ANZIAM 2025 Conference

2−6 February 2025
Pacific Bay Resort, Coffs Harbour

Australian Mathematical Society
Australian and New Zealand Industrial and Applied Mathematics

Contents

The talk abstracts in this volume have been prepared by their respective authors. The editors have made only minor typographical adjustments in the talk titles, following the conventions in `https://www.stylemanual.gov.au/`. The views, findings, conclusions and recommendations presented in this book reflect those of the individual authors.

We thank the organisers of the ANZIAM 2024 Conference for providing their LaTeX template. This document was typeset entirely in troff. Clickable links are in blue text.

Editors: Mariano Rodrigo and Natalie Thamwattana

Website: https://www.mathematics.org.au/sys/pages/plain.php?conf_id=67&page_id=39

ISBN: 978-0-6487562-5-5 (electronic)

1. Acknowledgement of Country

We acknowledge the Gumbaynggirr people as the Traditional Owners of the Coffs Harbour regions, their Elders past and present, and their continued connection with their land, waterways and community. We recognise that Aboriginal people have been doing mathematics on this Country for time immemorial, and respect Aboriginal ways of being, doing and knowing.

2. Conference Code of Conduct

ANZIAM is committed to a professional, open, productive and respectful exchange of ideas. These aims require a community and environment that fosters inclusion, provides mutual respect and embraces diversity. A condition of registering to attend the ANZIAM 2025 Conference and/or any associated satellite event is agreeing to the following Code of Conduct:

> Harassment in any form will not be tolerated. This includes, but is not limited to, speech or behaviour (whether in person, in presentations or in online discussions) that intimidates, creates discomfort, prevents or interferes with a person’s participation or opportunity for participation in ANZIAM’s vision and mission. We aim for ANZIAM to be an organisation where harassment in any form does not happen, including but not limited to: harassment based on race, gender, religion, age, colour, national or ethnic origin, ancestry, disability, marital status, sexual orientation or gender identity. Harassment includes but is not limited to: verbal comments that reinforce social structures of domination; sexual images in public spaces; deliberate intimidation, stalking or following; harassing photography or recording; sustained disruption of talks or other events; inappropriate physical contact; unwelcome sexual attention; and advocating for or encouraging any of the above behaviour.

Conference organisers will take seriously all reports of breaches of this Code of Conduct, and treat all parties with respect and due process without presupposition of guilt. Complaints will be handled with sensitivity, discretion and confidentiality. If a conference participant engages in harassing behaviour, they may be asked by the conference organisers to leave the conference. Any event participant who experiences or witnesses harassment should contact one of the following Code of Conduct representatives:

- Jennifer Flegg
- Bronwyn Hajek
- Mark McGuinness
- Claire Miller
- Vinesha Peiris
- Matthew Simpson
- Natalie Thamwattana

3. Conference Details and History

3.1. Organising committee

- Natalie Thamwattana, University of Newcastle (Chair)
- Juliane Turner, University of Newcastle (Secretary & admin support)
- Xiaoping Lu, University of Wollongong (Treasurer)
- Ravi Pethiyagoda, University of Newcastle (Webmaster & tech support)
- Mariano Rodrigo, University of Wollongong (Program & booklet)
- Pantea Pooladvand, University of New South Wales (Social events)
- Eva Stadler, University of New South Wales (Social events)

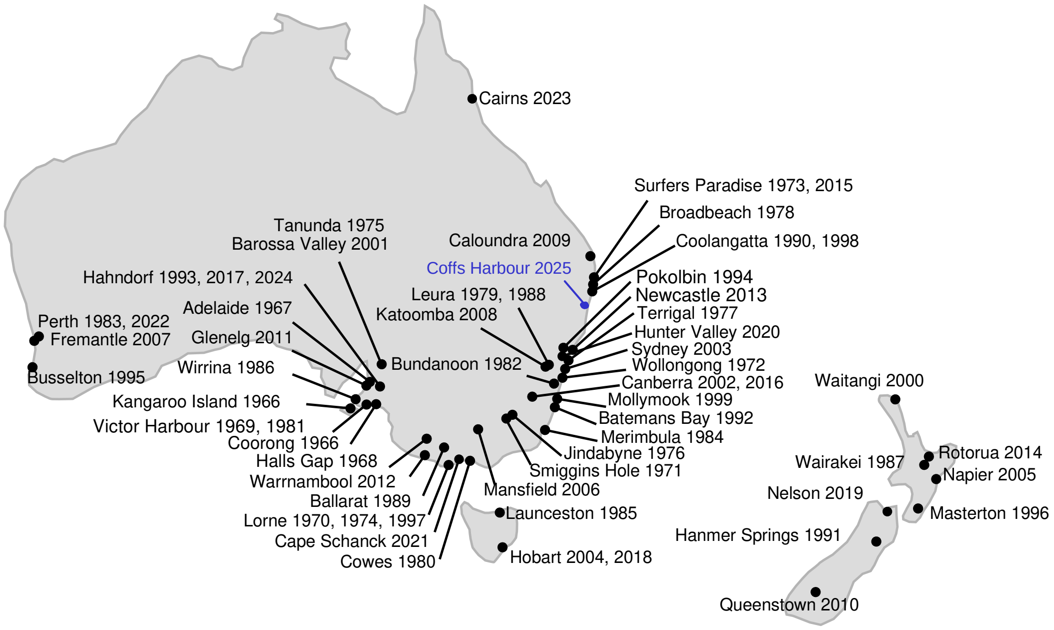
3.2. Invited speakers committee

- Scott McCue, Queensland University of Technology (Chair)
- Natalie Thamwattana, University of Newcastle (Conference rep)
- Jennifer Flegg, University of Melbourne
- Bronwyn Hajek, University of South Australia
- Chris Lustri, University of Sydney
- Fabien Montiel, University of Otago
- Claire Postlethwaite, University of Auckland
- Anja Slim, Monash University
- Michael Small, University of Western Australia
- Nan Ye, University of Queensland

3.3. Plenary speakers

- Prof Jared Bronski (University of Illinois Urbana-Champaign)
- A/Prof Vivien Challis (Queensland University of Technology)
- Dr Rebecca Chisholm (La Trobe University)
- Prof Mahdi Jalili (RMIT University)
- Prof Sunghwan (Sunny) Jung (Cornell University)
- Prof Hinke Osinga (University of Auckland)
- Prof Christopher Rycroft (University of Wisconsin−Madison)
- Prof Sungrim Seirin-Lee (Kyoto University)
- Prof Jean Yang (University of Sydney)

3.4. Past conference locations



1966	Kangaroo Island (August)	1986	Wirrina	2007	Fremantle
1966	Coorong (December)	1987	Wairakei	2008	Katoomba
1967	Adelaide	1988	Leura	2009	Caloundra
1968	Halls Gap	1989	Ballarat	2010	Queenstown
1969	Victor Harbor	1990	Coolangatta	2011	Glenelg
1970	Lorne	1991	Hanmer Springs	2012	Warrnambool
1971	Smiggin Holes	1992	Batemans Bay	2013	Newcastle
1972	Wollongong	1993	Hahndorf	2014	Rotorua
1973	Surfers Paradise	1994	Pokolbin	2015	Surfers Paradise
1974	Lorne	1995	Busselton	2016	Canberra
1975	Tanunda	1996	Masterton	2017	Hahndorf
1976	Jindabyne	1997	Lorne	2018	Hobart
1977	Terrigal	1998	Coolangatta	2019	Nelson
1978	Broadbeach	1999	Mollymook	2020	Hunter Valley
1979	Leura	2000	Waitangi	2021	Cape Schanck (online due to COVID-19)
1980	Cowes	2001	Barossa Valley	2022	Perth (online due to COVID-19)
1981	Victor Harbor	2002	Canberra	2023	Cairns
1982	Bundanoon	2003	Sydney	2024	Hahndorf
1983	Perth	2004	Hobart	2025	Coffs Harbour
1984	Merimbula	2005	Napier		
1985	Launceston	2006	Mansfield		

3.5. ANZIAM Medal

The ANZIAM Medal is awarded on the basis of research achievements or activities enhancing applied or industrial mathematics and contributions to ANZIAM. The first award was made in 1995. Past recipients are listed below.

1995	Renfrey Potts (U Adelaide)
1997	Ian Sloan (UNSW)
1999	Ernie Tuck (U Adelaide)
2001	Charles Pearce (U Adelaide)
2004	Roger Grimshaw (Loughborough U)
2006	Graeme Wake (Massey U)
2008	James Hill (UoW)
2010	Bob Anderssen (CSIRO)
2012	Robert McKibbin (Massey U)
2014	Kerry Landman (U Melbourne)
2016	Frank de Hoog (CSIRO Canberra)
2018	Phil Howlett (UniSA)
2019	Peter Taylor (U Melbourne)
2020	Larry Forbes (U Tasmania)
2021	Nalini Joshi (U Sydney)
2022	Phil Broadbridge (La Trobe U)
2023	Tony Roberts (U Adelaide)
2024	Hinke Osinga (U Auckland)

3.6. EO Tuck Medal

In honour of the late Ernest Oliver Tuck FAustMS FTSE FAA, ANZIAM has instituted a mid-career award for outstanding research and distinguished service to the field of applied mathematics. The inaugural EO Tuck Medal (two recipients) was presented at ANZIAM 2013. Past recipients are listed below.

2013	Geoffry Mercer (ANU)
	Shaun Hendy (VUW, Callaghan Innovation)
2015	Troy Farrell (QUT)
2017	Kate Smith-Miles (Monash U)
2018	Yvonne Stokes (U Adelaide)
2019	Scott McCue (QUT)
2020	Matthew Simpson (QUT)
2021	Michael Plank (U Canterbury)
2022	James McCaw (U Melbourne)
2023	Luke Bennetts (U Adelaide)
2024	Alex James (U Canterbury)

3.7. JH Michell Medal

In honour of John Henry Michell FRS, the JH Michell Medal is awarded to outstanding new researchers who have carried out distinguished research in applied or industrial mathematics, where a significant proportion of the research work has been carried out in Australia or New Zealand. Past recipients are listed below.

1999	Harvinder Sidhu (UNSW)
2000	Antoinette Tordesillas (U Melbourne)
2001	Nigel Bean (U Adelaide)
2002	Stephen Lucas (UniSA)
2004	Mark Nelson (UoW)
2006	Sanjeeva Balasuriya (U Sydney)
2007	Yvonne Stokes (U Adelaide)
2008	Carlo Laing (Massey U)
2009	Scott McCue (QUT)
2011	Frances Kuo (UNSW)
2012	Matthew Simpson (QUT)
2013	Terence O’Kane (CMAR, CSIRO)
2014	Ngamta Thamwattana (UoW)
2015	Barry Cox (U Adelaide)
2016	Joshua Ross (U Adelaide)
2017	Alys Clark (U Auckland)
2018	Claire Postlethwaite (U Auckland)
2019	Ryan Loxton (Curtin U)
2020	Jennifer Flegg (U Melbourne)
2021	Lewis Mitchell (U Adelaide)
2022	Elliot Carr (QUT)
2023	Christopher Lustri (Macquarie U)
2024	Vivien Challis (QUT)

3.8. TM Cherry Student Prize

A student prize was introduced in 1969 at Victor Harbor and is awarded annually for the best student talk presented at the conference. In May 1976, ANZIAM (then the Division of Applied Mathematics) adopted the title ‘TM Cherry Student Prize’ in honour of one of Australia’s leading scientists, Professor Sir Thomas MacFarland Cherry. Past recipients are listed below.

1969	R Jones (U Adelaide)
1970	J Rickard (UCL)
1971	J Jones (Mount Stromlo)
1974	RP Oertel (U Adelaide)
1975	RE Robinson (U Sydney)
1976	JP Abbott (ANU)
1977	J Finnigan (CSIRO)
	S Bhaskaran (U Adelaide)
1978	B Hughes (ANU)
	P Robinson (UQ)
1979	JR Coleby (U Adelaide)
	B Hughes (ANU)
1980	M Lukas (ANU)
1981	A Plank (UNSW)
1982	G Fulford (UoW)
	J Gear (U Melbourne)
1983	P Kovesi (UWA)
1984	A Kucera (UoW)
	S Wright (UQ)
1985	G Fulford (UoW)
	F Murrel (U Melbourne)
1986	A Becker (Monash U)
	K Thalassoudis (U Adelaide)
1987	M Rumsewicz (U Adelaide)
1988	W Henry (ANU)
1989	M Myerscough (U Oxford)
	J Roberts (U Melbourne)
1990	J Best (UoW)
1991	SK Lucas (U Sydney)
1992	SF Brown (UoW)
1993	D Standingford (U Adelaide)
1994	B Barnes (Monash U)
1995	A Buryak (ANU)
1996	A Gore (U Newcastle)
	D Scullen (U Adelaide)
1997	S Cummins (Monash U)
1998	J Clark (U Sydney)
	T Gourlay (U Adelaide)
1999	E Ostrovskaya (ANU)
2000	C Reid (Massey U)
2001	M Haese (U Adelaide)
2002	V Gubernov (ADFA)
	W Megill (UBC, UOW)
2004	K Mustapha (UNSW)
2005	J Looker (U Melbourne)
2006	C Fricke (U Melbourne)
2007	S Harper (Massey U)
2008	E Button (U Melbourne)
	M Haythorpe (UniSA)
2009	S Cohen (U Adelaide)
2010	L Mitchell (U Sydney)
2011	S Butler (U Sydney)
	J Caffrey (U Melbourne)
2012	J Nassios (U Melbourne)
2013	D Khoury (UNSW)
	T Vo (U Sydney)
2014	M Chan (U Sydney)
2015	H Tronnolone (U Adelaide)
2016	D Arnold (U Adelaide)
	A Jenner (U Sydney)
2017	C Miller (U Melbourne)
	E Hester (U Sydney)
2018	N Fadai (U Oxford)
	E Tredenick (QUT)
2019	E Musoke (U Auckland)
	C Li (UWA)
2020	R Crocker (U Adelaide)
2021	A Browning (QUT)
	R Valani (Monash U)
2022	A Zanca (U Melbourne)
	M Denes (UNSW)
2023	S Vollert (QUT)
	K Wawryk (Monash U)
2024	P Grant (QUT)

3.9. Cherry Ripe Prize

Since 1995, the students have run an alternative competition for the best non-student talk. Past recipients are listed below.

1995	Natashia Boland (U Melbourne)
1996	Andrew Pullan (U Auckland)
1997	Neville de Mestre (Bond U)
1998	David Stump (UQ)
1999	Mark McGuinness (VUW)
2000	Joseph Monaghan (Monash U)
	Andy Philpott (U Auckland)
2001	Phil Broadbridge (UoW)
2002	Ernie Tuck (U Adelaide)
	Larry Forbes (U Tasmania)
2004	Stephen Lucas (UniSA)
2005	Kerry Landman (U Melbourne)
2006	Vicky Mak (Deakin U)
	James Sneyd (U Auckland)
2007	Geoffry Mercer (UNSW)
2008	Neville de Mestre (Bond U)
2009	Philip Maini (U Oxford)
2010	Larry Forbes (U Tasmania)
2011	Larry Forbes (U Tasmania)
	Darren Crowdy (Imperial College)
2012	Martin Wechselberger (U Sydney)
2013	Scott McCue (QUT)
	Sheehan Olver (U Sydney)
2014	Peter Kim (U Sydney)
2016	Matthew Simpson (QUT)
	Melanie Roberts (IBM Research Australia)
2017	Christopher Green (QUT)
2018	Christopher Lustri (Macquarie U)
2019	Raúl Rojas (Freie Universität Berlin)
2020	Mike Meylan (U Newcastle)
	Peter Taylor (U Melbourne)
2021	J Nathan Kutz (U Washington)
2022	Jennifer Flegg (U Melbourne)
	Adrianne Jenner (QUT)
2023	Adrianne Jenner (QUT)
2024	Larry Forbes (U Tasmania)

3.10. AF Pillow Applied Mathematics Top-up Scholarship

The AF Pillow Applied Mathematics Trust offers an annual ‘top-up’ scholarship to a student holding either an Australian Postgraduate Award (APA) or equivalent award for full-time research in applied mathematics leading to the award of a PhD. The aim of the AF Pillow Applied Mathematics Top-up Scholarship is to increase the quality of postgraduate students in the field of applied mathematics in Australia. Past recipients are listed below.

2009	Christopher Lustri (QUT)
2010	Alex Badran (UoW)
2011	Michael Dallaston (QUT)
2012	Hayden Tronnolone (U Adelaide)
2013	Lisa Mayo (QUT)
2014	Audrey Markowskei (Macquarie U)
2015	Pouya Baniasadi (Flinders U)
2016	Alexander Tam (U Adelaide)
2017	Jody Fisher (Flinders U)
2019	Jesse Sharp (QUT)
2020	Matthew Berry (UoW)
2022	Eugene Tan (UWA)
2023	Noa Levi (QUT)
2024	Yong See Foo (U Melbourne)

3.11. Acknowledgements

The Organising Committee would like to express our heartfelt gratitude to John Banks from The University of Melbourne for his invaluable assistance in developing and maintaining the online conference registration system. We also extend our thanks to Michael Lydeamore from Monash University for his support in managing the financial aspects of the conference. We acknowledge the contributions of Chris Baker and Adriana (Age) Zanca, both from The University of Melbourne, for their efforts in organising the LGBTIQA+ & Allies breakfast and the WIMSIG lunch, respectively. Additionally, we are grateful to Gary Froyland from the University of New South Wales for his support through his Australian Research Council Laureate Fellowship. Finally, the committee sincerely appreciates the backing of the following organisations.

