect the same participant. Black thick line is the mean value for all subjects at that site. Abbreviations: Auck -Auckland, CS - cross section, CSF - cerebrospinal fluid, Chch - Christchurch, Dun - Dunedin, DAN - dorsal attention network, DMN - default mode network, FLAIR - fluid attenuation inversion recovery, GM - grey matter, HC - hippocampal, SWI - susceptibility weighted imaging, WM - white matter.

### Conclusion

We investigated the reproducibility (inter-site) and repeatability (overtime) of 15 quantitative MRI metrics in the context of an ongoing longitudinal study (the DPRCs) of MCI and dementia. Structural metrics exhibited excellent reproducibility across three sites and

repeatability over both days and up to five years. Resting state fMRI showed poorer reproducibility and repeatability, while perfusion MRI showed intermediate levels. Variability over time on the same scanner was comparable to variability measured on different scanners, and generally



short term repeatably was much better than long term repeatability. This work [3] provides both confidence in the robustness of many MRI-based metrics of dementia and highlights areas for improvement.

GM volume WM volume HC volume 1.5 1.5-1.5-10 1.0-0-0 0.5 0.5 0.5 2020 2072 2018 2020 2522 2018 2018 2020 2023 Q (modularity) **DMN connectivity DAN** connectivity 1.5+ 1.5 1.0 10.0 10.0 0.5 0.5 2018 2020 2018 2020 2023 2018 2020 202 GM perfusion WM perfusion Fibre density CS 1.51 1.54 1.5-1.0 00 1.0-0-0 0.5 0.5-0.5 2020 2018 2020 2022 2018 2023 2018 2020 2023 FLAIR GM/WM contrast FLAIR GM-CSF contrast T2 GM-WM contrast 1.5-1.5-1.54 10.0 10.00 0.5-0.5 0.5 2018 2020 2022 2018 2020 2022 2020 2018 2022 T2 GM-CSF contrast SWI GM-WM contrast SWI vessel contrast 1.5 1.5-10 0.5 0.5-0.51 2622 2018 2020 2018 2020 2022 2020 202

### Centre for eResearch support

All DPRC MRI data (from the hundreds of study participants and the six travelling heads described in this work) are stored on a Linux virtual machine (VM) hosted by the Centre for eResearch (CeR). Storing and analysing the data on the VM is useful for multiple reasons. 1) Multisite data can be stored in one location and processed centrally. This removes any extra variability in results from data collected between sites and over time (that we are trying to minimise) due to different image processing toolboxes used, 2) The DPRC research team is large and growing, as new members and students join they can easily be added to the VM users list, 3) Some MRI processing software is complicated to install and use. The CeR staff have been critical in helping install imaging software, including Docker packages and Python environments. 4) Some MRI processing software is compute and data intensive. CeR were able to find solutions for us, for example mounting different research drives to the VM and short term use of GPUs for specific data processing tasks. 5) MRI raw data sets and the processed data sets are large. CeR helped us with solutions to archive and backup the data.

Figure 3. Repeatability of metrics of interest measured at one site (Auckland). Circles represent relative values compared to baseline, measured in individual THs. Colours represent each participant. Grey lines indicate regression lines and shaded areas are 95% confidence intervals. Abbreviations: CS – cross section, CSF – cerebrospinal fluid, DAN – dorsal attention network, DMN – default mode network, FLAIR – fluid attenuation inversion recovery, GM – grey matter, HC – hippocampal SWI – susceptibility weighted imaging, WM – white matter.

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# Automating Data Collection and Generation for The Rongowai Mission

Adjunct Prof. Delwyn Moller - Department of Electrical, Computer, and Software Engineering Dr. Mike Laverick, Dr. Chris Seal, Yvette Wharton, Centre for eResearch

### Supporting the launch of Rongowai

Rongowai (Rongo - to sense; wai water) is an international collaborative mission hosting a next-generation **Global Navigation Satellite System** Reflectometry (GNSS-R) payload on board a commercial Q300 aircraft to collect climate data about New Zealand during flight. The mission is part of NASA's Cyclone Global Navigation Satellite System (CYGNSS) mission, and along with Air New Zealand, includes the University of Auckland, the University of Michigan responsible for building the device, Ministry of Business, Innovation, and Employment (MBIE), New Zealand Space Agency, Ohio State University and University of Canterbury. The Centre for eResearch at the University of Auckland plays a crucial role in the mission; communicating with the remote payload whenever it lands, ensuring that science and diagnostic data is downloaded, and subsequently processing the data into usable science products fit for research and eventually the wider community.

In the build up to the Rongowai "launch" date of the 13th September 2022 data pipelines were built and tested to ensure that the payload could communicate with the Science Payload Operation Centre (SPOC) infrastructure, and small webtools created to help the Air New Zealand installation crew monitor the status of the payload. After a tense hour on the morning of launch date, with the wider team tracking the maiden flight of Rongowai from Christchurch to Nelson using the mission's live-flight tracker, the team breathed a sigh of relief and



The Rongowai payload box during final bench testing at the University of Auckland prior to handing over of custodianship to Air New Zealand and aircraft installation.

a cheer of celebration as the first flight data of Rongowai was automatically downloaded upon arrival in Nelson!

### Automatic data retrieval from the NGRx

Rongowai flies roughly between 5-10 times a day, every day, from the early hours of the morning to through to midnight. It relies on a cellular modem to communicate with the SPOC when the plane has landed and flies to almost 20 airports around New Zealand each with varying levels of cellular reception. As such automated communication with Rongowai is required to ensure smooth operational status of the mission. When the payload lands it establishes a reverse SSH tunnel to the SPOC using its cellular modem, which in turn triggers a series of data transfer scripts

to download binary data from the payload. The scripts are designed to be robust enough to handle partial or interrupted downloads which can be caused by poor cellular connection or by aircraft events such as a craft powering down or taking off on its next flight. Included in the downloaded data are log files related to the onboard operations of Rongowai, and also payload engineering data used to monitor a wide range of values including component voltages, currents, temperatures, and more. Engineering data is automatically ingested into a near-live health dashboard for the Rongowai team to easily monitor the operational status of Rongowai, as well as the archiving of binary data to long term storage in case historical data is required in the future.