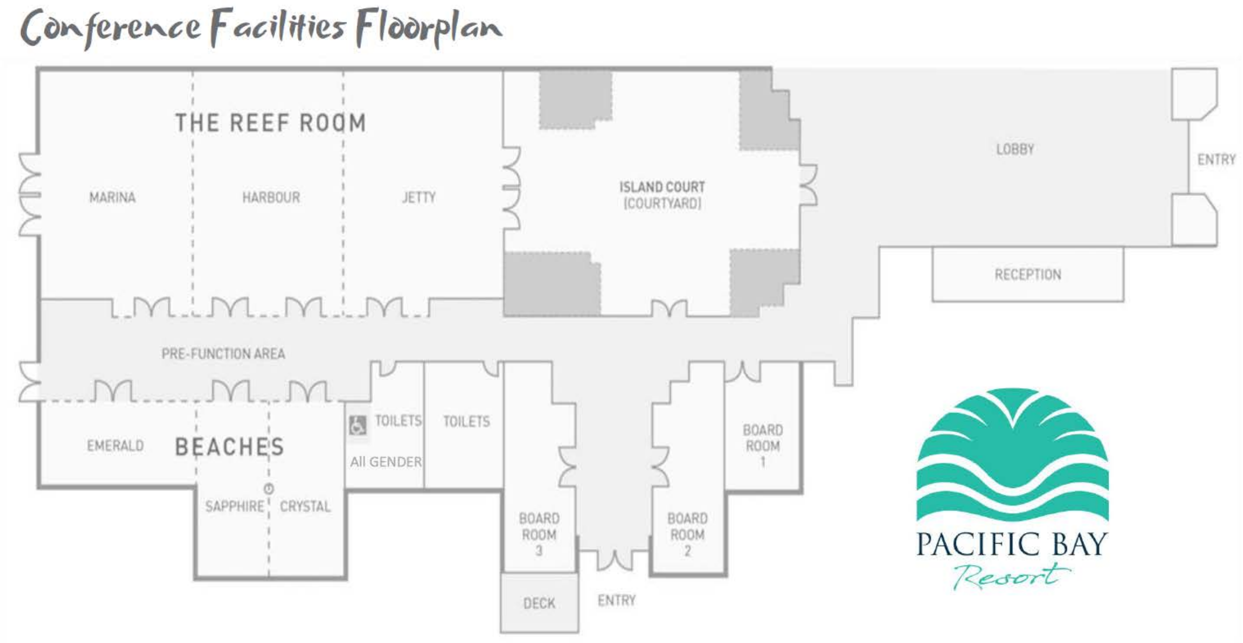
The Office of the NSW Chief Scientist & Engineer (OCSE) provides independent, evidence-based advice to government on how to address difficult policy problems. OCSE provides funding to the NSW research sector and brings academia, government and industry together to drive the commercialisation of research excellence for the benefit of the state, with a major focus on industry development. OCSE also supports a number of science outreach and engagement activities and events, including the annual Premier's Prizes for Science & Engineering.

We would also like to express our gratitude to the National Marine Science Centre at Southern Cross University in Coffs Harbour for generously providing venues free of charge for the MBSIG and SigmaOpt Workshops on Friday 7 February 2025.

4. Conference Overview

4.1. Conference venue

The conference will be held at the Pacific Bay Resort from 2−6 February 2025. The venue is located just 3 km north from Coffs Harbour. The Pacific Bay Resort is framed by ocean, mountains, natural forest and banana plantations. The resort map and conference facilities inside the resort's conference centre are shown below.



4.2. Conference reception

The welcome reception will be held from 18:30 on Sunday 2 February 2025 at the Bayside Restaurant/ Island Court. All conference delegates and registered guests are invited.

4.3. Conference dinner

The conference dinner will be held at the Pacific Bay Resort in the Reef Room on Wednesday 5 February 2025, beginning with pre-dinner drinks from 18:30.

4.4. Refreshment breaks and lunches

Morning and afternoon freshly brewed coffee, tea and light refreshments will be available. Lunches are included in the registration fee for delegates and their registered guests, and will be available at the Bayside Restaurant after the last presentations of the morning sessions.

Cafe-style coffees will be available for purchase at a coffee cart located within the conference centre.

4.5. Social media

ANZIAM attendees are encouraged to use social media from their personal accounts to share ideas from the conference. The conference hashtag is `#ANZIAM2025`. It is good practice to include a reference to the presenter and their affiliation, and please seek permission from the presenter before posting a photo of them or their presentation online.

4.6. Internet access

Delegates will be provided with WiFi internet access throughout the conference. Use the ‘Pacific Bay Conference’ network with password `PBRconf1`. Alternatively, you can scan the QR code below to access the internet:

4.7. Plenary lectures and contributed talks

All plenary lectures are scheduled to take place in the Reef Room. Each plenary talk will be 40 minutes long, with an additional 10 minutes for questions. There will be a 10-minute break between each plenary lecture and the preceding or following contributed talks to facilitate room transitions. Contributed talks will run concurrently in the Marina, Harbour, Jetty, Sapphire and Crystal Rooms. Each contributed talk will last for 15 minutes, followed by an additional five minutes for questions and room changeover.

4.8. Early career researcher networking lunch

The ECR networking lunch will take place at the Island Court on Monday 3 February 2025. This informal event aims to provide ECRs with an opportunity to network, share ideas and build a sense of community. The ECR networking lunch, organised by Pantea Pooladvand and Eva Stadler, is proudly supported by MACSYS and the Office of the NSW Chief Scientist & Engineer.

4.9. Student social event

All students are invited to the Charlesworth Pool on Monday 3 February 2025 for the student social event at 18:30. The event offers a wonderful opportunity to connect with fellow students in a relaxed atmosphere, complete with complimentary food and drinks available for purchase. Organised by ANZIAM student representative Georgia Weatherley, this gathering is made possible through the support of MACSYS.

4.10. LGBTIQA+ and Allies breakfast

The LGBTIQA+ and Allies Breakfast will take place at the outside deck of the Bayside Restaurant on Tuesday 4 February 2025 at 7:30. Everyone is welcome to attend. This event aims to celebrate the diversity within our community by providing an inclusive environment for LGBTIQA+ individuals and their allies to share their experiences and build a supportive network within the ANZIAM community.

Organised by Chris Baker, Pantea Pooladvand and Eva Stadler, the LGBTIQA+ and Allies breakfast is proudly supported by the Office of the NSW Chief Scientist and Engineer.

4.11. Women in Mathematics Special Interest Group lunch

The WIMSIG lunch is held at national ANZIAM conferences to promote and celebrate the contribution of women, trans, nonbinary and gender diverse people in the mathematical sciences. In 2024 − for the first time − the ANZIAM, JH Michell and EO Tuck medallists were all women! The WIMSIG lunch therefore aims to celebrate the achievements of the three women medallists and other women, trans, nonbinary and gender diverse people in mathematics. The event will feature a short panel discussion with audience polling followed by group conversations among participants. The panellists are the women invited speakers of the conference: Prof Hinke Osinga (ANZIAM medallist), A/Prof Vivien Challis (JH Mitchell medallist), Dr Rebecca Chisholm, Prof Jean Yang, and our guest from JSIAM, Prof Sungrim Seirin-Lee. Everyone is encouraged to attend and participate in the discussion. Tickets are free but you must have registered through the conference registration system by 25 January 2025.

The lunch will be held in parallel to the main conference lunch on Tuesday 4 February 2025 and will be held at the Island Court.

For information on, and some advice from, our women invited speakers, please see the Question-and-Answer interviews at https://austms.org.au/special-interest-groups/wimsig/wimsig-qas/anziam-2025-qa/

The 2025 WIMSIG lunch has been organised by Pantea Pooladvand, Eva Stadler and Adriana (Age) Zanca, with support from Prof Gary Froyland (UNSW Sydney) through his Australian Research Council Laureate Fellowship. Information on WIMSIG is available at https://austms.org.au/special-interest-groups/wimsig/

4.12. ANZIAM AGM

The 50th AGM of ANZIAM will be held at 19:30 (ACDT) on Tuesday 4 February 2025 in the Jetty Room. All ANZIAM members are welcome and encouraged to attend this meeting. The link for agenda and reports will be emailed to all members a week prior to the AGM. You may also join remotely using https://monash.zoom.us/my/srclarke?pwd=NnUzSjFmcDVvRVYzM1dqaHlMRHNpZz09&omn=84938173485

4.13. SigmaOpt workshop

SigmaOpt, the optimisation special interest group of ANZIAM, is holding a one-day workshop on the day after the ANZIAM 2025 Conference. The workshop will feature talks from five invited speakers, as well as the winner of the Student Best Paper Prize.

- When: Friday 7 February 2025, 9:45−15:30

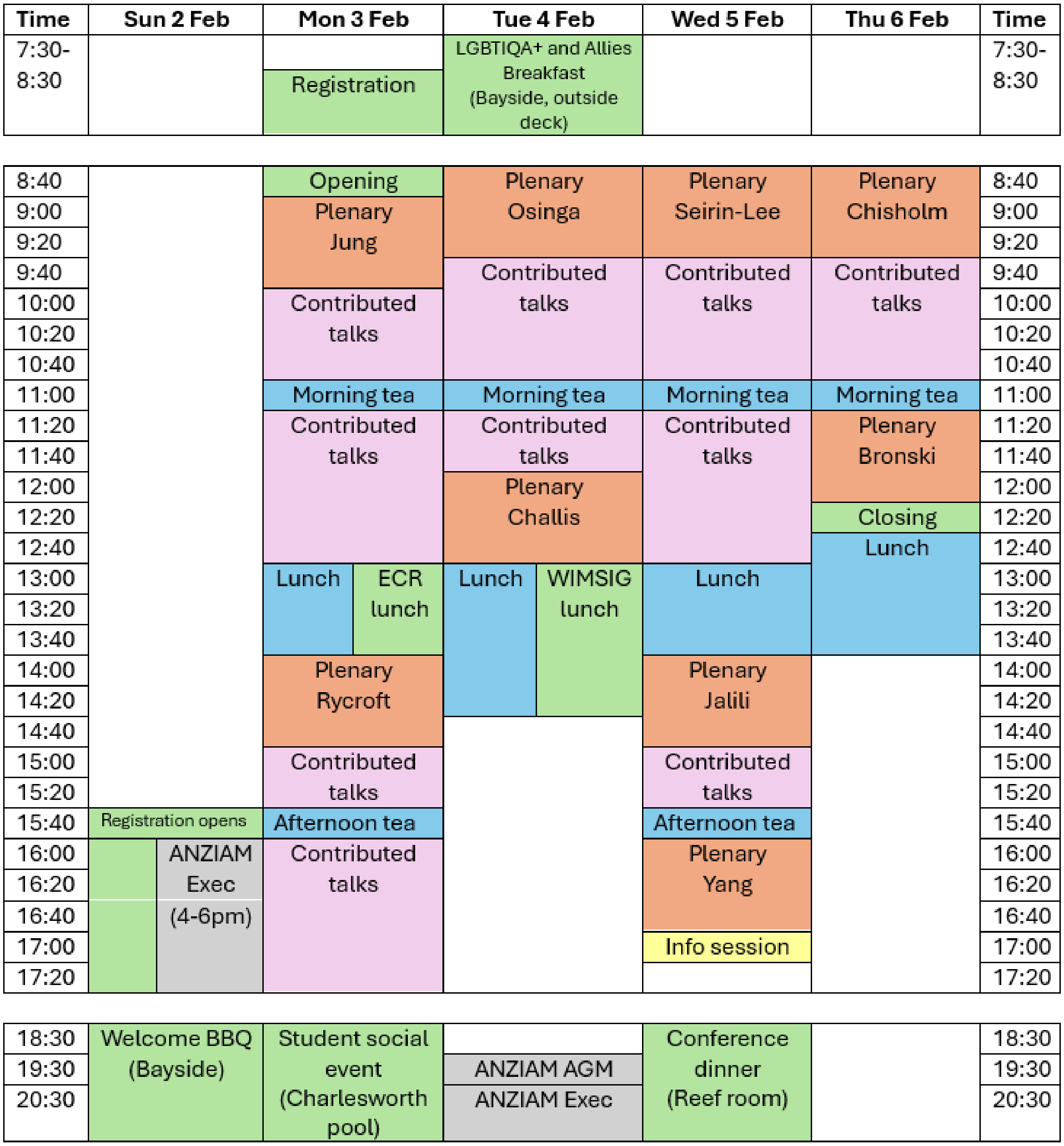
- **Where**: Tutorial Room A2.24A, National Marine Science Campus, Southern Cross University, Coffs Harbour
- **Cost**: $50 AUD (You must have registered through the conference registration system by 25 January 2025.)
- **Invited speakers**: Nam-Ho Nguyen (USyd), Felipe Atenas (UniMelb), Vinesha Peiris (Curtin), Alberto De Marchi (UniBw Munich, Germany), Winner of the Student Best Paper Prize (to be announced at the workshop)

4.14. Mathematical Biology Special Interest Group meeting

The annual one-day Mathematical Biology Special Interest Group (MBSIG) Workshop will be held after the ANZIAM 2025 Conference. The workshop will feature talks from five invited speakers and the winner of the Student Best Paper Prize.

- **When**: Friday 7 February 2025, 9:45−15:30
- **Where**: Lecture Theatre A1.02, National Marine Science Campus, Southern Cross University, Coffs Harbour
- **Cost**: $50 AUD (You must have registered through the conference registration system by 25 January 2025.)
- **Invited speakers**: Sami Al-Izzi (UNSW), Karina Arias Calluari (USyd), Thao Le (UniMelb), Michael Pan (UniMelb), Brock Sherlock (UNSW)

5. Conference Events at a Glance



Time	Sun 2 Feb	Mon 3 Feb	Tue 4 Feb	Wed 5 Feb	Thu 6 Feb	Time
7:30-8:30		Registration	LGBTIQA+ and Allies Breakfast (Bayside, outside deck)			7:30-8:30

Time	Sun 2 Feb	Mon 3 Feb	Tue 4 Feb	Wed 5 Feb	Thu 6 Feb	Time
8:40		Opening	Plenary Osinga	Plenary Seirin-Lee	Plenary Chisholm	8:40
9:00		Plenary Jung				9:00
9:20						9:20
9:40			Contributed talks	Contributed talks	Contributed talks	9:40
10:00		Contributed talks				10:00
10:20						10:20
10:40						10:40
11:00		Morning tea	Morning tea	Morning tea	Morning tea	11:00
11:20		Contributed talks	Contributed talks	Contributed talks	Plenary Bronski	11:20
11:40						11:40
12:00			Plenary Challis			12:00
12:20					Closing	12:20
12:40					Lunch	12:40
13:00		Lunch ECR lunch	Lunch WIMSIG lunch	Lunch		13:00
13:20						13:20
13:40						13:40
14:00		Plenary Rycroft		Plenary Jalili		14:00
14:20						14:20
14:40						14:40
15:00		Contributed talks		Contributed talks		15:00
15:20						15:20
15:40	Registration opens	Afternoon tea		Afternoon tea		15:40
16:00	ANZIAM Exec (4-6pm)	Contributed talks		Plenary Yang		16:00
16:20						16:20
16:40						16:40
17:00				Info session		17:00
17:20						17:20

Time	Sun 2 Feb	Mon 3 Feb	Tue 4 Feb	Wed 5 Feb	Thu 6 Feb	Time
18:30	Welcome BBQ (Bayside)	Student social event (Charlesworth pool)		Conference dinner (Reef room)		18:30
19:30			ANZIAM AGM			19:30
20:30			ANZIAM Exec			20:30

Note: For conference attendees staying at the Pacific Bay Resort, please be advised that there will be no dine-in dinner available at the Bayside Restaurant on Monday night. However, you can order take-away pizzas from the Bayside Restaurant (visit https://pacificbayresort.com.au/dining/), or you may arrange for a food delivery service to have your meal dropped off at reception. Alternatively, there is a restaurant at BreakFree Aanuka Beach Resort (Aanuka Beach House, see https://aanukabeachhouse.com.au/), which is approximately a 14-minute walk from the Pacific Bay Resort. Additionally, Coffs Harbour Town Centre offers a variety of restaurants and is located about a 7 to 10-minute drive from the Pacific Bay Resort. Dine-in service at the Bayside Restaurant will resume from Tuesday to Sunday, between 16:30 and 21:00.

6. Plenary Lectures

Each plenary talk will be 40 minutes long, with an additional 10 minutes for questions.

Day	Time	Plenary speaker	Talk title
MON	9:00	Sunghwan Jung	Animal behaviours in response to fluid instabilities: drinking, diving and shaking
MON	14:00	Christopher Rycroft	Uncovering the rules of crumpling with a data-driven approach
TUE	8:40	Hinke Osinga	‘Fingerprints’ of wild chaos
TUE	12:10	Vivien Challis	Computational design of piezoelectric metamaterials − a tour of topology optimisation methods and applications
WED	8:40	Sungrim Seirin-Lee	Mathematical dermatology based on skin eruption morphology connected to in vivo pathophysiological states
WED	14:00	Mahdi Jalili	AI, machine learning and optimisation for integration of electric vehicles into electricity grids
WED	16:10	Jean Yang	Translational potential of integrating two imaging data modalities
THU	8:40	Rebecca Chisholm	Multi-strain infectious disease dynamics
THU	11:30	Jared Bronski	Geometry of stability and eigenvalue problems

Animal behaviours in response to fluid instabilities: drinking, diving and shaking

Sunghwan Jung
Cornell University

Biological organisms have presumably adapted their behaviors or features in response to surrounding mechanical forces or instabilities to achieve better performance. In this talk, I will discuss three problems in which the dynamical system approach elucidates the physics behind animal behaviors. First, we investigated how cats and dogs transport water into the mouth using an inertia-driven (lapping) mechanism. We found that to maximize water intake per lap, both cats and dogs close the jaw at the column break-up time governed by unsteady inertia. This break-up (or pinch-off) time can be predicted using the stability analysis of the water column in which surface tension balances with inertia. Second, we studied how animals plunge-dive and survive from impact. Physical experiments using an elastic beam as a model for the body attached to different shapes revealed limits for the stability of the injuries during plunge-dive. The body response can be simplified as the Euler beam buckling problem with unsteady impact force on the diving front. Third, I will discuss the mechanism of releasing water lodged in the ear canal. For example, people often shake their head sideways to remove water out of ear canal after swimming or showering. This removal process involves high acceleration to push water out of a canal, which is analogous to the Rayleigh-Taylor instability. If time permits, I will briefly talk about how humans produce sound by clapping their hands, a process that can be modeled using classical Helmholtz resonance. (Back)

Uncovering the rules of crumpling with a data-driven approach

Christopher Rycroft
University of Wisconsin−Madison

When a sheet of paper is crumpled, it spontaneously develops a network of creases. Despite the apparent disorder of this process, statistical properties of crumpled sheets exhibit striking reproducibility. Recent experiments have shown that when a sheet is repeatedly crumpled, the total crease length grows logarithmically. This talk will offer insight into this surprising result by developing a correspondence between crumpling and fragmentation processes. We show how crumpling can be viewed as fragmenting the sheet into flat facets that are outlined by the creases, and we use this model to reproduce the characteristic logarithmic scaling of total crease length, thereby supplying a missing physical basis for the observed phenomenon.

This study was made possible by large-scale data analysis of crease networks from crumpling experiments. We will describe recent work to use the same data with machine learning methods to probe the physical rules governing crumpling. We will look at how augmenting experimental data with synthetically generated data can improve predictive power and provide physical insight. (Back)

‘Fingerprints’ of wild chaos

Hinke Osinga
University of Auckland

In a smooth world, curves, surfaces, and more generally, manifolds intersect each other transversely, if at all; tangencies are rare events that cannot be observed in experiments. In dynamical systems theory, therefore, it was long assumed that tangencies between invariant manifolds occur at isolated points when a parameter is varied, and the transition from tame to chaotic dynamics is mediated by a single tangential event. Recent theoretical work by Bonatti, Diaz, and others has shown that the boundary between tame and chaotic dynamics is, actually, more like a thick grey world that challenges our geometric intuition: tangencies may occur robustly, which is called wild chaos. This type of dynamics requires at least three dimensions for discrete-time systems, or four for a system of ordinary differential equations. This has been an impediment to our understanding of how steady states, periodic solutions, and their invariant manifolds organise wild chaotic dynamics.

In this talk, I will discuss how manifolds can have persistent tangential intersections as a parameter is varied. The starting point will be classical chaos in the planar Hénon map, a simple polynomial dynamical system. I will then consider a three-dimensional extension and explain its counter-intuitive properties: this map has one-dimensional invariant manifolds that cannot be avoided by other smooth curves. Hence, these one-dimensional manifolds behave as though they are two dimensional. With a careful combination of dynamical systems theory and advance computational methods, I will show what wild chaos and robust tangencies look like, how they arise, and why this matters for applications. (Back)

Computational design of piezoelectric metamaterials − a tour of topology optimisation methods and applications

Vivien Challis
Queensland University of Technology

Topology optimisation is a powerful computational approach for designing structures or microstructures for particular physical properties. The resulting designs can often be manufactured using modern additive manufacturing (or 3D printing) technologies. Topology optimisation typically combines numerical solution of the relevant state equations with a density- or level set-based description of the structure that facilitates optimisation of the design objective.

In this talk I'll introduce topology optimisation and outline two common approaches. I'll discuss a range of topology optimisation applications I've worked on during my career, including recent work optimising periodic piezoelectric metamaterials using our open source package GridapTopOpt.jl. (Back)

Mathematical dermatology based on skin eruption morphology connected to in vivo pathophysiological states

Sungrim Seirin-Lee
Kyoto University

The skin patterns of animals are formed through self-organization during development, whereas the skin eruption patterns observed on human skin reflect imbalances within the body. Both types of pattern formation share a common principle of spatial heterogeneity, where internal information is represented as shape. Urticaria is a common skin disorder characterized by wheals that appear in various shapes and typically disappear within hours or a day. Chronic spontaneous urticaria (CSU), a major subtype that can persist for years to decades, significantly impacts patients' quality of life. Although it is well accepted that the symptoms of urticaria are induced by the degranulation of skin mast cells and the release of various mediators, such as histamine, the mechanism of CSU remains elusive, largely due to the lack of animal models and specific clinical biomarkers. To address this, we developed a novel approach by integrating mathematical modeling, topological data analysis, in vitro experiments, and clinical data. Using this approach, we have constructed a new framework capable of inferring pathophysiological states from the shape of wheals and linking them to shape-specific treatments. This study proposes a practical framework in dermatology, enhancing both diagnostic accuracy and treatment efficacy by bridging mathematics and dermatology. (Back)

AI, machine learning and optimisation for integration of electric vehicles into electricity grids

Mahdi Jalili

RMIT University

Uptake of Electric Vehicles (EVs) is ramping up and EVs will soon be the dominant vehicle types offered in many markets including Australia. Distributions grids have not been originally designed to accommodate massive EV charging and uncoordinated charging might push the grid over its limits. On the other hand, EVs are batteries on the wheel and can support the grid and also homes through vehicle to grid technology. In this talk, I will present some recent advances on AI, machine learning and optimisation techniques for EV-grid integration. Such tools help reduce or delay network investments through providing optimal non-network solution, keeping energy affordability under control whilst maintaining reliability and security of electricity supply. Several case studies will be discussed on how AI and machine learning can be utilised to enable massive EV integration and supporting a net-zero future. (Back)

Translational potential of integrating two imaging data modalities

Jean Yang

University of Sydney

New spatial technologies have enabled the quantification of spatially resolved gene expression, advancing our understanding of the molecular basis of diseases. A key challenge lies in developing predictive models to bridge two data modalities, such as inferring spatial gene expression (cellular imaging) from more cost-effective H&E images (histopathology imaging). In this talk, I will first outline a statistical framework for evaluating the performance of such predictive models, emphasising the importance of generating diverse evaluation criteria. Beyond basic performance metrics comparing predictive estimates to ground truth, I will discuss the construction of evaluation criteria derived from survival analysis applied to real-world data such as The Cancer Genome Atlas, which enables us to capture translational insights between machine learning methods and clinical applications. Finally, I will explain how applying the evaluation framework to ten existing deep learning models informed the development of our new approach which leverages higher-resolution data to address the same problem. (Back)

Multi-strain infectious disease dynamics

Rebecca Chisholm

La Trobe University

In many models of infectious disease dynamics, an underlying assumption is that the pathogen (the organism causing the disease) exists in the host population as a uniform entity. This can be a reasonable assumption, for example, when modelling diseases caused by pathogens with a high level of genetic stability (e.g., the measles virus). When this assumption is not appropriate, models must sufficiently account for variation within the pathogen species that differentially affects important epidemiological characteristics such as a strain's virulence (severity of disease it causes), transmissibility, and/or response to interventions. A key complexity that arises in such models is the need to specify how pathogen strains interact within hosts directly and indirectly via the host immune response, often with little data to inform these assumptions which can significantly influence the predicted structure of pathogen populations. In this talk I will describe common approaches used to model multi-strain infectious disease dynamics. I will then describe some key insights gained into multi-strain infectious disease dynamics from the analysis of these model and via multi-strain model-based data analysis. (Back)

Geometry of stability and eigenvalue problems

Jared Bronski, Lee Deville, Robert Marangell, Vera Hur
University of Illinois Urbana-Champaign

Traveling waves and coherent structures are important features for understanding the behaviour of many physical systems, and the question of the stability of these features often leads to interesting mathematics. We present three models where we have been able to successfully analyze the stability using geometric ideas. (Back)

7. Contributed Talks

The program is shown on the following pages. The duration of each contributed talk will be 15 minutes with an additional five minutes for questions and changeover.

Student talks are marked with asterisks.

Monday 3 February (morning session)

8:00−8:30 Registration

8:40−9:00 Conference opening

9:00−9:50 **Plenary talk: Sunghwan Jung**
Animal behaviours in response to fluid instabilities: drinking, diving and shaking
Chair: Scott McCue

	Marina *Chair: Stuart Johnston*	**Harbour** *Chair: Kate Helmstedt*	**Jetty** *Chair: Ravindra Pethiyagoda*	**Sapphire** *Chair: Cecilia González-Tokman*	**Crystal** *Chair: Ilze Ziedins*
10:00−10:20	**Matthew Mack*** Many ODEs (and PDEs and an ABM) to a wound healing mechanism	**Sarah Vollert*** Calibrating mathematical models when data is limited: how to use non-empirical observations for parameterisation	**Mike Meylan** Analytic methods in hydroelasticity	**Gary Froyland** Emergence of quasi-stationary families of almost-invariant sets in convective fluids (including the atmosphere)	**Hritika Gupta*** Optimal call allocation policy for call centres
10:20−10:40	**Muhammad Asim Farooq*** Modeling interclonal cooperation in epithelial carcinogenesis using a vertex-based approach	**Matthew Adams** The mathematics of Pokémon breeding versus the mathematics of species trait evolution	**Amy-Rose Westcott*** Broadband capture of ocean wave energy: a 3D model	**Kevin Kühl*** Learning transfer operator dynamics on latent spaces	**David Wu** Patient movements in the Victorian hospital system: does time matter?
10:40−11:00	**James Osborne** Competing mechanisms for the buckling of an epithelial monolayer identified using multicellular simulation	**Celia Dowling*** Investigating zooplankton abundance using a seasonally forced model	**Ben Wilks** Layout and parameter optimisation of a wave energy park in an irregular sea	**Aleksandar Badza** Identifying atmospheric blocking events using the inflated generator	**Ashley Hanson*** Game theoretic decision making in service systems

11:00−11:20 Morning tea

Monday 3 February (morning session continued)

	Marina *Chair: Mary Myerscough*	**Harbour** *Chair: Rebecca Chisholm*	**Jetty** *Chair: Edward Hinton*	**Sapphire** *Chair: Bernd Krauskopf*	**Crystal** *Chair: Vivien Challis*
11:20–11:40	**Georgia Weatherley*** A moving-boundary model of lesion growth in multiple sclerosis	**Roslyn Hickson** Modelling the suppression of the global mosquito miscreants: *Aedes albopictus*	**Tharindi Amarathunge Achchige*** Pattern formation of precursor films: two species model	**Heath Dimsey*** Modelling the Bray–Liebhafsky oscillating reaction	**Connor Mallon** Topology optimisation for soft robotic grippers
11:40–12:00	**Ishraq Ahmed** Free cholesterol toxicity and impaired cell clearance in a lipid-structured model for atherosclerosis	**Md Nurul Anwar** Spatio-temporal agent-based modelling of malaria	**Radu Cimpeanu** Active control of liquid film flows: beyond reduced-dimensional models	**David C Groothuizen Dijkema*** Analysing dynamics near heteroclinic networks with a projected map	**Zachary Wegert*** Parallel level set-based optimisation of three-dimensional piezoelectric materials
12:00–12:20	**Joseph Ndenda** A mathematical model for smooth muscle cell phenotype switching in atherosclerotic plaque	**Maame Akua Korsah*** Model reduction and analysis: a case study of a malaria control model	**Michael Dallaston** Capillary levelling of thin liquid films of power-law rheology	**Matthew Lim*** The mathematics of collapse: geometric singular perturbation theory and rate-induced tipping phenomena in multiple-time-scale ecological models	**Liam Timms*** Coordinating a virtual power plant with a decentralised distributed algorithm
12:20–12:40	**Adelle Coster** Modelling macrophage action: insights from in vivo experiments	**Manuela Mendiolar** *Farauti and Furious*: modelling malaria mosquitoes for outbreak prevention	**Scott McCue** Unusual type of thin film rupture	**Timothy Earl Figueroa Lapuz*** The coordinate-independent geometric singular perturbation toolbox: model reductions of chemical reaction networks	**Thakshila Rajapaksha*** Convergence rate of the derivative-free *VU*-algorithm
12:40–13:00	**Luke Filippini*** Deterministic and stochastic modelling of anisotropic diffusion with a focus on the central nervous system	**Jennifer Flegg** A spatial multiscale mathematical model of malaria transmission	**Zayed Asiri*** A surrogate model of dispersive, variable density flow with application to seawater intrusion in offshore subsea aquifers	**Cecilia González-Tokman** Lyapunov–Oseledets spectrum for random metastable maps	**Nina Rynne*** Optimal control theory for climate temperature overshoot: separating mitigation and carbon dioxide removal
13:00–14:00	Lunch/ECR lunch				

Monday 3 February (afternoon session)

14:00−14:50 **Plenary talk: Cristopher Rycroft**
Uncovering the rules of crumpling with a data-driven approach
Chair: Anja Slim

	Marina *Chair: Domenic Germano*	**Harbour** *Chair: David Warne*	**Jetty** *Chair: Yvonne Stokes*	**Sapphire** *Chair: Brendan Florio*	**Crystal** *Chair: Bronwyn Hajek*
15:00−15:20	**Cecilia Olivesi*** A coupled agent-based and PDE model for angiogenesis applied to endometriosis	**Elise Mills*** Monte Carlo sampling: an application to Antarctic moss photosynthesis	**Minkush Kansal** Viscoelastic drop spreading: Cox−Voinov theory with normal stress effects	**Melanie Roberts** ShapleyX − a handy python tool for simulation-specific global sensitivity analysis	**David Plenty*** New non-Lie non-classical symmetry solutions of a class of reaction−diffusion equations
15:20−15:40	**Claire Miller** Modelling immune interactions with endometrial cells in endometriosis lesion onset	**Jessica Crawshaw** Modeling ranibizumab pharmacokinetics/pharmacodynamics in wet AMD: insights into VEGF suppression and drug retention through hierarchical Bayesian inference	**Matthew Walker*** A viscoplastic deposit on an oscillating plate	**Llewyn Randall*** Modelling amphitheatre gully erosion with coupled hydrology and erosion dynamics in two-dimensions	**Pierluigi Cesana** Space-time evolution of Volterra disinclinations

15:40−16:00 Afternoon tea

Monday 3 February (afternoon session continued)

	Marina *Chair: Adriana Zanca*	**Harbour** *Chair: Alexander Browning*	**Jetty** *Chair: Harvinder Sidhu*	**Sapphire** *Chair: Ben Wilks*	**Crystal** *Chair: Caroline Wormell*
16:00−16:20	**Noa Levi*** When therapeutic intervention is destined to fail	**Liam Gibson*** Modelling the rise of the adjunct population in colleges	**Larry Forbes** Mathematical fireworks	**Afnan Aldosri*** Wave scattering at a rectangular junction of four waveguides	**Aamir Yousuf*** Numerical analysis of a coupled thermoelastic diffusion plate model
16:20−16:40	**Mason Lacy*** Modelling T cell expansion in immune cell-mimicking scaffolds for adoptive cell therapy	**Zhao Mei Zheng*** Counting sheep ... or counting parameters in transmission models	**Graeme Hocking** Barotrauma in bats due to wind turbines	**Rehab Aljabri*** Simulating the vibrations of a circular ice shelf	**Bishnu Lamichhane** Gradient recovery based on a biorthogonal system
16:40−17:00	**Tommaso Lorenzi** PDE models for the spatial spread and evolutionary dynamics of heterogeneous cell populations	**Kartik Kamboj*** Assessing parameter identifiability in age-structured epidemic models with under-reporting	**Mark McGuinness** Modelling with differential equations − highlights	**Mitchell Bonham*** Tsunamis generated by a moving N-shaped atmospheric pressure wave	**Edoardo Fabbrini*** Modelling, analysis and finite element simulations of kinematically incompatible von Kármán plates
17:00−17:20	**Domenic Germano** Mathematical modelling of dendritic cell clustering for improved T-cell activation	**David Ceddia*** Mathematical modelling of athletic performance and the optimisation of training load	**Brendan Florio** Population balance modelling of polydisperse primary particles in the flocculation of minerals tailings	**Ravindra Pethiyagoda** Tsunami waves in a compressible ocean near a step-type topography	**Nicholas Peters*** Numerical methods for approximating the transfer and Koopman operators
17:20−17:40	**Yash Vats*** Modelling spike frequency adaption through higher-order fractional leaky integrate and fire model			**Anja Slim** Intruding into the atmosphere and oceans	
18:30	Student social event				

Note: For conference attendees staying at the Pacific Bay Resort, please be advised that there will be no dine-in dinner available at the Bayside Restaurant on Monday night. However, you can order take-away pizzas from the Bayside Restaurant (visit https://pacificbayresort.com.au/dining/), or you may arrange for a food delivery service to have your meal dropped off at reception. Alternatively, there is a restaurant at BreakFree Aanuka Beach Resort (Aanuka Beach House, see https://aanukabeachhouse.com.au/), which is approximately a 14-minute walk from the Pacific Bay Resort. Additionally, Coffs Harbour Town Centre offers a variety of restaurants and is located about a 7 to 10-minute drive from the Pacific Bay Resort. Dine-in service at the Bayside Restaurant will resume from Tuesday to Sunday, between 16:30 and 21:00.