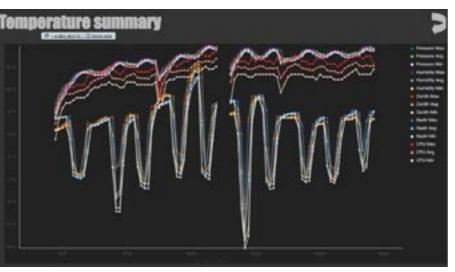


Live flight tracking of the first flight of Rongowai complete with simulated specular points (in pink). The live flight tracker can be viewed at https://spoc.auckland.ac.nz/status

### Automatic generation of Level-O and Level-1 data products

Both engineering and science data are downloaded from the payload in the form of binary data to ensure that the data is as small as possible when storing on board the remote payload and downloading over constantly changing cellular bandwidths. As a result the raw data retrieved from the Rongowai payload needs to be decoded from raw binary into more scienceready formats before it can be easily used.

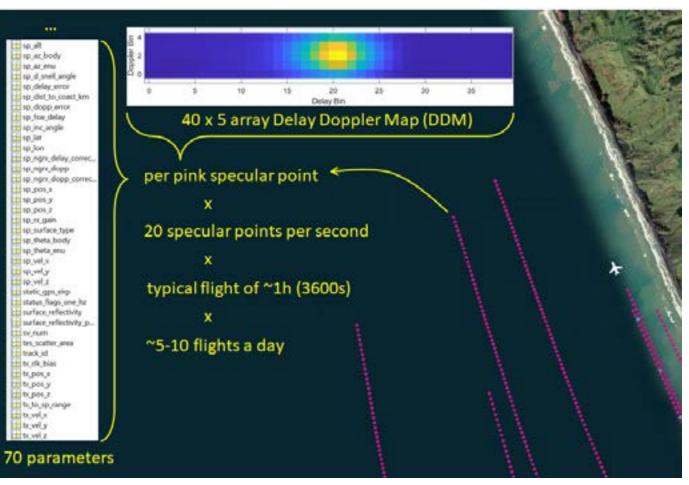
Nightly scripts are automatically run to convert the raw binary files into a series of decoded Level-O netCDF4 files that contain all the engineering and science data pertaining to each of the flights from that day. These files are then used to generate a new Level-1 netCDF4 file from which science algorithms can be developed and research performed. Both Level-0 and Level-1 files are archived to long term storage.



Snapshot of various temperature readings from several sensors onboard the payload, visualised using the engineering health dashboard. Each dip in temperature corresponds to a single flight with 10 flights being completed on this particular day.

The raw binary data has roughly a 10x decompression rate into netCDF4 files, a subtype of HDF5 files, and a typical file size for both Level-0 and Level-1 products is almost 300MB per 30

minutes of flying. With a typical flight time of 1 hour, and ~5 flights a day, Rongowai is set to produce ~6GB of binary, Level-0, and Level-1 data per day!



Visual example of the quantity of data produced by Rongowai for a Level-1 data product.

### Future work and data availability

We are currently productionising the automatic generation of Level-1 files which should be in place by early 2023. Once in place we will be working with collaborators at Takiwā to put in place data pipelines and visualisation tools to allow the exploration and retrieval of data, as well as preparing for future higher-level data products that will be developed in collaboration with the wider Rongowai team.

Further information on Rongowai can be found at the website https:// spoc.auckland.ac.nz/, and also in the previous case studies for Rongowai and the Science Payload Operation Centre, (https://www.eresearch.auckland. ac.nz/project/supporting-the-airborneremote-sensing-mission-rongowai/& https://www.eresearch.auckland.ac.nz/ project/developing-virtual-capabilitiesfor-the-science-payload-operationscentre/).

#### Press releases

zealand-skies sa-climate-science-mission-to-new-heights part-of-a-nasa-space-mission mate-science-mission-to-new-heights.htm https://www.youtube.com/watch?v=cSsDn6Son68

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- https://www.auckland.ac.nz/en/news/2022/09/27/the-rongowai-mission.html

# Ahuahu Great Mercury Island **Online Database**

Dr Joshua Emmitt, Research Fellow, Social Science; Dr Mike Laverick, Centre for eResearch



Figure 1: Excavation area (Area of Interest - AOI) on Ahuahu Great Mercury Island, New Zealand, as part of the Ahuahu Great Mercury Island Project.

### Background

Archaeologists are interested in human environment interrelationships over long spans of time and often engage in comparative analyses of these relationships. Data are compiled from a range of sources. The Archaeology eResearch Collaboration Initiative (ARCI) is a research group specialising in the management and analysis of data intensive archaeology. Currently the project is working with data from field projects in Egypt, New Zealand, Saudi Arabia, and Australia. These projects generate large amounts of data that need to be shared regularly between researchers around the globe.

Data acquired in the field consists of high resolution sampling of archaeological phenomena, recorded as a collection of geographic information with corresponding attribute information. It is not unusual for tens of thousands of observations to be collected during a field season. In addition, survey data can include photographs of archaeological features, including high resolution GigaPan imagery, and LIDAR point data. This data often includes complex file structures or large file sizes, the reading of which by specialist software such as ESRI's ArcGIS are not easily shared in a structured way amongst researchers, both domestic and

international. The Centre for eResearch provided access to the NeSI Data Fabric and customised servers which facilitated data sharing and collaboration, greatly increasing the productivity of the projects involved.

### Using CollectiveAccess to collaboratively record and manage archaeological data

CollectiveAccess is an open-source software designed to help catalogue and publish data collections. It is used by a number of institutions, museums, and galleries around the world as both

an internal platform to manage a wide range of collections and metadata, and also as a public-facing web platform to help present information on collections. CollectiveAccess implements its own intrinsic schema to broadly describe all major facets of a collection of data such as an object, object lots, collections, entities, places, media representations, and more. In addition to these broad descriptive tables CollectiveAccess allows you to create any amount of sub-schemas under its intrinsic schemas, as well as the ability to override and customise these intrinsic tables. Metadata fields and relational fields can be fully customised allowing CollectiveAccess, in addition to UI pages used to manage and explore data, allowing the software platform to be tailored to the needs of each specific deployment.