Tuesday 4 February (morning and afternoon sessions)

7:30−8:30 LGBTIQA+ and Allies breakfast

8:40−9:30 **Plenary talk: Hinke Osinga**
‘Fingerprints’ of wild chaos
Chair: Gary Froyland

	Marina *Chair: Alex Tam*	**Harbour** *Chair: Matthew Holden*	**Jetty** *Chair: Sergiy Shelyag*	**Sapphire** *Chair: Natalie Thamwattana*	**Crystal** *Chair: Xiaoping Lu*
9:40−10:00	**Ryan Murphy** Quantifying biological heterogeneity in nano-engineered particle-cell interaction experiments	**Grace Robinson*** Balancing competing priorities: optimising land use allocation	**Michael Small** Information spreading on real and imaginary networks	**Sami Al-Izzi** Continuum-geometric mechanics and design principles of odd active filaments	**Doungporn Wiwatanapataphee*** Fractional Black−Scholes model for pricing derivatives in the Australian energy market
10:00−10:20	**Obi Carwood*** Mathematical modelling of drug release from functionally-graded delivery systems	**Angus Lewis** Reading the shark’s barcode	**Daniel Herr*** On ripple search methods − rapid cycle detection protocols	**Kenji Kajiwara** Towards geometry of aesthetic shapes: Klein geometry, integrability and self-affinity	**Jordan Holdorf*** Evaluating investment potential in blue carbon ecosystems within emerging carbon markets
10:20−10:40	**Georgio Hawi*** Optimisation of locally advanced MSI-H/dMMR colorectal cancer treatment with neoadjuvant pembrolizumab using data-driven delay integro-differential equations	**Kaitlyn Brown*** Coral bleaching on the Great Barrier Reef: insights from a mathematical model	**Manu Kalia** Detecting communities in temporal networks with the inflated dynamic Laplacian for graphs	**Agnese Barbensi** Topologically steered simulations and the role of geometric constraints in protein knotting	**Xinyi Zhang*** Pricing knock-out options with transaction costs
10:40−11:00	**Cristina Koprinski*** Optimising chemotherapy for high grade serous ovarian cancer	**Luz Pascal*** When does non-stationarity matter for managing threatened ecosystems?	**Tristram Alexander** Human-interpretable clustering of short-text using large language models	**Barry Cox** Bucky-bowl dimples in graphene	**Kajanthan Shiyamasuntharam*** Thomas algorithm in the pricing of American option on coupon paying bond under the CIR interest rate model

11:00−11:20 Morning tea

Tuesday 4 February (morning and afternoon sessions continued)

	Marina *Chair: Adelle Coster*	**Harbour** *Chair: Maria Kleshnina*	**Jetty** *Chair: Justin Tzou*	**Sapphire** *Chair: Melanie Roberts*	**Crystal** *Chair: Benchawan Wiwatanapataphee*
11:20−11:40	**Behnaz Rahmani*** Understanding complex oscillations in a model of intracellular calcium dynamics	**Daniel Fraterman*** Modelling the evolution of ecologically scaffolded lifecycles	**Stuart Johnston** The role and benefit of heterogeneity in migratory animal populations	**Josiah Murray*** Solving for railway deformations using Weeks’ method and undetermined coefficients	**Augustinas Sukys** Approximating solutions of the Chemical Master Equation using neural networks
11:40−12:00	**Catheryn Gray** Exploring Akt dynamics: modelling spatial and temporal regulation	**Tace Stewart*** Navigating the maze: a synthesis of dynamic conservation planning methods for a changing environment	**Mariano Rodrigo** From crowded streets to serene retreats: managing overtourism through mathematics	**Patrick Grant*** Wood you believe it? A model for simulating moisture migration and swelling in engineered wood products	**Thomas Williams*** Using neural networks for inference problems in genetic epidemiology

12:10−13:00 **Plenary talk: Vivien Challis**
Computational design of piezoelectric metamaterials − a tour of topology optimisation methods and applications
Chair: Mark McGuinness

13:00−14:30 Lunch/WIMSIG lunch

19:30−20:30 ANZIAM AGM

Wednesday 5 February (morning session)

8:40−9:30 **Plenary talk: Sungrim Seirin-Lee**
Mathematical dermatology based on skin eruption morphology connected to in vivo pathophysiological states
Chair: Matthew Simpson

	Marina *Chair: Pascal Buenzli*	**Harbour** *Chair: Eva Stadler*	**Jetty** *Chair: Michael Dallaston*	**Sapphire** *Chair: Hinke Osinga*	**Crystal** *Chair: Boris Baeumer*
9:40−10:00	**Alexander Browning** Heterogeneity in temporally fluctuating environments	**Jiahao Diao** Should public health policy exempt cases with low viral load from isolation during an epidemic?: a modelling study	**Hugh Michalski*** The effect of obstacle length and height in supercritical free-surface flow	**Courtney Quinn** Exploring partial tipping through variation in forcing timescale	**Thisaakhya Jayakody*** An application of the time-inhomogeneous Markovian binary tree to female families
10:00−10:20	**Brock Sherlock*** Queuing, even GLUT4 has to do it	**Joel Miller** The ethical implications of the SIR epidemic final size relation	**Andrey Pototsky** Large-scale vortices in electromagnetically driven horizontal soap films	**Samuel Bolduc-St-Aubin*** State-dependent delays in feedback loops: insights from an El Niño-Southern Oscillation model	**Justin Tzou** Levy flight search in 2-D geometries
10:20−10:40	**Lucy Ham** Collective action: cell fate control in space and time	**Matthew Berry** Adapting vaccination strategies for Mpox	**Sergey Suslov** Vortices in electromagnetically driven films: physical nature and bifurcation characteristics	**John Bailie*** Bifurcations of resonance tongues in a periodically climate model	**Parul Tiwari** Metamodelling for geometric Brownian motion using polynomial chaos expansion
10:40−11:00	**Shahak Kuba*** A stochastic model of biological tissue growth in confined spaces	**Steffen Docken** Insights into the natural obstacles that slow early HIV spread based on analysis of Simian Immunodeficiency Virus experiments	**Tomoo Yokoyama** Classification of streamline topology of vortex flows in doubly periodic domains	**Siwen Deng*** Oscillatory instability of localised spot pattern in the Schnakenberg reaction−diffusion system in defected 3D domains	**Zhou Zhou** Major-minor mean field game of stopping: an entropy regularisation approach
11:00−11:20	Morning tea				

Wednesday 5 February (morning session continued)

	Marina *Chair: Ryan Murphy*	**Harbour** *Chair: Chris Baker*	**Jetty** *Chair: Douglas Brumley*	**Sapphire** *Chair: Courtney Quinn*	**Crystal** *Chair: Robert Cope*
11:20−11:40	**Rodney Dharma*** Bacterial encounter rates and residence times in microbial symbiosis	**Ruarai Tobin*** Multi-strain infection dynamics with an immunity-structured model	**Yvonne Stokes** The complex stability landscape for drawing of holey fibres	**Sam Doak*** Invariant manifolds and wild chaos	**David Warne** A Bayesian hierarchical framework for capturing experimental variability in flow cytometry data
11:40−12:00	**Aidan Patterson*** An analytic solution to a hole opening problem for a bacterial colony	**Isobel Abell*** Incorporating human behaviour when modelling animal disease outbreaks	**Olle Ponten*** Directed helical motility of active particles in the zero-Reynolds number limit	**Davide Papapicco*** Slowly, then all at once: uncovering the dynamics of a catastrophe	**Andreas Heinecke** Unsupervised statistical learning in ancient numismatics
12:00−12:20	**Hayden Tronnolone** Creating a nutrient-based model for cylindrical yeast growth	**Pratyush Kollepara*** Effect of contact structure on the realised generation intervals of an outbreak	**Xinyi Yang*** Resolving the hydrodynamics of non-spherical microswimmers	**Juan Patiño-Echevería*** Global bifurcations in a 4D Lorenz-like system	**Harry McArthur*** A MCMC framework for differentially-private synthetic data generation
12:20−12:40	**Kai Li*** An off-lattice discrete model to characterise filamentous yeast colony morphology	**Thao Le** Simulating emergency animal disease outbreaks and response	**Siluvai Selvan*** Modelling mass transport due to ciliary carpets: Rotlet model	**Bernd Krauskopf** Phase resetting and the geometry of isochrons	**Yong See Foo*** Inferring reaction networks from dynamics
12:40−13:00	**Alex Tam** Accidental and regulated cell death in yeast biofilms	**Tianxiao Hao** Estimating real-time epidemic trends from multiple streams of surveillance data	**Edward Hinton** Trapping of viscous liquid atop a granular mush	**Tony Roberts** Constructing accurate multi-continuum micromorphic homogenisations in multi-D space-time	**Michael Groom** Entropic learning enables skilful forecasts of ENSO phase at up to two years lead time
13:00−14:00	Lunch				

Wednesday 5 February (afternoon session)

14:00−14:50 **Plenary talk: Mahdi Jalili**
AI, machine learning and optimisation for integration of electric vehicles into electricity grids
Chair: Michael Small

	Marina *Chair: Mark Flegg*	**Harbour** *Chair: Manuela Mendiolar*	**Jetty** *Chair: Matthew Adams*	**Sapphire** *Chair: Bishnu Lamichhane*	**Crystal** *Chair: Mariano Rodrigo*
15:00−15:20	**Adriana Zanca** Theoretical and mathematical models of cell fate	**James McCaw** How immune dynamics shape multi-season epidemics: a continuous-discrete model in one dimensional antigenic space	**Maria Kleshnina** Resilience in the evolution of cooperation: measuring the effect of inequality	**Alexander Johnston** Efficient inference for differential equation models without numerical solvers	**Boris Baeumer** A non-separable Hawkes process modelling earthquake frequencies
15:20−15:40	**Thomas Cummings, Yang Zhao** Clone wars: modelling tumour resistance in CAR-T cell therapy	**Oliver Eales** Viral kinetics of H5N1 infections in dairy cows	**Matthew Holden** Should we really expand protected areas to save threatened species?	**Caroline Wormell** An efficient statistic for bounding the spectrum of data-driven operators	**Benchawan Wiwatanapataphee** Fractional advection−diffusion modelling in fluid dynamics with spatially varying diffusion coefficients

15:40−16:10 Afternoon tea

16:10−17:00 **Plenary talk: Jean Yang**
Translational potential of integrating two imaging data modalities
Chair: Peter Taylor

17:00−17:20 **Information session: Peter Taylor**
Fraudulent publishing in the mathematical sciences

18:30 Conference dinner

Thursday 6 February (morning session)

8:40−9:30 **Plenary talk: Rebecca Chisholm**
Multi-strain infectious disease dynamics
Chair: James McCaw

	Marina *Chair: James Osborne*	**Harbour** *Chair: Joel Miller*	**Jetty** *Chair: Larry Forbes*	**Sapphire** *Chair: Tony Roberts*
9:40−10:00	**Matthew Simpson** Parameter identifiability, parameter estimation and model prediction for differential equation models	**Eva Stadler** Reconciling neutralising antibody titres across assays	**Dave Smith** Fokas diagonalisation	**Judy Bunder** Boundary conditions for multiscale equation-free modelling
10:00−10:20	**Michael Pan** Incorporating thermodynamic constraints into parameter estimation for dynamic models of cell metabolism	**Michael Lydeamore** Modelling chytridiomycosis transmission in frogs	**Bronwyn Hajek** Nonlinear backward diffusion and regularisation options	**Daisuke Tagami** A preconditioner of iterative domain decomposition methods based on a multigrid strategy
10:20−10:40	**Pascal Buenzli** Beyond linear elasticity using discrete models of cellular tissues	**Robert Cope** Quantifying uncertainty in worm egg counts with bulk sampling	**Robert Marangell** Floquet theory and stability analysis for Hamiltonian PDEs	**Wei-Chang Yeh** Enhancing Monte Carlo simulation efficiency through optimal computing budget allocation for network reliability analysis
10:40−11:00	**Jeremy Worsfold** Stochastic limit cycles in the Togashi−Kaneko model of an autocatalytic system	**Richard Creswell** Bayesian approaches to characterising the accuracy of diagnostic tests for Buruli Ulcer	**Chris Lustri** Stokes' phenomenon in complex solutions to nonlinear PDEs	**Xiaoping Lu** Utility indifference approach for option pricing

11:00−11:30 Morning tea

11:30−12:20 **Plenary talk: Jared Bronski**
Geometry of stability and eigenvalue problems
Chair: Robert Marangell

12:20−12:30 Presentation of the Cherry Ripe Prize and Closing Remarks

12:30−14:00 Lunch

8. Abstracts

8.1. Plenary talks

Geometry of stability and eigenvalue problems

Jared Bronski, Lee Deville, Robert Marangell, Vera Hur
University of Illinois Urbana-Champaign

Traveling waves and coherent structures are important features for understanding the behaviour of many physical systems, and the question of the stability of these features often leads to interesting mathematics. We present three models where we have been able to successfully analyze the stability using geometric ideas. (Back)

Computational design of piezoelectric metamaterials − a tour of topology optimisation methods and applications

Vivien Challis
Queensland University of Technology

Topology optimisation is a powerful computational approach for designing structures or microstructures for particular physical properties. The resulting designs can often be manufactured using modern additive manufacturing (or 3D printing) technologies. Topology optimisation typically combines numerical solution of the relevant state equations with a density- or level set-based description of the structure that facilitates optimisation of the design objective.

In this talk I'll introduce topology optimisation and outline two common approaches. I'll discuss a range of topology optimisation applications I've worked on during my career, including recent work optimising periodic piezoelectric metamaterials using our open source package GridapTopOpt.jl. (Back)

Multi-strain infectious disease dynamics

Rebecca Chisholm
La Trobe University

In many models of infectious disease dynamics, an underlying assumption is that the pathogen (the organism causing the disease) exists in the host population as a uniform entity. This can be a reasonable assumption, for example, when modelling diseases caused by pathogens with a high level of genetic stability (e.g., the measles virus). When this assumption is not appropriate, models must sufficiently account for variation within the pathogen species that differentially affects important epidemiological characteristics such as a strain's virulence (severity of disease it causes), transmissibility, and/or response to interventions. A key complexity that arises in such models is the need to specify how pathogen strains interact within hosts directly and indirectly via the host immune response, often with little data to inform these assumptions which can significantly influence the predicted structure of pathogen populations. In this talk I will describe common approaches used to model multi-strain infectious disease dynamics. I will then describe some key insights gained into multi-strain infectious disease dynamics from the analysis of these model and via multi-strain model-based data analysis. (Back)

AI, machine learning and optimisation for integration of electric vehicles into electricity grids

Mahdi Jalili

RMIT University

Uptake of Electric Vehicles (EVs) is ramping up and EVs will soon be the dominant vehicle types offered in many markets including Australia. Distributions grids have not been originally designed to accommodate massive EV charging and uncoordinated charging might push the grid over its limits. On the other hand, EVs are batteries on the wheel and can support the grid and also homes through vehicle to grid technology. In this talk, I will present some recent advances on AI, machine learning and optimisation techniques for EV-grid integration. Such tools help reduce or delay network investments through providing optimal non-network solution, keeping energy affordability under control whilst maintaining reliability and security of electricity supply. Several case studies will be discussed on how AI and machine learning can be utilised to enable massive EV integration and supporting a net-zero future. (Back)

Animal behaviours in response to fluid instabilities: drinking, diving and shaking

Sunghwan Jung

Cornell University

Biological organisms have presumably adapted their behaviors or features in response to surrounding mechanical forces or instabilities to achieve better performance. In this talk, I will discuss three problems in which the dynamical system approach elucidates the physics behind animal behaviors. First, we investigated how cats and dogs transport water into the mouth using an inertia-driven (lapping) mechanism. We found that to maximize water intake per lap, both cats and dogs close the jaw at the column break-up time governed by unsteady inertia. This break-up (or pinch-off) time can be predicted using the stability analysis of the water column in which surface tension balances with inertia. Second, we studied how animals plunge-dive and survive from impact. Physical experiments using an elastic beam as a model for the body attached to different shapes revealed limits for the stability of the injuries during plunge-dive. The body response can be simplified as the Euler beam buckling problem with unsteady impact force on the diving front. Third, I will discuss the mechanism of releasing water lodged in the ear canal. For example, people often shake their head sideways to remove water out of ear canal after swimming or showering. This removal process involves high acceleration to push water out of a canal, which is analogous to the Rayleigh-Taylor instability. If time permits, I will briefly talk about how humans produce sound by clapping their hands, a process that can be modeled using classical Helmholtz resonance. (Back)

‘Fingerprints’ of wild chaos

Hinke Osinga

University of Auckland

In a smooth world, curves, surfaces, and more generally, manifolds intersect each other transversely, if at all; tangencies are rare events that cannot be observed in experiments. In dynamical systems theory, therefore, it was long assumed that tangencies between invariant manifolds occur at isolated points when a parameter is varied, and the transition from tame to chaotic dynamics is mediated by a single tangential event. Recent theoretical work by Bonatti, Diaz, and others has shown that the boundary between tame and chaotic dynamics is, actually, more like a thick grey world that challenges our geometric intuition: tangencies may occur robustly, which is called wild chaos. This type of dynamics requires at least three dimensions for discrete-time systems, or four for a system of ordinary differential equations. This has been an impediment to our understanding of how steady states, periodic solutions, and their invariant manifolds organise wild chaotic dynamics.

In this talk, I will discuss how manifolds can have persistent tangential intersections as a parameter is varied. The starting point will be classical chaos in the planar Hénon map, a simple polynomial dynamical system. I will then consider a three-dimensional extension and explain its counter-intuitive properties: this map has one-dimensional invariant manifolds that cannot be avoided by other smooth curves. Hence, these one-dimensional manifolds behave as though they are two dimensional. With a careful combination of dynamical systems theory and advance computational methods, I will show what wild chaos and robust tangencies look like, how they arise, and why this matters for applications. (Back)

Uncovering the rules of crumpling with a data-driven approach

Christopher Rycroft
University of Wisconsin−Madison

When a sheet of paper is crumpled, it spontaneously develops a network of creases. Despite the apparent disorder of this process, statistical properties of crumpled sheets exhibit striking reproducibility. Recent experiments have shown that when a sheet is repeatedly crumpled, the total crease length grows logarithmically. This talk will offer insight into this surprising result by developing a correspondence between crumpling and fragmentation processes. We show how crumpling can be viewed as fragmenting the sheet into flat facets that are outlined by the creases, and we use this model to reproduce the characteristic logarithmic scaling of total crease length, thereby supplying a missing physical basis for the observed phenomenon.