In tandem with the Centre for eResearch we are currently trialling a CollectiveAccess deployment, using the Nectar Research Cloud, specifically tailored to the needs of the Ahuahu Great Mercury Island project and more broadly the needs of the Archaeology eResearch Collaboration Initiative (ARCI). The CollectiveAccess deployment will be used to collaboratively record, manage, and explore archaeological data and metadata relating to the Ahuahu Great Mercury Island project. For example this will include metadata on the following, and much more:

- artefacts (various stones, shells, bones, etc)
- features (pits, postholes, ovens, walls, etc)
- · the spatial and conceptual metadata relating to where the above were discovered (such as deposits, layers, cuts, structures, areas of interest, and more)
- people and entities involved in discovering and documenting the above
- · media representations of the above (photos, videos, documents, shape files, etc)
- · sources of media (Cameras, Drones, Tablets, Stations, etc)





Figure 3: A screenshot of a trial configuration of CollectiveAccess, set up to represent the archeological data and metadata captured by the Ahuahu Great Mercury Island project.

We are currently in the process of implementing our project schema, previously co-developed with the Centre for eResearch here [1] and detailed further here [2], into a CollectiveAccess equivalent that can display and manage the project data and metadata in an intuitive manner. This process includes the creating CollectiveAccess sub-schema representations and corresponding UI pages to describe the schemas. In addition we are currently exploring

#### Notes

[1] https://www.eresearch.auckland.ac.nz/project/arci-archaeology-eresearch-collaboration-initiative/ [2] https://link.springer.com/article/10.1007/s10816-018-9399-6Annual Survey

Figure 2: Example of the recording process of a single object (sample/artefact) from a specific layer of an excavation area(check with Josh - source:\_https:// www.aucklandmuseum.com/about-us/ blog/2015/investigations-underway-atcoralie-bay)

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how the CollectiveAccess software workflows can be used to ingest years of existing project data and metadata, as well as future excavation work. The Centre for eResearch is helping to document the process of sub-schema creation, metadata and UI customization, and the general technical process of installing, maintaining, and upgrading the CollectiveAccess instance for the eventual transition from trial to production.

# **VRhook: A Data Collection Tool for VR Motion Sickness Research**

Elliott Wen, Research Fellow, Auckland Bioengineering Institute

### Introduction

VR gaming has been gaining widespread popularity in recent years, with the annual market revenue projected to reach \$84 billion by 2028 [1]. However, up to 40% of users suffer from VR motion sickness with symptoms like fatigue, disorientation, and nausea [2, 3]. These adverse effects can severely undermine the user experience. To inform users about potential motion sickness, VR game stores like Oculus and Steam display a comfort rating for each game. These comfort ratings are determined by human experts who can identify common risk factors inside the application, such as frequent multi-axis rotation, excessive movement speed, and use of wide field of view [4]. However, a significant drawback of this approach is the highly labor-intensive rating process, which does not scale with the growing game industry.

Recently, researchers have proposed the use of machine learning approaches to identify the presence of motion

sickness [5, 6]. Despite the progress made, many of these studies pointed out that their models are constrained by the size of training datasets. To improve the model generalization, they need to acquire larger datasets, containing many thousands of video clips of VR experiences and the corresponding risk factors [7]. Unfortunately, conventional data acquisition strategies cannot meet this requirement. Manual annotation by human experts is expensive and does not scale. An alternative is

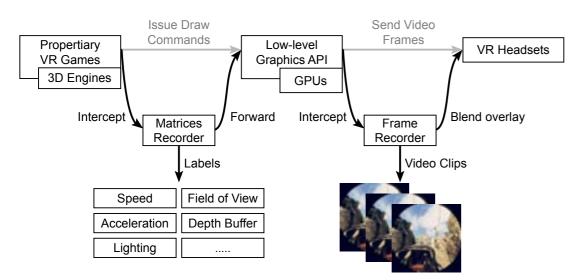
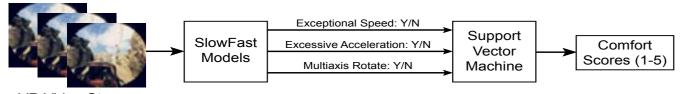


Figure 1: Backbone techniques of our data collection tool



VR Video Stream

Figure 2: Machine Learning ppeline run in Nectar GPUs.

to use custom-made VR games for data collection, however this could create generalizability issues. Finally, modifying existing VR games to extract the data would require source code access, which is practically impossible due to the proprietary nature of the games.

To overcome these challenges, we present a novel data collection tool named VRhook, which can automatically extract labeled data from a wide range of real-world VR games without accessing their source codes (see Figure 1). This is achieved via Dynamic Hooking [8], where we inject custom code into run-time memory to intercept low-level graphics pipeline data, particularly video frames and their associated transformation matrices. In computer graphics, transformation matrices apply motion effects to 3D models and project them into a two dimensional video frame for presentation. The matrices thus can be used to extract many useful labels such as rotation, speed, and acceleration, which have been linked to motion sickness [9, 10]. In addition to data capturing, our tool can inject additional rendering commands to display ingame overlay information. This allows us to incorporate a previously validated dial mechanism. [11] to collect selfreported comfort scores from users. By combining the extracted labels, the self-reported comfort scores, and the video frames, we can construct many motion sickness detection models from prior work. In this way, our tool could stimulate new machine learning based research on VR sickness.