This study was made possible by large-scale data analysis of crease networks from crumpling experiments. We will describe recent work to use the same data with machine learning methods to probe the physical rules governing crumpling. We will look at how augmenting experimental data with synthetically generated data can improve predictive power and provide physical insight. (Back)

Mathematical dermatology based on skin eruption morphology connected to in vivo pathophysiological states

Sungrim Seirin-Lee
Kyoto University

The skin patterns of animals are formed through self-organization during development, whereas the skin eruption patterns observed on human skin reflect imbalances within the body. Both types of pattern formation share a common principle of spatial heterogeneity, where internal information is represented as shape. Urticaria is a common skin disorder characterized by wheals that appear in various shapes and typically disappear within hours or a day. Chronic spontaneous urticaria (CSU), a major subtype that can persist for years to decades, significantly impacts patients' quality of life. Although it is well accepted that the symptoms of urticaria are induced by the degranulation of skin mast cells and the release of various mediators, such as histamine, the mechanism of CSU remains elusive, largely due to the lack of animal models and specific clinical biomarkers. To address this, we developed a novel approach by integrating mathematical modeling, topological data analysis, in vitro experiments, and clinical data. Using this approach, we have constructed a new framework capable of inferring pathophysiological states from the shape of wheals and linking them to shape-specific treatments. This study proposes a practical framework in dermatology, enhancing both diagnostic accuracy and treatment efficacy by bridging mathematics and dermatology. (Back)

Translational potential of integrating two imaging data modalities

Jean Yang
University of Sydney

New spatial technologies have enabled the quantification of spatially resolved gene expression, advancing our understanding of the molecular basis of diseases. A key challenge lies in developing predictive models to bridge two data modalities, such as inferring spatial gene expression (cellular imaging) from more cost-effective H&E images (histopathology imaging). In this talk, I will first outline a statistical framework for evaluating the performance of such predictive models, emphasising the importance of generating diverse evaluation criteria. Beyond basic performance metrics comparing predictive estimates to ground truth, I will discuss the construction of evaluation criteria derived from survival analysis applied to real-world data such as The Cancer Genome Atlas, which enables us to capture translational insights between machine learning methods and clinical applications. Finally, I will explain how applying the evaluation framework to ten existing deep learning models informed the development of our new approach which leverages higher-resolution data to address the same problem. (Back)

8.2. Contributed talks

Incorporating human behaviour when modelling animal disease outbreaks

Isobel Abell*
The University of Melbourne

Outbreaks of emergency animal diseases, such as Foot-and-Mouth Disease and Avian Influenza, can have far reaching consequences on animal welfare, food security and international trade. In an effort to reduce overall spread of a disease between properties, pre-emptive culling strategies may be employed alongside testing and vaccination strategies. Culling strategies must always be carefully considered to minimise both the impact of an outbreak against and the number of animals culled. However, management strategies that require the mass culling of animals may create a disincentive for farmers to report their infection to relevant authorities.

This project explores the impact human behaviour, i.e. farmers reporting infection, has on the overall spread of animal diseases. We construct an agent-based model incorporating animal-to-animal spread of disease and disease spread between properties in a network. We vary the reporting rate of infected properties and investigate its impact on a variety of management strategies, including pre-emptive culling, testing and vaccination. (Back)

The mathematics of Pokémon breeding versus the mathematics of species trait evolution

Matthew Adams
Queensland University of Technology

In the video game series ‘‘Pokémon’’ it is possible to pass on traits (in the form of Natures, Stats and movesets) from parent Pokémon to child Pokémon, which is a form of microevolution. Later games in the Pokémon game series also acknowledge that macroevolution can take place, via introduction of specific regional forms separated by time period (Hisui versus Sinnoh) or spatial isolation (Alola, Galar and Paldea). However, Pokémon does not (to my best knowledge) acknowledge that trait evolution can also affect the ability of a species population to survive long-term in the wild.

In this talk I overview recent mathematical work that uses generalised Lotka-Volterra models and stochastic speciation events to explain how species macroevolution can lead to complex ecosystems with many species coexisting simultaneously. While this theoretical work addresses a serious ecological question regarding how natural ecosystems can become increasingly complex over time, it also has a novel parallel to the number of Pokémon species increasing from 151 (in the original games) to 1025 (in the most recent games). (Back)

Free cholesterol toxicity and impaired cell clearance in a lipid-structured model for atherosclerosis

Ishraq U Ahmed, Mary R Myerscough
The University of Sydney

The resolution of chronic inflammation involves a dynamic balance between cell death and the clearance of dying cells via efferocytosis. In nonresolving atherosclerotic plaques, this balance is disrupted due to the accumulation of high levels of intracellular cholesterol. Cholesterol is initially stored within the cell in the form of cholesterol esters, but some of this is hydrolysed to form free cholesterol. Excess free cholesterol is cytotoxic to macrophages, and impairs their efferocytic ability and promotes necrotic cell death. In nonresolving plaques, the impairment of cellular function and increase in cell death rates can lead to the formation of a necrotic core.

In this talk, we present a preliminary partial integro-differential equation model for the early development of atherosclerotic tissue, where the cell population is structured by cholesterol content. Cells can accumulate cholesterol by ingesting it from LDL or dead cells, and can reduce their cholesterol load by proliferating. The model includes cell death via both apoptosis and necrosis, where necrotic material is ingested by live cells more slowly than apoptotic material. Death rates themselves depend on the levels of esterified and free cholesterol, where the relative levels of each are obtained from a coupled single-cell ODE model that describes intracellular cholesterol processing. With this model, we study how free cholesterol-induced cell death can lead to full tissue necrosis if efferocytosis rates are insufficient. We also consider how cell proliferation can help mitigate tissue necrosis by lowering intracellular cholesterol loads. (Back)

Continuum-geometric mechanics and design principles of odd active filaments

Sami Al-Izzi
UNSW Sydney

We derive continuum equations describing the dynamics of of active filaments in the continuum limit with non-reciprocal odd active terms. These terms are traditionally forbidden in continuum mechanics by the Maxwell-Betti reciprocal relations, but are permissible in systems that are driven by the local injection of energy (e.g. living systems or robotic materials). These equations describe the continuum limit of various mechanical and robotic systems that are capable of generating self-sustained unstable travelling waves. We discuss the mapping between discrete mechanisms and the continuum limit and insights that the continuum limit can provide for the rational design of discrete mechanisms. We solve the full non-linear dynamics for odd filaments connected in a loop for the two lowest order active stresses along with the steady states found in odd buckling filaments with fixed ends and compare to experimental realizations using robotic filaments. (Back)

Human-interpretable clustering of short-text using large language models

Justin K Miller, **Tristram J Alexander**
The University of Sydney

Clustering short text is a difficult problem, due to the low word co-occurrence between short text documents. This work shows that large language models (LLMs) can overcome the limitations of traditional clustering approaches by generating embeddings that capture the semantic nuances of short text. In this study clusters are found in the embedding space using Gaussian Mixture Modelling (GMM). The resulting clusters are found to be more distinctive and more human-interpretable than clusters produced using the popular methods of doc2vec and Latent Dirichlet Allocation (LDA). The success of the clustering approach is quantified using human reviewers and through the use of a generative LLM. The generative LLM shows good agreement with the human reviewers, and is suggested as a means to bridge the ‘validation gap’ which often exists between cluster production and cluster interpretation. The comparison between LLM-coding and human-coding reveals intrinsic biases in each, challenging the conventional reliance on human coding as the definitive standard for cluster validation. (Back)

Wave scattering at a rectangular junction of four waveguides

Afnan Aldosri*
The University of Newcastle

In this talk, we consider the scattering of linear waves in two dimensions by a rectangular region at the junction of four waveguides. A solution to the frequency domain problem is obtained by exploiting reflective symmetry to reduce the full problem to sub-problems defined on one quadrant of the junction. These sub-problems are solved using the eigenfunction matching method. The solution to the problem in the full region is then recovered from the solutions to the sub-problems. Finally, the solution in the time domain is constructed as a superposition of the frequency domain solutions and visualised for a range of incident pulses and waveguide geometries. (Back)

Simulating the vibrations of a circular ice shelf

Rehab Aljabri*
The University of Newcastle

A mathematical model is presented to investigate the vibrations in the time domain of circular ice shelves under different boundary conditions. The system is modelled using the shallow-water equations, which reduces the problem to a sixth-order partial differential equation. It is shown that this equation is separable in cylindrical coordinates, and the solution is expanded in Bessel functions. Different boundary conditions are investigated, clamped and free circular and no-flux and no-pressure conditions. These are the standard simplified boundary conditions considered in ice shelf modelling. The modes of vibration are calculated, and the time-dependent motion is simulated. Even for this idealised model, the ice shelf shows a very complex motion in the time domain. (Back)

Pattern formation of precursor films: two species model

Tharindi Amarathunge Achchige*, Bronwyn Hajek, Alex Tam, Marta Krasowska
University of South Australia

Precursor films formed by ionic liquids have the potential to be excellent lubricants for high-end applications. These precursor films create different types of patterns on different substrates and the effectiveness of the lubricating layer depends on the pattern they form. We aim to use mathematical modelling to select suitable pairs of ionic liquid-solid substrates to be used as lubricants by analysing the patterns formed by various ionic liquids on different substrates. The model considers a system of interacting particles, which in the continuum limit of short-range attraction yields a fourth-order thin-film-like equation for the density of cations and anions. Two-species Cahn-Hilliard-like equations are used considering anions and cations of the ionic liquid molecules as two distinct species. In this talk, I present how the two-species model illustrates the patterns formed by ionic liquid molecules, along with the linear stability analysis. Comparing the linear stability analysis results with experiments will allow us to quickly screen ionic liquids to improve lubrication. (Back)

Spatio-temporal agent-based modelling of malaria

Md Nurul Anwar, Camelia Walker, Jennifer Flegg
The University of Melbourne

Plasmodium falciparum malaria is responsible for the majority of malaria morbidity and mortality each year and is the deadliest out of the five malaria-causing parasites. Mathematical models can be used to simulate the transmission dynamics of malaria. We have developed a spatio-temporal agent-based model to capture the transmission dynamics and the impact of spatially distributed interventions on malaria transmission. We incorporate spatiotemporal estimates of mosquito suitability and household data from Vietnam to model the interaction between human and mosquito agents. Individuals are localised in space, both in households and grouped in villages. Mosquitoes are also modelled as agents and are either localised in households or travelling between households. We investigate different strategies to select households to distribute additional interventions that can lower disease burden more effectively while assuming a limited budget for malaria intervention. (Back)

A surrogate model of dispersive, variable density flow with application to seawater intrusion in offshore subsea aquifers

Zayed M Asiri*, Anthony D Miller, Sergiy Shelyag
Flinders University

In coastal hydrology, knowing the location of the dispersive fresh-saltwater transition zone is important, but challenging as it involves dispersive and variable density effects. Identifying the transition zone requires intensive numerical computations to solve the flow and dispersive transport equations. Here, a surrogate model of seawater intrusion in offshore subsea aquifers is presented. This model is trained using a factorial sampling of a five-parameter non-dimensional parameter space to correct a semi-analytical sharp-interface model to take into account the mixing zone and provides a prediction for the 5% and 50% seawater concentration lines. This model provides a good prediction to these concentration lines and since it does not require solving the flow and dispersive transport equations, it can be used to rapidly assess the vulnerability of subsea aquifers with offshore extension to saltwater intrusion. (Back)

Identifying atmospheric blocking events using the inflated generator

Aleksandar Badza, Gary Froyland
University of New South Wales

Extreme weather events such as heatwaves are often attributed to atmospheric blocks, which are large quasi-stationary masses of air which (as the name suggests) ‘‘block’’ regular westerly wind flow and result in prolonged extreme weather patterns. In this talk, we demonstrate how to identify these blocks using the inflated generator, a new mathematical operator used to identify quasi-stationary families of almost-invariant sets (which blocks are an example of). We show how these families of sets obtained from the inflated generator are able to illustrate the full spatiotemporal extent of two blocking events responsible for some of the worst heatwaves that occurred during the European summer of 2003, and how this method provides a viable alternative for diagnosing blocking events in comparison to three well-documented and frequently used geophysical block detection proxies. (Back)

A non-separable Hawkes process modelling earthquake frequencies

Boris Baeumer, Conor Kresin, Yifu Tang, Ting Wang
University of Otago

The rate of occurrence of earthquakes of a certain magnitude clearly depends on the time and magnitude (and location) of past earthquakes. Current models for earthquake occurrence rate mainly build in the dependence on time (and location) of past earthquakes and treat the association of rate and magnitude separately. We present a parsimonious model for the occurrence rate by dealing with time and magnitude of earthquakes simultaneously and demonstrate the performance of such model using long-term earthquake records that contain multiple mainshock-aftershock sequences. (Back)

Bifurcations of resonance tongues in a periodically climate model

John Bailie*, Priya Subramanian, Bernd Krauskopf
The University of Auckland

Resonance is a phenomenon encountered in many fields of science when a system is subjected to external forcing or coupling. Generally, these systems have dynamics on a stable invariant torus that may be characterized by the rotation number ρ, given by the ratio of the involved frequencies. For rational values of ρ, the system is said to be in resonance, and the flow on the torus converges to a stable periodic solution. We investigate the overall resonance structure of an invariant torus that exists in a bounded region of a parameter plane.

As a case study, we examine a periodically forced planar model for vertical mixing in the North Atlantic with three bifurcation parameters: a threshold η above which mixing is convective, a virtual salinity flux μ, and amplitude c of the seasonal variation of this flux. For positive forcing $c > 0$, there exists a region of the (μ, c)-plane, bounded by a curve of torus bifurcation, with a two-dimensional stable invariant torus. We develop an algorithm for computing the rotation number with $\rho = \frac{p}{q}$ for q up to 10^4, and in doing so, present classification of the resonance structure in terms of the extrema of the rotation number ρ. (Back)

Topologically steered simulations and the role of geometric constraints in protein knotting

Agnese Barbensi, Alexander R Klotz, Dimos Gkountaroulis
The University of Queensland

We introduce a method to determine the optimal pathway by which a polymer may knot or unknot, while subject to a given set of physics, and we investigate the effect of imposing geometric constraints. We show that with protein-like geometric constraints, the frequency of twist knots increases, similar to the observed abundance of twist knots in protein structures. (Back)

Adapting vaccination strategies for Mpox

Matthew Berry, Raina MacIntyre, Deborah Cromer, Adam Hacker, Miles Davenport, David Khoury
University of New South Wales

During an outbreak of Mpox with limited vaccines available, critical decisions around how to maximise the impact of the available vaccines are critical. Using a simple model for infection, we can evaluate different vaccination strategies and examine which strategies minimise the number of cases. To do this we apply a correlate of protection for Mpox to account for waning of immunity. (Back)

State-dependent delays in feedback loops: insights from an El Niño-Southern Oscillation model

Samuel Bolduc-St-Aubin*, Bernd Krauskopf, Priya Subramanian
University of Auckland

Time-delayed negative feedback processes play crucial roles across various fields of research and are frequently modelled by delay differential equations (DDEs). Typically, these models assume constant delays, yet this is a simplification: real-world delays, such as in climate science, often vary with the state of the system. This makes state dependence of delays an appealing consideration from a modelling perspective. In this work, we examine a DDE model of the El Niño-Southern Oscillation, which drives unpredictable changes in Pacific sea surface temperature and atmospheric conditions. It features an instantaneously switching feedback term with a delay implicitly defined by the state variable. We show that, when the system responds to distinct consecutive events in chronological sequence, this type of state-dependent delay does not alter the system's dynamics compared to a constant delay. This surprising result provides a theoretical justification for what has been observed in this DDE ENSO model with smooth switching. (Back)

Tsunamis generated by a moving N-shaped atmospheric pressure wave

Mitchell Bonham*

The University of Newcastle

Atmospheric pressure waves from a volcanic eruption can generate tsunamis with a speed and reach well beyond waves caused by usual mechanisms (e.g. earthquakes). To model a tsunami generated by a moving atmospheric pressure, a one-dimensional linear wave model incorporating a decaying N-shaped atmospheric pressure wave will be presented. Using a novel numerical method, the wave model is solved for an atmospheric pressure wave representative of the recent Hunga-Tonga Hunga Ha'apai (HTHH) 2022 volcanic eruption. The outcomes of the one-dimensional linear wave model will be compared to the HTHH 2022 tsunami. (Back)

Coral bleaching on the Great Barrier Reef: insights from a mathematical model

Kaitlyn Brown*, Michael Bode

Queensland University of Technology

Coral reefs across the world are at serious risk due to the ongoing effects of mass bleaching incidents that have been observed over the last three decades. The destabilisation of coral reef ecosystem is expected to have catastrophic implications for essential ecosystem services. There is an urgent need to improve our mechanistic understanding of coral bleaching dynamics to inform effective intervention and conservation efforts. We have developed a model of community-scale coral dynamics via a coupled system of nonlinear ordinary differential equations. Coral bleaching is represented as a continuously evolving state of the modelled population and underlying symbioses are captured implicitly. System dynamics analysis was used to validate the conceptual framework and provided valuable insights into the mechanisms driving the resilience and robustness of a reef's bleaching response. Using data observed on the Great Barrier Reef, we parametrised the model and observed multiple correlations providing further insight into the mechanisms of bleaching and inspiring future data collection. (Back)

Heterogeneity in temporally fluctuating environments

Alexander Browning

University of Oxford

Many biological systems regulate phenotypic heterogeneity as a fitness-maximising strategy in uncertain and dynamic environments. Analysis of such strategies is typically confined both to a discrete set of environmental conditions, and to a discrete (often binary) set of phenotypes specialised to each condition. In this talk, we extend on both fronts to encapsulate both a discrete and continuous spectrum of phenotypes arising in response to two broad classes of environmental fluctuations that drive changes in the phenotype-dependent growth rates. We present a series of analytical and semi-analytical results that reveal regimes in which both discrete and continuous phenotypic heterogeneity is evolutionary advantageous. (Back)

Beyond linear elasticity using discrete models of cellular tissues

Pascal R Buenzli
Queensland University of Technology

Biological tissues often involve large deformations and differential creation of new material within the tissue. This makes their mechanical behaviour hard to capture mathematically. Mathematical models based on continuum mechanics usually rely on linear elasticity theory; extending these models to large deformation and to tissue growth is highly nontrivial. In this contribution, we build on recent developments of simple discrete models of mechanical interactions between cells and their continuum limit to derive evolution equation of tissue stress during mechanical relaxation. These nonlinear partial differential equations (PDEs) depend on the restoring force laws assumed for the mechanical behaviour of the cells. These PDEs provide a very good approximation of the discrete models for any deformation. At small deformations, these equations can be linearised to match linear elasticity theory. (Back)

Boundary conditions for multiscale equation-free modelling

Judy Bunder
University of South Australia

Patch dynamics equation-free modelling efficiently simulates on-the-fly macroscale solutions of complex multiscale problems. In simulations, sparse ‘patches’ in space-time are coupled across both space and time to capture the emergent macroscale dynamics. Recently, we developed self-adjoint patch coupling that ensures symmetries of the multiscale problem are preserved in the macroscale simulation. However, this self-adjoint coupling is defined to be identical for each patch and is therefore unable to cope with fixed boundary conditions. Here we present an adaptation of self-adjoint patch coupling suitable for boundary conditions. This adaptation uses reflections about the fixed boundaries to ensure the boundary conditions are correctly applied and the simulation still preserves self-adjointness. (Back)

Mathematical modelling of drug release from functionally-graded delivery systems

Obi Carwood*
Queensland University of Technology

A key challenge in drug delivery within diffusion-based models is accounting for drug molecules that bind to the carrier device and remain unreleased from the capsule. A well-established approach to model this behaviour is the inclusion of a reaction term that irreversibly removes drug concentration without release. Consequently, determining the total fraction of drug released becomes a complex problem that analytical, numerical, and stochastic methods can be implemented to solve. In this work, functionally graded delivery systems are analysed, where diffusion and reaction-rate terms are allowed to vary spatially. The aim is to derive closed-form analytical expressions for the fraction of drug released and validate these expressions through comparisons with numerical and stochastic solutions. (Back)

Mathematical modelling of athletic performance and the optimisation of training load

David Ceddia*
The University of Melbourne

In order to improve at an activity, it is generally agreed upon that it requires practice. How this practice should be structured, however, is not a generally agreed-upon thing. In this talk, I will introduce the topic of mathematically modelling a change in athletic performance in response to a training load. Specifically, I will introduce two prominent athletic performance models from the literature: the Banister et al. (1975) Fitness-Fatigue Impulse Response Model and the Busso (2003) Variable Dose-Response Model. I then ask: given these models of athletic performance, what is the training load that maximises the change in performance over a fixed period?