### **GPU** support from Nectar

In our work, we implement VRhook on Nectar GPU instances. We automate the execution and generate a dataset from 5 real-world roller coaster games. On average each game lasted for 4 minutes. In total, we gathered approximately 1200 one second video clips. Each clip contained 180 video frames (90 for each eye) at a resolution of 1832 × 960. These frames' MVP matrices were recorded and analyzed to generate three types of binary labels for each clip, including 1) fast/slow speed, 2) fast / slow acceleration, and 3) multiple-axis rotation detected / not detected. Using this dataset, we further develop a machine learning based pipeline to detect the presence of factors that contribute to motion sickness and predict the comfort score for a given game play video as shown in Figure 2. We used two V100 32 GB

### **Risk Factor Excessive Spee** Excessive Acceler Multi-axis Rota SVM Accura 0.70

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- DAAAM & Proceedings, vol. 28, 2017.
- 1658-1682, 2020.

- - 2017.
- 193-215, 2001.
- ments, vol. 17, no. 3, pp. 283-292, 2008.

GPUs from Nectar cloud to train the model. We set the number of epochs to 5 and the batch size to 32. The learning rate was  $1e^{-4}$  and the training wall time was 12 hours. The performance of our system is shown in Table 1. We managed to publish this work at The ACM Symposium on User Interface Software and Technology (UIST 2022). We really appreciate valuable technical support from many friendly CeR staff members in the Nectar cloud.

	First Pipeline Stage				
	Accuracy	F1 Score			
ed	0.76	0.71			
ation	0.78	0.75			
tion	0.78	0.76			
Second Pipeline Stage					
cy	Weighted F1 Score				
	0.69				

Table 1: Pipeline performance

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[3] D. M. Johnson, "Introduction to and review of simulator sickness research," 2005. [4] E. Chang, H. T. Kim, and B. Yoo, "Virtual reality sickness: a review of causes and measurements," International Journal of Human-Computer Interaction, vol. 36, no. 17, pp.

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[9] R. H. So, A. Ho, and W. Lo, "A metric to quantify virtual scene movement for the study of cybersickness: Definition, implementation, and verification," Presence, vol. 10, no. 2, pp.

[10] F. Bonato, A. Bubka, S. Palmisano, D. Phillip, and G. Moreno, "Vection change exacerbates simulator sickness in virtual environments," Presence: Teleoperators and Virtual Enviro

[11] N. McHugh, S. Jung, S. Hoermann, and R. W. Lindeman, "Investigating a physical dial as a measurement tool for cybersickness in virtual reality," in 25th ACM Symposium on Virtual Reality Software and Technology, 2019, pp. 1–5.

# Accounting for Errors in Data **Improves Divergence Time Estimates** in Single-cell Cancer Evolution

Kylie Chen, PhD Candidate, School of Computer Science

### Introduction

Single-cell sequencing provides a new way to explore the evolutionary history of cells. Compared to traditional bulk sequencing, where a population of heterogeneous cells is pooled to form a single observation, single-cell sequencing isolates and amplifies genetic material from individual cells, thereby preserving the information about the origin of the sequences. However, single-cell data are more error-prone than bulk sequencing data due to the limited genomic material available per cell. Here, we present error and mutation models for evolutionary inference of single-cell data within a mature and extensible Bayesian framework, BEAST2 [1].

Our framework enables integration with biologically informative models such as relaxed molecular clocks and population dynamic models. Our simulations show that modeling errors increase the accuracy of relative divergence time and substitution parameters. We reconstruct the

phylogenetic history of a colorectal cancer patient and a healthy patient from single-cell DNA sequencing data. We find that the estimated times of terminal splitting events are shifted forward in time compared to models which ignore errors. We observed that not accounting for errors can overestimate the phylogenetic diversity in single-cell DNA sequencing data as shown in Figure 1.

We estimate that 30-50% of the apparent diversity can be attributed to error. Our work enables a full Bayesian approach capable of accounting for errors in the data within the integrative Bayesian software framework BEAST2.

### Use of Nectar GPUs

In our work, we provide a full Bayesian framework for inferring cell evolution histories and population dynamics using single-cell DNA data. We developed and optimized error models for singlecell DNA evolution. We present two error models for single-cell data: GT16

(allelic dropout/sequencing error) where parameters are sampled, and GT16 GL [2] where data uncertainty is based on phred scores from empirical single-cell variant callers. We performed Bayesian inference on single-cell DNA data using Monte Carlo Markov Chain sampling.

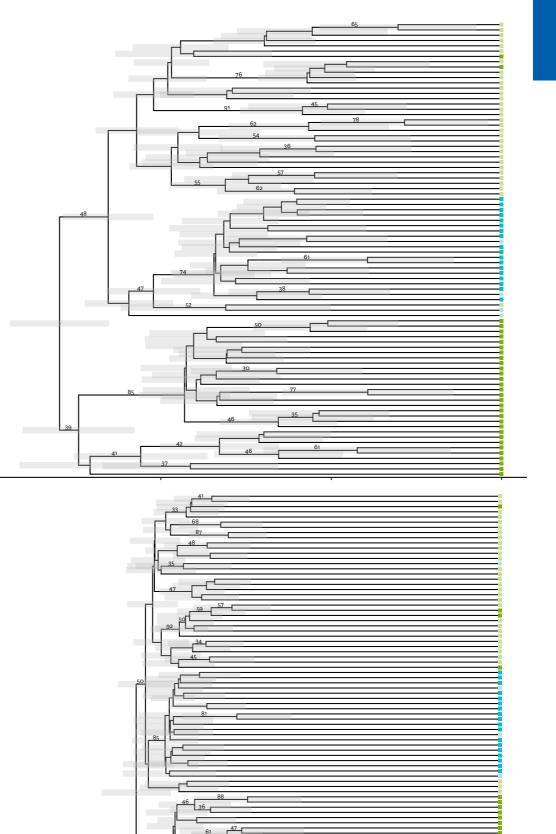
Our software was optimized to use a high performance GPU library, Beagle [3] for computing the likelihood probabilities. For analysis of large real datasets (25k sites, 26 cells), our GPU optimization can lead to a 30X decrease in computational time compared to the unoptimized code. The runtime efficiency for this dataset is 36 hours per million samples (no optimization), 4 hours per million samples (Beagle no GPU), and 1 hour per million samples (Beagle with GPU).

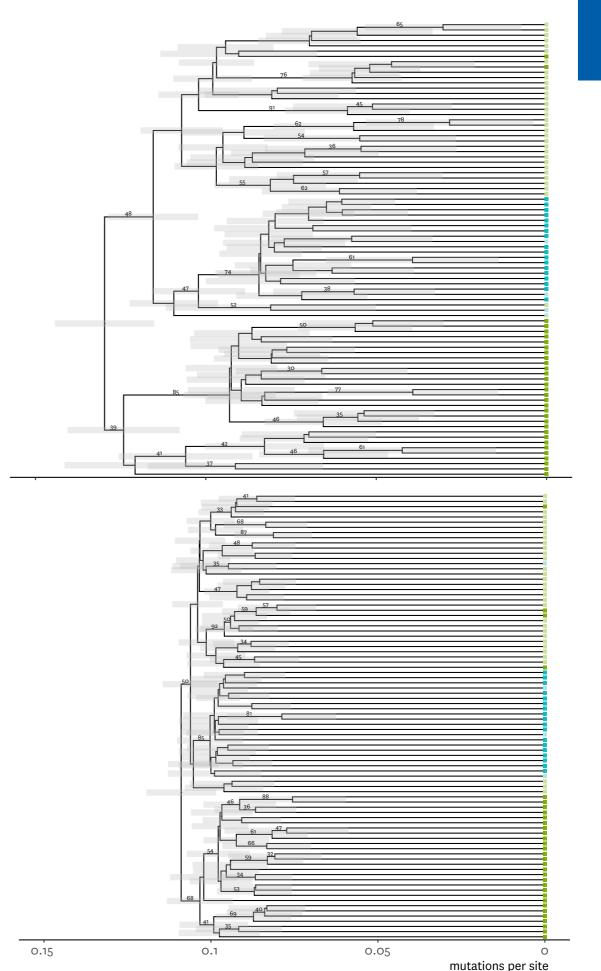
This work is published in Molecular Biology and Evolution, Volume 39, Issue 8, August 2022, msac143 (https://doi. org/10.1093/molbev/msac143)



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Normal (missorted) Cell type Normal . Tumour metastatic

Figure 1 Phylogenetic history of a colorectal cancer patient and a healthy patient from single-cell DNA sequencing data. p.s. The horizontal meaurement axis is applied to both top and bottom graphs.

# Tumour primary

.

47

14

# **ANNUAL SURVEY**

### **Survey Results**

The Centre conducts an independent University-wide researcher survey each year. In order to capture as many research outputs as possible, we tied the 2022 annual survey with the year-end PBRF (Performance-Based Research Portfolio) reporting cycle to avoid multiple response efforts.

This annual survey is to understand how our service offerings are able to meet researchers' needs and demands, and their views on what the important eResearch services are, and how we can make continuous improvements to these services. Another important outcome from the survey is to pinpoint

the critical investment that may be prioritised as part of the University's strategic capital planning. Figure 1. below is the measure of researchers satisfaction level with our various services based on a total of 627 replies.

### **Researchers** Feedback

Thanks to the responses from our researchers, we have received largely positive comments about our services. Here are small samples of feedback and comments about our services and the improvement that we can make going forward.

85% satisfied 85% 0 55% . 30%  $\vdots$ 14% 1% 1%

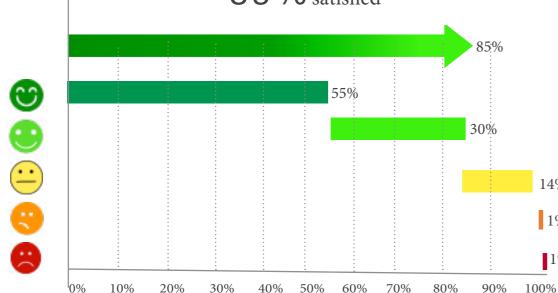
> The above graph shows the level of satisfaction with the services provided by the Centre for eResearch - reported by researchers through annual survey in 2022.

### project is in a secure location. I was impressed with the quick set up of the

Thanks very much.

It is incredibly helpful to know that the data we are collecting for this research drive. At times, I have found it a little tricky to navigate accessing the research drive and also where to go for assistance and help. -- Faculty of Education and Social Work.





### **Researchers'** quotes:

I really like using the NectarVM service, it has helped us develop our research work through access to computational resources. Our research would not have been possible without Nectar. We have also benefited from commissioned project support. Nick and Noel have been great, have written useful codes, and have been easy to deal with. They are both really professional, accurate and have supported our research. I am just chuffed that we learnt about the Centre for eResearch! -- Faculty of Law

With my technologist hat on, it would be great to have MyTardis or similar online to provide comprehensive data and metadata delivery for our sequencing instruments. We have solutions / workarounds in place but something more integrated and streamlined would really help data management. In general I have had incredible support from CeR and am very grateful for this. Thank you! -- School of Biological Sciences

This is a fantastic service, and without it my research would be impossible.

#### -- School of Computer Science

I appreciate all the help and support that I received from Yvette, Jenny, Nick, Noel and Andrew. I enjoyed working with your team. Thank you. -- Architecture and Planning

I am very happy with the services. Several research outputs are expected in 2023, made possible by using these services. -- School of Medicine

I receive adequate support when I ask for it. I have let some things that were not working ideally just sit there as issues because I didn't have time to get to asking ... but the service by eResearch has been amazing. -- School of Environment

I very much appreciate the diversity of research storage. I realise I don't always know exactly the difference between the support we get from NeSI vs eResearch staff but in all cases, the support and advice are hugely helpful and timely. -- School of Biological Sciences

UOA DropBox has become really central to my work, especially with the pandemic and the need to access all my files both from home and in the office. It is far more intuitive and accessible than other options, and works well with my various teams. -- Humanities, Classics and Ancient History

Dropbox continues to enable in some spaces where SharePoint will not accept the types of files we need to work with. Please do not remove this service. -- Liggins Institute

All VMs/drives are correct, in use, and fit our needs very well - thank you! -- Engineering Science

This is a great service for large team projects, thank you! -- Politics and International Relations