Ideally, we would expect the optimised training loads derived from these models to align with common training practices of elite athletes, displaying trends such as periodisation and tapering. Such an agreement is not, however, observed. I will then detail potential modifications to an athletic performance model that elicit periodisation and tapering. Additionally, I discuss the possible incorporation of an injury risk model into an athletic performance model as a means of eliciting these training behaviours. (Back)

Space-time evolution of Volterra disinclinations

Pierluigi Cesana, Alfio Grillo, Marco Morandotti, Andrea Pastore
Kyushu University

The dynamics of a system of particles subject to a 4th order potential field modeling the space-time evolution of wedge disclinations is studied, focusing on finite systems of disclinations within a circular domain. Existence theorems for the trajectories of these disclinations are presented, considering both the dynamics without predefined preferred directions of motion in an isotropic medium and the dynamics in which the disclinations move parallel to predefined directions, modeling a crystalline material. The analysis is illustrated with a number of numerical solutions to demonstrate various relevant configurations. `https://arxiv.org/abs/2408.15457` (Back)

Active control of liquid film flows: beyond reduced-dimensional models

Radu Cimpeanu, Oscar A Holroyd, Alexander W Wray, Susana N Gomes
University of Warwick

The ability to robustly and efficiently control the dynamics of nonlinear systems lies at the heart of many current technological challenges, ranging from drug delivery systems to ensuring flight safety. Most such scenarios are too complex to tackle directly, and reduced-dimensional modelling is used in order to create viable mathematical representations of the target systems. This simplified setting allows for the development of rigorous control-theoretical approaches, but the propagation of their effects back up the hierarchy and into real-world systems remains a significant challenge. Using the canonical setup of a liquid film falling down an inclined plane under the action of active controls, we develop a multi-level modelling framework containing both analytical models and direct numerical simulation techniques acting as a cohesive computational platform.

Three separate approaches will be described: 1. a simple yet powerful analytically-informed feedback strategy via blowing/suction (Cimpeanu et al., Nonlinear Dynamics 104, 2021), 2. a linear-quadratic regulation optimal control methodology (Holroyd et al., SIAM J. Appl. Math. 84, 2024), and 3. a model-predictive control loop using electrostatic effects aimed at dripping prevention (Wray et al., Physical Review Fluids 7, 2022). In each case the extended ranges of applicability of the hybrid mechanisms, as well as the detailed effects of the controls in terms of stability and treatment of nonlinearity, are examined in detail. This helps us gain a systematic understanding of the information transfer inside the flows, ultimately informing next-generation interfacial control strategies. (Back)

Quantifying uncertainty in worm egg counts with bulk sampling

Robert Cope
University of New England

Sheep are infected with parasitic worms, such as the Barber’s pole worm. Large burdens of these worms in a mob of sheep can be detrimental, so farmers need to assess the worm burden to inform management decisions. Worm burden is assessed using a faecal worm egg count (WEC) test, and each test has a cost, and so strategies to minimise the number of tests required while providing sufficiently accurate estimates to inform management decisions are of value. In this talk, I will describe the mathematics of WEC tests, and the probability distribution of relevant test outputs under both standard strategies (where each sample is tested separately), and bulk sampling (where samples are combined). Specifically, we are able to obtain expressions for the variance of an estimated mob WEC in terms of the underlying parameters of the worm burden in the mob, and relevant details of the WEC process (including lab-specific parameters, and how the test is applied). These results can directly inform the strategies that farmers and laboratories use when managing sheep. (Back)

Modelling macrophage action: insights from in vivo experiments

Adelle Coster, Mary Myerscough
University of New South Wales

Atherosclerotic plaques are the result of the buildup of fats, cholesterol, and other substances in and on the artery walls. Macrophages serve as central mediators of inflammatory and metabolic signalling within atherosclerotic plaques. Their abundance and activation states dynamically shift during the progression and regression of atherosclerosis. In vivo data of plaque development is hard to obtain − both from an experimental and ethical perspective.

Macrophages play a critical role by ingesting lipids derived from low-density lipoproteins ‘‘bad cholesterol’’) and the membranes of dead and dying cells through a process known as efferocytosis. In a study by Ford et al. (2019, Proc. R. Soc. B), macrophage lipid accumulation was quantified in vitro under conditions where the only source of internalised lipid was efferocytosis.

Here we seek to understand the possible dynamics underlying macrophage lipid accumulation. We present a simple mathematical model to encode the major processes acting, and to replicate features observed in the experimental data. These results provide a foundation for developing more comprehensive models of atherosclerosis. (Back)

Bucky-bowl dimples in graphene

Barry J Cox, Amir Karton, Ngamta Thamwattana
University of South Australia

The Buckminsterfullerene, or bucky-ball (C_{60}), is a well-known molecular structure composed of 60 carbon atoms arranged in a spherical shape, resembling a soccer ball. A related class of molecules, known as bucky-bowls, includes compounds such as corannulene ($C_{20}H_{10}$) and sumanene ($C_{21}H_{12}$). These molecules can be conceptualized as truncated versions of bucky-balls, where the curvature is reduced, and hydrogen atoms are used to stabilize the structure.

When bucky-balls and bucky-bowls interact with graphene, a remarkable phenomenon occurs: the molecules induce a dimple in the graphene sheet. This dimple is driven by van der Waals forces, which cause a deformation in the otherwise flat graphene structure. The resulting change in geometry is not merely aesthetic; it significantly impacts the chemical and electrical properties of graphene. These changes present exciting possibilities for the development of nano-electro-mechanical devices, where such deformations can be harnessed for novel applications.

In this talk, we will present a variational model designed to predict the characteristics of these graphene dimples induced by bucky-bowls and bucky-balls. We will also introduce a numerical approach that can be applied to a broad range of similar axisymmetric systems, demonstrating its potential for exploring other types of molecular-graphene interactions and complex nanostructures. (Back)

Modeling ranibizumab pharmacokinetics/pharmacodynamics in wet AMD: insights into VEGF suppression and drug retention through hierarchical Bayesian inference

Jessica Crawshaw, Antonello Caruso, Michael Gertz, David Augustin, Philip Maini, Eamonn Gaffney
Queensland University of Technology

Wet age-related macular degeneration (AMD) is a disease which slowly destroys ones' central vision, with a huge impact on quality of life. It is the leading cause of central blindness worldwide. Wet AMD is characterised by neovascularisation, triggered by an unhealthy abundance of vascular endothelial growth factor (VEGF). These newly formed capillaries allow fluids to seep into the retina, damaging the local photoreceptors (critical light sensing cells). Currently, there is no definitive cure for wet AMD. As such, intraocular injections of anti-angiogenic drugs to reduce the abundance of retinal VEGF is the clinical gold standard for disease management, slowing the progression of vision loss. However, injections into the eye are unpleasant, and the fluid dynamics within the eye leads to relatively rapid drug elimination, resulting in the need for regular intraocular injections.

In this talk, we will present and analyse a pharmacokinetic/pharmacodynamic (PK/PD) model of a standard-of-care antibody, ranibizumab, targeting VEGF. This model has been developed to improve our understanding of the ocular pharmacology of ranibizumab, and to provide a robust understanding of ranibizumab retention in the eye. Results from this PK/PD model are compared to published animal (cynomolgus monkey) and human data. We present a hierarchical Bayesian inference strategy to determine relevant parameter distributions. Using this strategy, we provide an insight into the clinically observed inter-patient variability in VEGF suppression and drug retention. Finally, this model establishes the initial basis for a computational framework we are developing to mathematically compare the ocular PK/PD of ranibizumab with novel therapeutic strategies and other clinical anti-VEGF drugs in the treatment of AMD. (Back)

Bayesian approaches to characterising the accuracy of diagnostic tests for Buruli Ulcer

Richard Creswell, Ben Lambert, Astrid C Erber
The University of Melbourne

Buruli Ulcer (BU) disease, caused by infection of the skin with Mycobacterium ulcerans, is a neglected tropical disease present in some regions of Asia, Australia, Africa, and South America. Early treatment is important for optimal patient outcomes, but symptoms of early stage disease are somewhat nonspecific, motivating the development and deployment of disease testing strategies. Although PCR testing for BU is known to provide high diagnostic accuracy, the extensive technical requirements of PCR (e.g., thermal cycling) may be unavailable or impractical in regions where BU is prevalent. The loop mediated isothermal amplification (LAMP) test has emerged as a more practical alternative, and a multitude of experiments have been performed in which patients are simultaneously subjected to both a PCR and LAMP test for BU. In the present study, we use these data to assess the accuracy of the LAMP test for BU by inferring both experiment-specific and global estimates of LAMP sensitivity and specificity. We develop and implement Bayesian hierarchical approaches which share information across experiments, while accommodating for heterogeneity. We demonstrate both the utility of Bayesian hierarchical approaches in improving the precision of parameter estimates and discovering structure in complex data, as well as pitfalls arising from limited quantities of data or unintentionally informative prior distributions. Further fields of computational biological data analysis where we believe similar considerations relating to Bayesian hierarchical methods are applicable are also briefly discussed. (Back)

Clone wars: modelling tumour resistance in CAR-T cell therapy

Thomas Cummings, **Yang Zhao**
The University of Melbourne

Chimeric antigen receptor (CAR)-T cell therapy is a revolutionary immunotherapy that engineers T cells to target cancer cells more effectively, and has shown significant efficacy in blood cancers. Despite its success, variability in patient responses and the emergence of tumour resistance are not well understood. Clonal tracing data from mouse experiments show that the clonal composition of a relapsed tumour changes sharply as the initial CAR-T dosage is increased. This is reminiscent of bistability in dynamical systems.

Compartment modelling provides a framework for exploring different hypotheses of resistance development. By treating sensitive and resistant tumour cells as separate compartments, we investigate the possible long-term resistance patterns. Under simplifying assumptions, we analytically determine the stability of certain steady states to evaluate their biological viability. This allows us to hypothesise parameter regimes that support observations of bistability.

In reality, the observed switch-like behaviour may not necessarily be explained by bistability, but the extinction of certain clones at small cell numbers, which cannot be adequately described by deterministic continuous-state models. A preliminary investigation reveals that the switch-like behaviour can be reconstructed by considering a population to be extinct when its size drops below a threshold. (Back)

Capillary levelling of thin liquid films of power-law rheology

Michael Dallaston
Queensland University of Technology

The levelling of a perturbed thin liquid film due to surface tension can be used to measure the viscosity of fluids at low shear rates. We show how the modelling of the dynamics of such films extends to the case of power-law fluids, which presents mathematical challenges due to the non-analyticity of the power-law model at zero shear. We examine the distinct dynamics of both periodic and localised disturbances, and show via numerical simulations how a general initial condition will evolve toward the appropriate universal (self-similar) solution in each case. (Back)

Oscillatory instability of localised spot pattern in the Schnakenberg reaction−diffusion system in defected 3D domains

Siwen Deng*, Shuangquan Xie, Justin Tzou
Macquarie University

In a bounded 3D domain, we analyze the translational and amplitude oscillatory instabilities of a localized one-spot pattern in a two-component RD system. For the translational instability, stability is dictated by a 3×3 nonlinear matrix eigenvalue problem, where the matrix entries are derived from a Green's function reflecting the domain's geometry. The most unstable eigenvalue sets the oscillation frequency at onset, while the corresponding eigenvector determines the oscillation mode. We explore how localized defected domain and perturbed spherical domain influence this instability.

For the amplitude instability, we study the Hopf bifurcation (HB) threshold's dependence on the feed rate A. When $A < A_\varepsilon$ with $A_\varepsilon > 13.56$ (a saddle point tied to ε), τ_H is $O(1)$ and a hybrid asymptotic-numerical method is applied to obtain the threshold. When $13.56 \leq A < A_\varepsilon$, two distinct HB thresholds exist. No bifurcation occurs for $A > A_\varepsilon$ in the $\tau = O(1)$ regime. For $A > 13.56$, the HB threshold $\tau_H = O(\varepsilon^{-3})$ depends on the inner eigenvalue problem spectrum. Thus, three HB thresholds appear when $13.56 \leq A < A_\varepsilon$: two at$O(1)$ and one at$O(\varepsilon^{-3})$. We show that there is no intermediate regime between $O(1)$ and$O(\varepsilon^{-3})$. Full numerical solutions of the 3D Schnakenberg PDE validate these results. (Back)

Bacterial encounter rates and residence times in microbial symbiosis

Rodney Dharma*
The University of Melbourne

Microbial symbiosis is highly prevalent in microecology, and can be found in marine and aquatic environments, as well as soil and groundwater. Despite its ubiquity, there are still many outstanding questions on the role that microbial behaviours, such as chemotaxis (ability for microorganisms to navigate towards or away from chemical gradients) and motility (ability to make directed motion) play in shaping these interactions. Recent developments showed that chemotaxis enhances metabolic exchange between motile marine bacteria and non-motile picophytoplankton cells. This marks a shifting paradigm on what is known to be possible, as bacterial chemotaxis towards such small targets was traditionally thought to be impossible. Cell-cell interactions between co-moving chemotactic bacteria remain overlooked with many studies assuming a well-mixed continuum/bulk approximation. Using agent-based modelling, we simulate metabolic exchanges between two microbial species in a spatially heterogeneous environment, and in doing so, (1) resolve the encounter rates between two mutualistic bacterial populations and (2) quantify the total time a bacterium can spend within close vicinity of its targets. Our modelling indicates that chemotaxis enhances metabolite exchanges between co-moving cells by increasing the frequency and duration of fleeting interactions between targets, and that larger targets enable bacterial colonisation, resulting in longer-lasting interactions. Moreover, by enabling mutual chemotaxis and simulating bacterial cross-feeding, we observe the onset of strong bacterial aggregation, even for low exudation rates and hence smaller targets. (Back)

Should public health policy exempt cases with low viral load from isolation during an epidemic?: a modelling study

Jiahao Diao, Rebecca H Chisholm, Nicholas Geard, James M McCaw
The University of Melbourne

As demonstrated during the COVID-19 pandemic, non-pharmaceutical interventions, such as case isolation, are an important element of pandemic response. The overall impact of case isolation on epidemic dynamics depends on a number of factors, including the timing of isolation relative to the onset of contagiousness for each individual instructed to isolate by public health authorities. While there is an extensive literature examining the importance of minimising the delay from exposure to direction to isolate in determining the impact of case isolation policy, less is known about how underlying epidemic dynamics may also contribute to that impact. In particular, empirical observation, and modelling studies, have shown that as an epidemic progresses, the distribution of viral loads among cases systematically changes. In principle, this may allow for more targeted and efficient isolation strategies to be implemented. Here, we developed a multi-scale agent-based model to investigate the potential for isolation strategies that account for cases viral loads to be incorporated into policy. We compare the impact and efficiency of alternative strategies in which all cases, regardless of their viral load, are required to isolate and strategies in which some cases may be exempt from isolation. Our findings show that, following the epidemic peak, the vast majority of cases identified with a low viral load are in the declining phase of their infection and so contribute little to overall contagiousness. This naturally prompts the question as to the potential public health value of discontinuing isolation for such individuals. Our numerical investigation of this ‘adaptive’ strategy shows that exempting individuals with low viral loads from isolation following the epidemic peak leads to a modest increase in new infections. Surprisingly, it also leads to a drop in efficiency, as measured by the average number of infections averted per isolated case. Our findings therefore suggest caution in adopting flexible or adaptive isolation policies. Our multi-scale modelling framework is sufficiently flexible to enable extensive numerical evaluation of more complex isolation strategies, incorporating more disease-specific biological and epidemiological features, supporting the development and evaluation of future public health pandemic response plans. (Back)

Analysing dynamics near heteroclinic networks with a projected map

David C Groothuizen Dijkema*, Vivien Kirk, Claire M Postlethwaite
University of Auckland

A heteroclinic cycle is a particular solution structure found in dynamical systems, typically composed of a collection of saddle equilibria and heteroclinic orbits connecting them in a cyclic manner. Trajectories near an attracting heteroclinic cycle visit all saddles in order, spending increasingly long periods of time near each saddle before making a rapid switch to the next one. Systems with heteroclinic cycles can be used to model intransitive interactions and intermittent phenomena.