The virtual machine is helpful in allowing remote access to data processing software. The data storage drive is helpful in allowing centralised data storage so we do not need to maintain several external hard drives. -- Faculty of Science Technical Services

The Dropbox has been invaluable in facilitating my collaborations. I anticipate further research outputs in the coming years. -- Psychology

We occasionally have problems when multiple users are accessing a shared file, resulting in the duplication of files. -- School of Environment

Current access to GPUs and storage is invaluable to my research. I find CeR staff are knowledgeable and able to sort out any issues quickly. Future needs: I will always need more storage - especially if variations of datasets need to be stored. It would be great to have a Local UoA object store for AI labelling and modelling tasks. Future projects are likely to be several hundred TBs in size with clinical images combined with genomics. Note: I have had some issues with research drive not wanting to pull back my data from archive and timing out, thus my desire for a more transparent Object Store. On the GPU side - higher memory is always a plus. Perhaps an A6000 or H100 80GB would be a nice addiiton. -- Molecular Medicine and Patholoav

It would be great to alter the name of the Dropbox folder so that it is not in the file path which does not allow easy path determination for older software packages to navigate too.

-- School of Biological Sciences

Thank you so much for your help! -- *Psychology* 

Currently I am in need of support in the AI space, which I am in discussion with CeR about. -- School of Environment

The eResearch staff and the services offering are absolutely fantastic. DropBox, however, is horrible and confusing to use. We are stuck with using two different email addresses to use Google docs integration function on DropBox. It would also be great to share a folder with a specific group with access that the owner chooses using a link - currently the view only link is easy to create, but the edit permissions link is not always available for some reason. Google Drive offers this and we miss it. -- School of Environment I am very impressed with the provisioning of services in terms of the quality and quantity. Very happy with the support I get when I need it. -- *Physics* 

The eResearch team are always exceptionally responsive and helpful with any queries, including installation of specialised software onto the VM. Very happy with the service and facilities provided. -- Faculty of Engineering

Is there a low-friction way to quickly spin up a decently powerful Linux/ Windows instance? I mean for up and running in under 10 minutes from when I decide I need it without asking anyone for approval with the ability to give access to anyone at UoA and to persist data for weeks and months. (Memory state does not matter) Nectar is just too much pain for this use case (e.g. not low friction). Say 6GB ram, 500GB SSD, 8+ recent cores. -- Accounting and Finance

Thanks for keeping me running on the virtual machine associated with my research, it is essential to my PhD research. More research outputs to follow shortly! -- *Electrical*, *Computer and Software Engineering* 

Organise workshops for data processing in relation to 3D and spatial data -- Social Sciences

Appreciate the service because it allows easy data storage between relevant people in the project. -- School of Medical Science

I found your service highly valuable. Thanks. -- Mechanical Engineering

Centre for eResearch could have a higher profile within the University.

From a technical point of view the BIRU research network drive works very well for our unit. -- Faculty of Medical and Health Technical Services It would really helpful if creative outcomes - which, after all, are accepted by the TEC for PBRF purposes - are included in the dropdown menu. (It never feels good to have to describe your research as "other"). I have made several video works with the footage I am storing and will continue to do so, including next year (2023) as part of a larger research project. Thank you for the storage - it's a huge help. -- Fine Arts

The unlimited Dropbox storage is definitely critical for data storage. What happened with the University's migration from Google to OneDrive caused a lot of trouble, and the same issue needs to be prevented from the research support side.

#### -- Electrical, Computer and Software Engineering

Overall I was happy with the resources provided which facilitated my research. My suggestion would be to create some documentation that could save a lot of time for someone who is new to research, on what resources are available and how to use them. -- School of Computer Science

1) Communications. There are still people requesting high-powered (and expensive laptops) to work with data and don't know that CeR provides many free solutions. The majority of academics do not understand the services provided by CeR. 2) Training: I recommend creating a how-to guide going through the steps towards common goals. For example, how do I create and access a Windows virtual machine? An end-to-end guide would be great, showing all steps from requesting resources to accessing the VM remotely. -- Information Systems and Operations Management

Although I was always able to book and use an appropriate GPU for my virtual machine, having more available GPU could be beneficial as I will rely on these even more in the near future. -- Marine Science Thank you very much for the support towards our research, it is truly an essential service to keep our data safe. -- Medical Science, Anatomy and Medical Imaging

We have extensively used the Dropbox services provided through the UoA. That has been instrumental for our group over many years, and I would encourage the University to continue that and resist turning the University into a Microsoft "one shop only". -- Faculty of Science Administration

Thank you for this service. The ability to add new research drives/projects for new students and collaborations makes handling research data a lot more smooth. This service definitely helps make data management less painful. -- Liggins Institute

I have received the support that I need. Thanks. -- *Statistics* 

I would like to thank the Nectar and eResearch team for the amazing service! I have found Nectar VMs to be efficient and easy to setup for my research. -- School of Computer Science

Communication with support was difficult regarding setting up the Dropbox folder. A simple request needed repeated reminders, and it took a long time to complete. -- *Mechanical Engineering* 

All excellent. -- School of Environment

Keep up the great work. Many thanks. -- School of Environment

Nothing additional to what has been already provided. Excellent support from Tom this year. -- School of Chemical Sciences

Thank you for this service. -- School of Medicine

Staff have been incredibly helpful and responsive. Service much appreciated. -- Population Health, Epidemiology and Biostatistics Setting up / mapping the network drive was incredibly straightforward and easy! I had only recently done this, so there are no results to disclose yet. -- *Psychology* 

I have used my resource allocation to perform data analysis that required more RAM, CPU and disk than available on my other UoA computing resources. The resources have always been available and accessible, and through the associated documentation and videos I have been able to create and replace VMs using the available preconfigured images. In future I may need to process sizable images and videos, in which case I will explore the Nectar GPU resources. -- *Physics* 