A heteroclinic network is a connected union of heteroclinic cycles. Trajectories near a heteroclinic network can exhibit complex dynamics. They may be attracted to one cycle within the network, possibly visiting a finite number of other cycles first, or they may be attracted to a larger subset of cycles of the network, visiting them in regular or irregular sequences. Regions of parameter space associated with the different asymptotic behaviour can form highly intricate patterns, including Farey-like concatenation.

This talk will discuss how a particular piecewise-smooth map can be used to investigate the complex dynamics near heteroclinic networks. (Back)

Modelling the Bray−Liebhafsky oscillating reaction

Heath Dimsey*
University of Tasmania

Oscillating chemical reactions often show colour-changing temporal oscillations when stirred and form spatial patterns when left to self-diffuse. However, the Bray-Liebhafsky reaction − one of the first oscillating chemical reactions discovered − does not produce visible changes while it oscillates. This difficulty has meant that the potential for the Bray-Liebhafsky reaction to form spatial patterns has remained largely unexplored.

We will investigate several methods to predict the temporal and spatial behaviour observed in this reaction. We suggest a novel mathematical model for the kinetic behaviour. We incorporate a spatial dimension into the system which enables prediction of one- and two-dimensional spatial patterns within cylindrical and rectangular dishes. We discuss the range and stability of the various patterns that may form. (Back)

Invariant manifolds and wild chaos

Sam Doak*, Hinke Osinga, Bernd Krauskopf
The University of Auckland

Wild chaos is a type of robust higher-dimensional chaotic dynamics. One of its defining characteristics is the presence of robust heterodimensional cycles, which include non-transverse intersections between stable and unstable manifolds. The persistence of non-transverse intersections is counter-intuitive: for example, such behaviour in three dimensions necessitates robust intersections between two one-dimensional manifolds. Consequently, such curves must ‘behave’ as if they were a surface, facilitating robust intersections with other one-dimensional manifolds.

We focus on a promising potential candidate for a discrete-time dynamical system exhibiting wild chaos, of which there are very few explicit examples. The defining diffeomorphism has dimension three, is volume preserving, and is quadratic with quadratic inverse. We illustrate the emergence of wild chaos in this system by first considering the one-dimensional manifolds of its two fixed points. Indeed, these curves appear to have ‘surface-like’ properties. We show that each fixed point lies in a different hyperbolic set, distinguished by the dimensions of their unstable manifolds. Moreover, the one-dimensional manifolds of these hyperbolic sets intersect to give rise to robust heterodimensional cycles. We also discuss how these manifolds disentangle from each other as a parameter is varied, thereby highlighting specific changes in the manifold geometry that could represent a mechanism to produce wild chaos. (Back)

Insights into the natural obstacles that slow early HIV spread based on analysis of Simian Immunodeficiency Virus experiments

Steffen S Docken, Agatha Macairan, Timothy E Schlub, Christine M Fennessey, Taina T Immonen,
Deborah Cromer, Brandon F Keele, Miles P Davenport
UNSW Sydney

Immediately following HIV transmission, there is an extended period of low infected cell count, during which, the virus may be more vulnerable to clearance via the immune system. A better understanding of the obstacles inhibiting viral expansion may provide insight into how to therapeutically harness the immune system to more effectively clear HIV early after exposure.

To examine the relative magnitude of various viral obstacles, we use a barcoded Simian Immunodeficiency Virus (SIV) animal model of HIV infection, which allows the simultaneous tracking of multiple lineages within an animal or in vitro culture. We posit that each obstacle results in a stochastic delay to when the virus overcomes said obstacle, and indeed, within a week of infection of rhesus macaques, we see wide heterogeneity in lineage sizes (up to 10^5-fold differences), indicative of stochastic delays in early viral spread. By comparison to the heterogeneity in viral production by single cells, we estimate the relative contribution to the cumulative early infection obstacle by variability in viral production of the first infected cell (23%) vs. variability in the conduciveness to viral replication of the first site of infection (77%). These estimates are based on variance of log-lineage size (lineage sizes are lognormally distributed) in rhesus macaques ($1.25\,(\log_{10}\text{copies})^2$) and viral production by individual cells taken from a rhesus macaque $0.31\,(\log_{10}\text{copies})^2$). We further dissect the obstacle caused by the first infected cell into the portion driven by cellular phenotype and inherent stochasticity of cellular infection (11% and 12% of the cumulative obstacle, respectively), based on viral production by a cell line ($0.17\,(\log_{10}\text{copies})^2$), which expresses a more uniform phenotype than macaque cells. Further work is needed to characterize the anatomical, cellular, and viral properties that drive these obstacles. Additionally, the quantifications presented here are based on persistent lineages, but it would be interesting to examine the impact these early obstacles have on extinction probability. (Back)

Investigating zooplankton abundance using a seasonally forced model

Celia Dowling*
The University of Melbourne

Rising sea-surface temperatures are causing spatial and temporal changes in the distribution of zooplankton in our oceans. This complicates foraging for higher-trophic species who feed primarily on zooplankton. Therefore, understanding the impact of temperature on planktonic dynamics is of great import to wildlife conservationists and researchers. The Nutrient-Phytoplankton-Zooplankton (NPZ) model is a type of population-level continuum model that has been used for decades to model the relationship between nutrients entrained from deep nutrient-rich waters, phytoplankton biomass, and zooplankton concentrations in the well-mixed layer of the ocean. However there are few NPZ-type models that have been extended to take into account seasonal changes in the mixed-layer depth, the stratification of water columns due to heat, and ocean dynamics, and can undergo dynamics and stability analysis. In this talk, I extend Edwards and Brindley's 1996 NPZ model to include dependence on a seasonally changing mixed-layer depth and heat-induced vertical stratification. I detail how the mixed layer depth and proxy for quantifying the impact of stratification can be computed from temperature-depth profiles made accessible by the Environmental Research Division's Data Access Program (ERDAPP). To accurately represent the ocean, I add ocean current dynamics (via advection and diffusion) to the model. I parameterise and solve the resulting rectangular mesh of partial differential equations for a case study in the North Atlantic Ocean near the Canary Islands archipelago. Summer phytoplankton blooms assisted by strong eddies and autumnal phytoplankton blooms induced by severe vertical stratification of the water columns are recovered by my constructed model, qualitatively matching the dynamics of the Canary Island region. (Back)

Viral kinetics of H5N1 infections in dairy cows

Oliver Eales, James McCaw, Freya Shearer
The University of Melbourne

Since early-2024 unprecedented outbreaks of highly pathogenic avian influenza H5N1 clade 2.3.4.4b have been ongoing in dairy cows in the United States with significant consequences for the dairy industry and public health. Understanding of key epidemiological parameters is required to support outbreak response, including predicting the likely effectiveness of interventions and testing strategies. Here we pool limited publicly available data from three studies of naturally and experimentally infected dairy cows. We use Bayesian statistical models to quantify Ct value trajectories of infected dairy cows and the relationship between Ct value and the log-titre of infectious virus, a proxy for infectiousness. We estimate that following infection peak Ct values are rapidly reached within 1−2 days with a population mean Ct value of 17.0 (13.6, 20.3). We identify a critical threshold Ct value of 21.5 (20.2, 23.4), with values of Ct value above this threshold representing little-to-no infectious viral load. Finally, we estimate the distribution of the duration of infectiousness for dairy cows (i.e. the duration their Ct value remains above the critical threshold) with a population mean of 6.3 (2.9, 12.6) days. (Back)

Modelling, analysis and finite element simulations of kinematically incompatible von Kármán plates

Edoardo Fabbrini*, Pierluigi Cesana, Andrés A León Baldelli
Kyushu University

In the first part of the talk, I investigate the existence and regularity of solutions for kinematically incompatible von Kármán thin plates. The mathematical model consists of two coupled, nonlinear, fourth-order elliptic partial differential equations. The kinematic incompatibility arises from the presence of Volterra wedge disclinations in the crystalline lattice and enters the mathematical formulation as a discrete distribution of Dirac delta measures. The existence of solutions is established using the direct method in the calculus of variations, following a similar approach to Ciarlet's proof for kinematically compatible plates. The regularity of solutions is demonstrated under additional assumptions regarding the regularity of the plate boundary and the external load. In the second part of the talk, I introduce a C0-Discontinuous Galerkin formulation for the numerical solution of the von Kármán plate problem. I then identify the relevant nondimensional parameters and conduct numerical experiments by varying these parameters in appropriate ranges. A direct application of this study is in the continuum modeling of graphene sheets with wedge disclinations in the crystal lattice. (Back)

Modelling interclonal cooperation in epithelial carcinogenesis using a vertex-based approach

Muhammad Asim Farooq*
The University of Sydney

This study uses a vertex-based computational model based on CHASTE to investigate interclonal cooperation within cell populations. We analyze interactions between mutated cell types with distinct hyperproliferative and invasive properties. Modeling the cooperative dynamics between these clones shows how cellular heterogeneity affects tissue growth and invasion, enhancing the understanding of tumor progression and therapeutic target predictions. (Back)

Deterministic and stochastic modelling of anisotropic diffusion with a focus on the central nervous system

Luke Filippini*, Adrianne Jenner, Elliot Carr
Queensland University of Technology

Neurological diseases and disorders are the subject of an extensive area of research that is of significant importance to the scientific community and wider population. Notable examples include autism, multiple sclerosis, and nervous system cancers, such as glioblastoma, which currently remain incurable. This is primarily due to the structural complexity of the nervous system and the impracticalities of surgical examination and/or resection. Hence, indirect methods, such as magnetic resonance imaging and mathematical modelling, are frequently relied upon to yield meaningful insight into the physiological processes that drive disease progression.

In this talk, we discuss both deterministic and stochastic approaches for modelling anisotropic particle diffusion on a lattice, motivated by potential applications to neurological diseases and disorders. Here, we consider anisotropic diffusion informed by a single diffusion tensor. In particular, the stochastic framework is derived from a numerical discretisation of the diffusion equation obtained using the finite volume method (FVM). We discuss the limitations of using a traditional square or rectangular lattice, in terms of obtaining strictly positive jump probabilities, and present a more promising approach using a hexagonal lattice. Most notably, the latter approach yields a valid stochastic framework for any reasonable diffusion tensor, as opposed to the former approach, which remains valid only for a restricted range of diffusion tensors. (Back)

A spatial multiscale mathematical model of malaria transmission

Jennifer A Flegg, Shoshana Elgart, Somya Mehra, Mark B Flegg
The University of Melbourne

The epidemiological behavior of *Plasmodium vivax* malaria occurs across spatial scales including within-host, population, and metapopulation levels. On the within-host scale, *P. vivax* sporozoites inoculated in a host may form latent hypnozoites, the activation of which drives secondary infections and accounts for a large proportion of *P. vivax* illness; on the metapopulation level, the coupled human-vector dynamics characteristic of the population level are further complicated by the migration of human populations across patches with different malaria forces of (re-)infection. To explore the interplay of all three scales in a single two-patch model of *Plasmodium vivax* dynamics, we construct and study a system of eight integro-differential equations with periodic forcing (arising from the single-frequency sinusoidal movement of a human sub-population). Under the numerically-informed ansatz that the limiting solutions to the system are closely bounded by sinusoidal ones for certain regions of parameter space, we derive a single nonlinear equation from which all approximate limiting solutions may be drawn, and devise necessary and sufficient conditions for the equation to have only a disease-free solution. Our results illustrate the impact of movement on *P. vivax* transmission and suggest a need to focus vector control efforts on forest mosquito populations. The three-scale model introduced here provides a more comprehensive framework for studying the clinical, behavioral, and geographical factors underlying *P. vivax* malaria endemicity. (Back)

Population balance modelling of polydisperse primary particles in the flocculation of minerals tailings

Brendan Florio
Murdoch University

Polymer flocculants are used to encourage the aggregation of solid particles such that they settle at the bottom of gravity ‘‘thickeners’’ to separate wase solids and liquids in the minerals industry. Population-balance models are used to describe the aggregation process and predict behaviour under various scenarios. Traditional models have poor predictive power when the primary particles have polydisperse size distribution, due to their assumption that all aggregates of the same mass have the same settling and collision properties. In this talk, we will present a novel method which accounts for both the mass and composition of fractal-like aggregates to better capture the complex behaviour of gravity thickeners, where polydisperse inputs are typical. (Back)

Inferring reaction networks from dynamics

Yong See Foo*, Adriana Zanca, Jennifer Flegg, Ivo Siekmann
The University of Melbourne

Reaction network inference aims to identify, from observing system dynamics, the unknown interactions between species of the system. This is evidently an important problem for understanding biochemical systems, though the approach is also applicable to epidemiological and ecological settings. Many reaction network inference methods involve fitting a model built from a large library of candidate reactions to data. In this talk, we will demonstrate how model construction can be easily automated with the Julia package `Catalyst.jl`. However, the problem of reaction network inference can be confounded by *dynamically equivalent* networks, i.e. structurally distinct networks that can produce the same dynamics. This symmetry can be broken by penalising model complexity, encouraging the model fit to return parsimonious networks. Unfortunately, it is not straightforward to design a penalty term that appropriately addresses issues of spurious false positives, local minima in reaction space, and hyperparameter selection. We will demonstrate why L_1 regularisation (which is standard in classical regression) is inadequate for reaction network inference and explore other promising alternatives. (Back)

Mathematical fireworks

Larry K Forbes
University of Tasmania

The pyrotechnics industry is now a big business, and it includes fireworks for festive occasions (such as New Year's Eve) and various military applications. Typically, what is wanted is first a loud bang, followed by bright coloured lights, and occasionally a stroboscopic display. Designing fireworks that will produce these effects is not at all easy, and a lot of research has been carried out in this field. Safety concerns are often paramount, as a result of both the explosion itself and the possible toxicity of some of the reagents. In addition, measurements are often not practical in such a hostile environment. This talk looks at a very simple model of these pyrolytic reactions, proposed recently by some Russian authors. We will present a reasonably straightforward analysis of this model, which nevertheless reveals surprising behaviour. The system can have multiple steady states and large-amplitude oscillations in time. In addition, the system can exhibit ‘‘tipping points’’ which separate the basins of attraction of very different behaviour types. The mathematics underlying these events is fairly simple to explain, but in a laboratory they could appear random or unstable, and could be hazardous. (Back)

Modelling the evolution of ecologically scaffolded lifecycles

Daniel Fraterman*, Edward F Green, Andrew J Black
The University of Adelaide

In order to understanding the evolution of multicellular organisms, we first require that the organisms themselves are capable of evolution. We consider stochastic models in which the environment plays a role in scaffolding a primitive lifecycle for a cluster of cells. This lifecycle ensures that the cluster produces similar offspring, allowing for evolution by natural selection to occur on the group level. By creating deterministic approximations to our model and employing an adaptive dynamics approach, we study the evolution of the traits of these cell clusters. This allows us to find and consequently understand the factors that dictate the optimal lifecycle for the current environment. (Back)

Emergence of quasi-stationary families of almost-invariant sets in convective fluids (including the atmosphere)

Gary Froyland, Aleks Badza
UNSW Sydney

Macroscopic features of dynamical systems such as almost-invariant sets and coherent sets provide crucial high-level information on how the dynamics organises phase space. I will introduce a numerical method to identify the emergence and disappearance of time-parameterised families of almost-invariant sets in time-dependent dynamical systems. Using this spectral approach I will diagnose the onset and decay of atmospheric blocking events from wind velocity data and identify the formation and collapse of turbulent superstructures in Rayleigh-Benard convection. (Back)

Mathematical modelling of dendritic cell clustering for improved T-cell activation

Domenic PJ Germano, Federico Frascoli, Robyn Araujo, Peter Kim
The University of Sydney

Understanding the dynamics of the immune system in response to cancer remains an open challenge. For example, T-cells are known to play a crucial role in identifying and removing cancers, although the particular mechanisms that regulate T-cell activation and response quality are not known. Recent evidence suggests that both homotypic and heterotypic dendritic cell (DC) clustering in the lymphatic system can enhance the T-cell response. Heterotypic DC clusters are also associated with elevated PDL1 expression, which raises the hypothesis that DC clusters may optimize T-cell quality over quantity.

In this work, we present a mathematical framework to investigate this interplay between DC clustering and T-cell activation. The model incorporates T-cell taxis driven migration, antigen accumulation via D-T-cell interaction, and DC local clustering. Due to their comparatively slow migration, DCs are modelled as stationary cells, while the T-cells undergo a biased random walk. By simulating how DC clustering can improve T-cell activation, we are able to demonstrate that a robust immune response can emerge.