We are in the first year of our Marsden Grant Research Project, so just getting underway. Your team have provided invaluable and high quality support to set up secure research storage for our project. as part of our hapūled, kaupapa Māori research, we are developing a significant new archive (including wide range documents, photography and videography content) for education and research purposes that will eventually be publicly accessible and transferred to/held by a designated external repository. So a secure and adequate data storage is crucial during this development phase. We also received expert advice from an eResearch engagement specialist on our ethics application earlier in the year that was invaluable and other ways your team can assist our research. -- Faculty of Education and Social Work, Te Puna Wananga

Setting up the Dropbox seems to be harder for some people than necessary. -- Bioengineering Institute

The services provided are good as I would expect of a research-led university. -- Accounting and Finance

It would be helpful to understand the range of support available from CeR. -- School of Medicine

An easier way to add my research students to the VM would be useful. -- Learning, Development and Professional Practice

First and foremost thank you. Without the research VM, the prototyping and analysis of hours of data would have been impossible. If any improvement I could suggest, it would be toward disk speed. The speeds appear to be well below that of a normal computer SSD. -- Medical Science

I am very happy with the services provided, the staff at UoA are available whenever needed and are very helpful. I wish all services at the UoA were like this.-- *Bioengineering Institute* 

Thank you so much for your wonderful support. Earlier this year my students needed to use the VM; without access to the VM, there was no way for them to continue their research. -- *Electrical*, *Computer and Software Engineering* 

The software coaching/consulting delivered to my research group was extremely helpful. -- *Bioengineering Institute* 

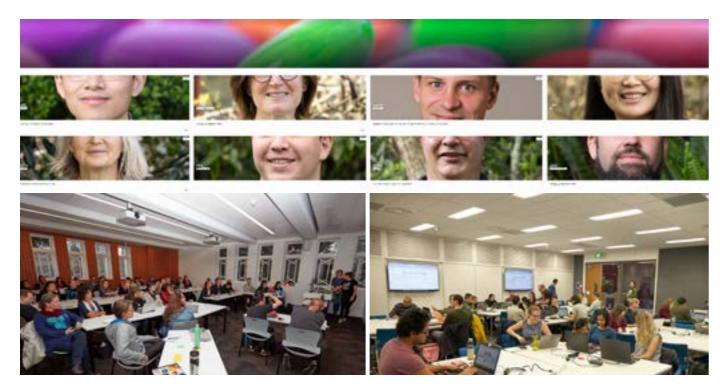
Thanks once again for all your support - it is really appreciated. -- *Physics* 

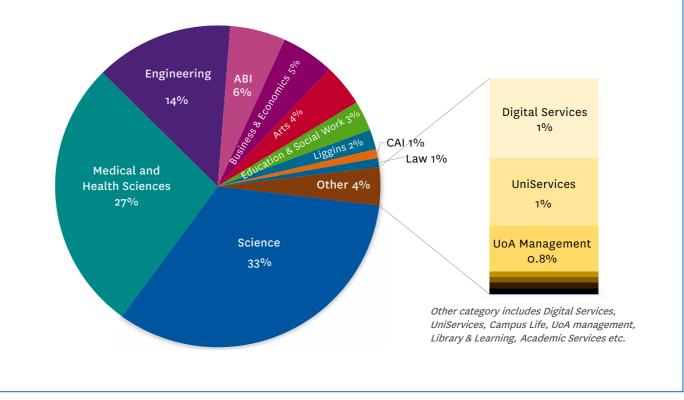
I would have liked a tutorial on how to re-connect easily to the drive from my home PC. -- Faculty of Education and Social Work

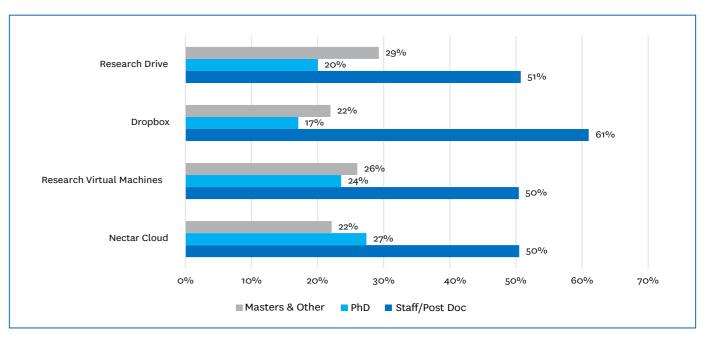
# **OPERATIONAL METRICS**



The operational metrics are collected from events/workshops participants organised by the Centre, and from the Centre's automated Project Database throughout the year.







Number of researchers on active projects that are split by their roles and the services that the Centre for eResearch provides in 2022.

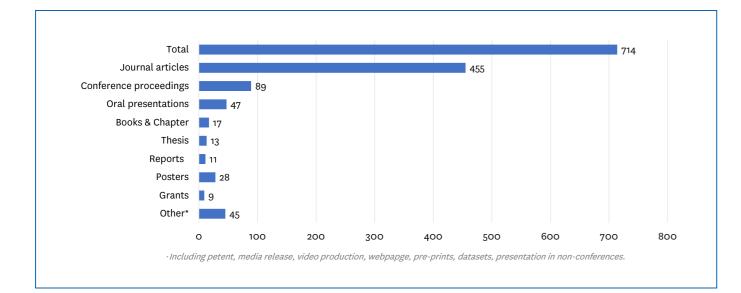
Number of researchers supported by the Centre for eResearch that are split by faculty and large scale research institutes in 2022.

# **RESEARCH OUTOMES**

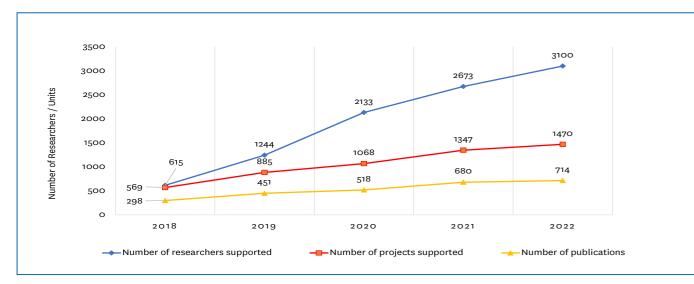
Summary of Research **Outcomes** 

The following research outcomes were captured through the Centre's annual survey with researchers who have responded to the survey. However, these outcomes only represent some of the University researchers' endeavours.

The list includes a small fraction of O4 2021, which was not accounted for in the last report. The top figure summarises research outcomes by category, and the bottom figure shows the growth of CeR research support over the past 5 years.



Number of research outcomes by key categories that are captured by the Centre for eResearch annual survey in 2022.



Growth of the Centre for eResearch research support for the past 5 years, incluing the number of total researchers supported, research projects and research publicaitons captured through annual survey each year.

### Appendix

### **Journal Articles**

- 1. A.P. Martin, C. Lim, M. Kah, M.S. Rattenbury, K.M. Rogers, E.L. Sharp, R.E. Turnbull, (2022) Soil Pollution Driven By Duration of Urbanisation and Dwelling Ouality in Urban Areas: An Example from Auckland, New Zealand, Applied Geochemistry Volume 148, January 2023, 105518 2.
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### **Oral Presentation**

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- Bogdan, B., Buklijas, T., Greenhalgh, C. 3. (2022) Historical Approaches to The Auckland Steroid Trial. Liggins Institute Celebration, Liggins Institute, The University of Auckland.
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- Charlie Ruffman. Macdiarmid Institute. Towards Zero Carbon - Catalytic Architectures Theme Meeting.
- 6 Chris Wilson Making Online Spaces Safer Presentation to He Whenua Taurikura Hui Nov 2022
- Clothier, P. I., & Macdonald, M. (2022). 7. Kowhaiwhai and Fluid Dynamics. in 10th Fluids in New Zealand (Finz) Workshop. Auckland, New Zealand (Virtual).
- 8 Dickson, M. 2022 Keynote Presentation at The New Zealand Coastal Society Conference, November 2022.
- Esti De Graaff. A Review of Placental Pathology By Ethnicity Amongst Extremely Preterm Perinatal Deaths, PSANZ 2022.
- 10. Glass, M., Talmage, A., Wade, K., & Warren, P. (2021, October), Neuro Choirs in Aotearoa New Zealand: Music Therapists Approaches & Perspectives. Music Therapy New Zealand Research Special Interest Group Webinar #7. Youtube. Https://www Youtube.Com/Watch?V=Cwdyf5lbv3e
- 11. Hui Hui Phua. Pancreatic function of preterm-born lambs at one-year of age at the Liggins Research Day 2022.
- 12. Hui Hui Phua. A Microscopic Study of the Endocrine Pancreas of Preterm-Born Lambs at One-Year of Age at the Queenstown Research Week 2022

- 13. Jane Allison. Novel Insights Into The Structure and Function of Dengue Virus NS1 Protein. Research Week Infectious Disease Satellite Meeting, Queenstown 29-30.08.2022
- 14. J. Leung, D. Vatsalan, and N.A.G. Arachchilage, "Feature Analysis of Fake News: Improving Fake News Detection in Social Media." Submitted to the Symposium on Usable Security and Privacy (USEC) 2023(jleu075)
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- 19. Marama Muru-Lanning, Keri Mills, Ngāhui Harrison, Gerald Lanning, Charmain Tukiri. Te Ora a Ururoa: Learning from the Mahi of Kaitiaki (2022) 29 Public History Review 55 20. Megan Tuck, Data Stored in The Resilience
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- 22. Michael Pudiihartono, UoA 3MT Doctoral Finalist 2022 | The uncharted DNA: From junk to gold https://youtu.be/tt8sNzwCWTs 23. Michael Zhang. Speeding Up Column
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- 31. Pisaniello, A., Handley, K. M., White, W. L., and Clements, K. D. (2022) Sources of Variation in The Hindgut Microbiome of The Herbivorous Marine Fish Kyphosus Sydneyanus (Silver Drummer). New Zealand Microbiological Society (NZMS). 21-24 November, Wellington, New Zealand 32. Rajika Munasinghe. An Efficient, On-Resin Fmoc SPPS Preparation of Daptomycin, New Zealand Institute of Chemistry Conference
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- Association Annual Meeting 36. Russel, M., Buklijas, T. (2022). Democratic Reform in N7 Local Government: Innovations Abroad and Their Potential Uses in Aotearoa
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- 41. Stefano Schenone. The Clues in The Sand - Sediment Biogenic Structure Provides Insight Into Benthic Species and Ecosystem Functioning. NZMSS 2022.
- 42. Svetlana Daly, Soft Skills: Why Should NZABA Conference.
- 43. Talmage, A. (2021, October 15). Voices in Harmony: Choral Singing Therapy with Older Adults with Acquired Neurogenic Communication Difficulties . HOPE Foundation Knowledge Exchange Day. Online.
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- 47. Ziva Louisson. Temporal Dynamics of Crop Associated Microbes, New Zealand, Microbiological Society (NZMS) 2022.

### Posters

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- Megan Tuck. 70 Years of Shorelinechange 9. in South Taranaki. NZ Coastal Society Conference 2022.
- 10. Michael Pudjihartono. Interpretation ff The Role Of Germline And Somatic Non-Coding Mutations In Cancer: Expression And Chromatin Conformation Informed Analysis.
- 11. Paredes-Mariño J, White JDL, Dürig T, Baxter R. Cronin S.I. Kula T. Ukstins I. Wu J. Adams D, Brenna M, Brooks-Clarke I. (2022, Nov 29-Dec 1) A Tale of Extreme Fragmentation: The Volcanic Ash from Hunga Eruption. GSNZ Annual Conference, Palmerston North New Zealand. P.P. 207.
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- 17. Simpson, J., Van Wijk, K., and Adam, L (Dec 2021). The Effects of Pressure, Temperature, and Microstructure on The Nonlinear Softening and Recovery of Fault Rocks. Virtual Poster Presented and The American Geophysical Union Fall Meeting, San Francisco, December 2021.
- 18. Svetlana Daly. Soft Skills: Why Should We Care. Faculty of Science Research Showcase 2022
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