This mechanistic framework provides insights into the balance between T-cell quantity and quality of an immune response. It also offers a platform for hypothesis testing to optimise immunotherapy strategies and pathways. (Back)

Modelling the rise of the adjunct population in colleges

Liam Gibson*, Alex James
The University of Canterbury

The college system in America is a complex ecosystem of hierarchy, competition, and the promise of social mobility. Over the last few decades, a new type of academic has arisen in this ecosystem: the adjunct. Those employed on short fixed-term teaching and instructional contracts. We apply mathematical models from population dynamics and ecology to study this ecosystem. Is this system stable? Is there a unique fixed point or multiple attractors? This research has implications for the social science theory and institutional policy. (Back)

Lyapunov−Oseledets spectrum for random metastable maps

Cecilia González-Tokman
The University of Queensland

We discuss recent advancements in the analysis of the Lyapunov-Oseledets spectrum of transfer operator cocycles associated to random metastable maps. These findings provide detailed insights into the random (and stationary) physical measures of these systems and yield asymptotic estimates for the rates of correlation decay. (Based on joint works with Joshua Peters and Anthony Quas.) (Back)

Wood you believe it? A model for simulating moisture migration and swelling in engineered wood products

Patrick Grant*, Ian Turner, Steven Psaltis, Maryam Shirmohammadi
Queensland University of Technology

Wood and sawn timber have been used in construction for millennia, but the dimensions of the sawn boards limited traditional building sizes. Modern glue-lamination techniques have revolutionised the building and construction industry, enabling the creation of large-scale engineered wood products (EWPs) that far exceed the size of the original timber. This advancement allows for the construction of mid- to high-rise mass timber buildings; a good example is the mass timber office building known as '25 King' in Brisbane. This research focuses on cross-laminated timber (CLT) EWPs, which are significantly lighter and offer comparable strength characteristics to their steel and concrete counterparts. CLT panels are composed of layers of timber boards with alternating longitudinal grain direction, and a glue line separates each layer. Timber swells as it takes on moisture, which can cause internal stresses within the timber. In an EWP, moisture migration can induce a shear stress along the glue line, particularly if one board is wet and swelling while the other board remains dry. This shear stress can result in delamination of the glue line, which is classified as a severe structural failure.

To model these highly nonlinear moisture ingress and swelling processes, we first generate a virtual representation of the EWP and then employ a two-equation variant of the well-established TransPore model to simulate the moisture migration and heat transfer within the EWP. The resulting three-dimensional computational model uses a vertex-centred finite volume method spatial discretisation scheme to produce a large system of stiff ordinary differential equations (ODEs). The resulting system of ODEs is solved numerically using the exponential Euler method implemented in a Jacobian-free Krylov subspace framework with variable stepsize controlled via local error estimation. The glue line in the EWP is treated as an imperfect contact boundary condition with an experimentally calibrated interfacial transfer coefficient. Lastly, the moisture fields are passed to the ABAQUS FEA software to compute the swelling stresses and strains in a post-processing procedure where experimental data is used to calibrate the moisture-dependent swelling coefficients. Moreover, the flexibility in the model allows for varying climatic conditions to be accounted for, ranging from the hot and humid conditions in north Queensland to the cold and dry conditions in South Australia. The model parameters have been fitted using experimentally determined moisture ingress data to enhance the predictive capability of the overall computational approach. (Back)

Exploring Akt dynamics: modelling spatial and temporal regulation

Catheryn Gray
University of New South Wales

Correct spatial and temporal localisation is crucial for any cellular signalling component. In the mammalian insulin signalling pathway, the activation of Akt/PKB functions as a pivotal, low-threshold switch that is critical for glucose uptake. However, detailed data regarding its cellular location and phosphorylation state remains sparse.

In this talk, a mean-field model that encapsulates current experimental insights into Akt signalling dynamics is presented. The model operates on two distinct timescales−signalling and physical transport−wherein the transportation of Akt often represents the rate-limiting step.

The outputs of the model are consistent with the observed steady-state behaviour of the underlying biological system, and also exhibit the transient overshoot behaviour which is a necessary characteristic of the activation of Akt. (Back)

Entropic learning enables skilful forecasts of ENSO phase at up to two years lead time

Michael Groom, Davide Bassetti, Illia Horenko, Terence O'Kane
CSIRO

This paper builds on previous work in applying the entropy-optimal Sparse Probabilistic Approximation (eSPA) machine learning algorithm to the task of classifying the phase of ENSO, as determined by the Niño3.4 index (Groom et al., *Artif. Intell. Earth Syst.*, 2024). In this study, only observations and reanalyses from the satellite era are employed when training and validating the entropic learning models, and a full set of hindcasts are performed over the period from 2012 to 2022 (with a maximum lead time of 24 months) in order to determine out-of-sample skill. The features used for prediction are the leading principal components from a delay-embedded EOF analysis of global sea surface temperature, the vertical derivative of temperature at the equator and the zonal and meridional wind stresses in the tropical Pacific.

Despite the limited number of data instances available for training (ranging from 350 monthly averages for the earliest hindcast to 520 as of December 2024), eSPA is shown to avoid overfitting in this small data regime and produces categorical forecasts with comparable skill to the combined (model-based) probabilistic forecasts produced from the International Research Institute for Climate and Society (IRI) ENSO prediction plume. At lead times longer than those available from the IRI plume, eSPA maintains skill out to 15 months in terms of the ranked probability skill score and 24 months in terms of the area under the Reciever Operating Characteristic curve, all at a small fraction of the computational cost of running a dynamical ensemble prediction system. Furthermore, eSPA is shown to successfully forecast the 2015/16 and 2018/19 El Niño events at 24 months lead time, the 2016/17, 2018/19 and 2020/21 La Niña events at 24 months lead time and the 2021/22 and 2022/23 La Niña events at 14 and 12 months lead time. (Back)

Optimal call allocation policy for call centres

Hritika Gupta*
The University of Melbourne

We aim to solve a continuous time Markov decision process in order to find optimal call allocation policy for call centres in finite time horizon with skills-based routing. To achieve this, we use several approximation models involving Approximate Value Iteration and Forward Pass Algorithms. We draw a comparison of these models and the set of threshold policies using simulations and demonstrate how to calculate the transient waiting time distributions of customers for the threshold policies. This method could be employed by call centres to meet targets set by clients in terms of the proportion of calls that are answered within a specified time. (Back)

Nonlinear backward diffusion and regularisation options

Bronwyn Hajek, Tom Miller, Alex Tam, Ian Lizarraga, Robby Marangell, Martin Wechselberger
University of South Australia

Nonlinear reaction-diffusion equations are used widely to model many different systems and processes, particularly in biology. In particular, backward diffusion, where the nonlinear diffusivity is negative for some regions, is sometimes used to model aggregation and can produce sharp travelling fronts and shocks in the solution. In this talk, I'll discuss various regularisation options, the choice of which impacts both the shock length and its speed. Geometric singular perturbation theory (GSPT) can be used to show that a new shock selection rule is equivalent to both a nonlinear regularisation and a composite regularisation, and to predict the correct travelling wave speed. (Back)

Collective action: cell fate control in space and time

Lucy Ham
The University of Melbourne

Cellular systems exhibit remarkable multistability, enabling genetically identical cells to adopt diverse states across time and space. This talk explores the principles underlying cell fate decisions, focusing on how cell-to-cell communication and spatial gene regulatory networks can govern multicellular organisation. Using stochastic models, we show how feedback loops and paracrine signalling drive transitions from ephemeral to stable cell states. We provide insights into the role of noise control strategies and phase transitions in enhancing system stability, offering a framework to understand the fundamental limits of phenotypic emergence in multicellular organisms. Specifically, we demonstrate that the spatial spread of phenotypic regions is constrained by a cubic-root scaling law, highlighting a trade-off between signalling robustness and spatial precision. This highlights the delicate balance required during development to maintain tissue structure and informs the design of robust synthetic systems with precise control over cell fate. (Back)

Game theoretic decision making in service systems

Ashley Hanson*
The University of Melbourne

This research originates from a paper written by Knight, Komenda and Griffiths, which studied the interaction between a system of two intensive care units (ICUs) in a game theoretic setting. In this project, we extend the model proposed in their paper to consider multiple ICUs. Whilst the study of ICUs is an application of our model, the proposed model is designed for a more general setting where there are multiple facilities. In each facility, customers are served by parallel servers. An arriving customer is either assigned to a facility or is rejected from entering the system. (Back)

Estimating real-time epidemic trends from multiple streams of surveillance data

Tianxiao Hao, Saras M Windecker, Katherine L Senior, James M McCaw, Freya M Shearer,
Gerard E Ryan, Nick Golding
The Kids Research Institute Australia

Accurately assessing the real-time epidemic growth or decline is important to managing infectious diseases. This is not straightforward, as new infections take time to become reported in disease surveillance systems, and not all infections are reported. This means our picture of epidemic trends is time-lagged and confounded by reporting trends. The time-varying rates at which infections become reported are particularly difficult to estimate, and they differ across surveillance data streams, e.g., infections become cases or hospital admissions at different rates. We propose a statistical model for estimating epidemic trends from multiple streams of surveillance data, while accounting for stream-specific imperfect reporting rates. We model the numbers of daily new infections using a non-parametric function of time. We then model the expected observed data streams arising from such infections using forward convolutions representing reporting delays, and stream-specific reporting rates. Leveraging the joint inference on infection numbers from different surveillance data streams, we fit the model to data and simultaneously estimate infection numbers and the reporting rates. Using a simulated respiratory epidemic and the resulting simulated surveillance data, we demonstrate the fitting and validation of the model, implemented in R using Hamiltonian Monte Carlo. We also showcase features of the model and its R implementation useful in practical real-time or near-real-time data analysis settings. (Back)

Optimisation of locally advanced MSI-H/dMMR colorectal cancer treatment with neoadjuvant pembrolizumab using data-driven delay integro-differential equations

Georgio Hawi*, Peter S Kim, Peter P Lee
The University of Sydney

Colorectal cancer (CRC) poses a major public health challenge due to its increasing prevalence, particularly among younger populations, with it being the third most commonly diagnosed cancer and the second leading cause of cancer-related deaths worldwide as of 2024. Microsatellite instability-high (MSI-H) CRC and deficient mismatch repair (dMMR) CRC comprise 15% of all CRC, and have shown remarkable response to immunotherapy, especially with PD-1 inhibitors. Despite this, there is still a significant need to optimise immunotherapeutic regimens to maximise clinical efficacy and patient quality of life, whilst minimising monetary costs. Mathematical models are a promising avenue for treatment optimisation, and we use delay integro-differential equations to model the interactions and dynamics of various cell types, immune checkpoints, damage-associated molecular patterns (DAMPs), and cytokines. We provide deterministic equations for the concentrations of cancer cells, DAMPs, CD4+ and CD8+ T cells, dendritic cells (DCs), cancer-associated fibroblasts (CAFs), neutrophils, macrophages, NK cells and various cytokines of pro-inflammatory (IL-2, IFN-γ, TNF, IL-12, IL-1β) and immunosuppressive (TGF-β, IL-10, IL-4, IL-6) nature. We consider these cells and their phenotypes, noting that many of these cell types are being modelled deterministically for the first time in cancer, paving the way for a deeper understanding of the complex underlying immune dynamics. We consider two compartments: the tumour site and the tumour-draining lymph node (TDLN), taking into account phenomena such as DC migration, T cell proliferation, acquired resistance to pembrolizumab, and CD8+ T cell exhaustion and reinvigoration. The parameter values and initial conditions for the model are estimated from experimental data, incorporating various pharmacokinetic, bioanalytical, and radiographic studies, as well as deconvolution of bulk RNA-sequencing data from the TCGA COADREAD database. We finally optimise CRC treatment with neoadjuvant pembrolizumab − one of the most commonly used PD-1 inhibitors. We maximise treatment efficacy and efficiency in locally advanced MSI-H/dMMR CRC patients whilst accounting for toxicity, and improve upon currently FDA-approved therapeutic regimens for metastatic MSI-H/dMMR CRC. We demonstrate that a single medium-to-high dose of pembrolizumab is sufficient for effective tumour eradication, whilst being efficient, safe and practical. (Back)

Unsupervised statistical learning in ancient numismatics

Andreas Heinecke
The University of Newcastle

Die analysis is an important tool of ancient economic history. Yet, manual die studies are too labor-intensive to comprehensively study large coinages such as those of the Roman Empire. From a computer vision viewpoint, such studies present a challenging unsupervised clustering problem, involving an unknown and large number of highly similar semantic classes (usually hundreds) of imbalanced sizes, for which training examples would be extremely time-expensive to obtain and are thus not available. We address this problem through determining dissimilarities derived from specifically devised re-weighted Gaussian process-based keypoint features in a Bayesian distance microclustering clustering framework. The covariance structure of the re-weighted Gaussian process can be efficiently approximated via convolutions. The resulting method can reduce the time investment necessary for large-scale die studies by several orders of magnitude, in many cases from years to weeks, and provide data towards longstanding controversial debates on the economic history of ancient states. (Back)

On ripple search methods − rapid cycle detection protocols

Daniel Z Herr*, Brett A Norval
CSIRO

Cycle detection in directed graphs is central to numerous processes in both theoretical and applied domains, including network analysis, circuit design, and scheduling. Traditionally, algorithms like depth-first search have been the methods of choice for identifying cycles, with complexity often bounded by $O(E+V)$, where E is the number of edges and V the number of vertices. While this has proven sufficient for many large-scale applications, the growing complexity of modern datasets is motivating interest in new techniques that can exploit graph structure and mathematical properties.

In this work, we present a set of simple yet powerful number-theoretic approaches that demonstrate clear advantages over existing cycle detection algorithms. These novel methods derive from elementary arithmetic manipulations, but they exhibit appealing theoretical properties when deployed in cycle-finding routines. Empirical evidence suggests that our number-theoretic operators significantly reduce redundant searches and streamline the detection of cycles.

We undertake a rigorous assessment of these methods through comparative runtime analysis, benchmark tests, and theoretical complexity discussions. The results highlight favourable scalability and improved time to detection, indicating potential to outperform standard DFS-based strategies in certain classes of graphs. Moreover, we argue that these new algorithms offer compelling insights into the structure of cycles, reinforcing their role not only as a computational tool but also as a lens into the deeper combinatorial properties of networks.

Through this presentation, we hope to stimulate further research into number-theoretic procedures for graph analysis and encourage the exploration of alternative paradigms to established cycle detection routines. (Back)

Modelling the suppression of the global mosquito miscreants:*Aedes albopictus*

Matthew Ryan, Manuela Mendiolar, Dan Pagendam, **Roslyn Hickson**, Brendan Trewin
CSIRO and James Cook University

Aedes albopictus mosquitoes are competent vectors for the spread of at least 24 different arboviruses, including dengue fever, Ross River virus, and Japanese encephalitis, but remain relatively less studied than their more urban cousins, *Aedes aegypti*. We model an Incompatible Insect Technique (IIT) based intervention for mosquito control, with bidirectional incompatibility between two (or more) strains of *Wolbachia*. We explore the expected time until population suppression and a proxy for cost (numbers of mosquitoes released) of such an intervention. We further explore for a single locale how immigration and emigration of mosquitoes between areas might affect these factors, and reversibility of the intervention − an important consideration in modern *Wolbachia*-based mosquito control programs. (Back)

Trapping of viscous liquid atop a granular mush

Edward Hinton, Anja Slim
The University of Melbourne

We consider the gravity-driven motion of viscous liquid propagating above a dense granular medium that obeys a $\mu(I)$-rheology. Initially, the pool of liquid depresses the granular layer to form levees at its edges. Next, these levees are pushed outwards by the gravity-driven slumping of the liquid, but the levees are not surmounted. In the third stage, the top of the levee is pushed out beyond the rest of the levee. This segregates the liquid into a pond trapped by the remnant of the original levees, and a slowly spreading thin film ahead of the levees. The trapped fraction of liquid depends on the extent of the early granular erosion, which in turn is controlled by the initial shape of the deposit and the yield criterion of the granular layer. The key physical ingredients that lead to such dynamics are inertia-less flow and a lower layer with a yield criterion. The latter gives rise to the all-important levees, which lead to the eventual trapping. The alternative regime of a viscous liquid spreading beneath a granular mush will also be discussed. (Back)

Barotrauma in bats due to wind turbines

Graeme C Hocking, Wafaa Mansoor
Murdoch University

Wind turbines are notorious for causing bird deaths due to collisions with the blades. This is an intense area of study, not least because Government Environmental Acts require prior analysis of the impact of wind farms. Less well known is the damage done to bats due to large pressure variations due to the flow past the rotors. A preliminary examination of this will be presented to determine possible mechanisms for “barotrauma”. (Back)

Should we really expand protected areas to save threatened species?

Matthew Holden
The University of Queensland

Several international agreements have called for rapidly expanding protected areas to improve biodiversity. However, increasing the size and/or number of protected areas comes at an opportunity cost. We could use money allocated to protected area expansion for other management interventions. In this talk, I will use mathematical population dynamic models of species in protected areas to examine whether bigger protected areas are better for threatened species and biodiversity. (Back)

Evaluating investment potential in blue carbon ecosystems within emerging carbon markets

Jordan Holdorf*, Melanie Roberts, Ivan Diaz-Rainey, Chris Brown
Griffith University

Nature markets, particularly carbon markets, present a promising financial opportunity for ecosystem conservation and restoration projects. These markets enable projects to generate financial returns while addressing global climate goals. However, the viability of such investments depends on many factors, including restoration costs, carbon sequestration rates, the risk of climate events, and market conditions such as carbon credit values.

This study applies a temporal model developed to optimise the timing of investment for conservation under climate uncertainty. Under varying market conditions, we assess the viability of investing in different Blue Carbon ecosystems−mangroves, salt marsh, and seagrass. Using stochastic dynamic programming, we analyse conservation projects across three distinct carbon credit values, evaluating how variations in restoration costs and carbon sequestration rates influence project outcomes.

Our findings identify the types of viable projects under different carbon credit scenarios and market conditions. This work underscores the critical role of integrating financial and ecological dynamics in decision-making frameworks. It provides actionable insights for policymakers and investors to prioritise and scale conservation efforts in Blue Carbon ecosystems effectively. (Back)

An application of the time-inhomogeneous Markovian binary tree to female families

Sophie Hautphenne, **Thisaakhya Jayakody***, Peter Taylor
The University of Melbourne

Female family dynamics vary from one country to another. These differences can be investigated using mathematical models. We apply matrix analytic methods and show that the time-inhomogeneous Markovian binary tree model is suitable for modelling the lifetime of a woman and the long-term behaviour of a whole female family generated by a single woman. Using this model, we introduce a recursive formula to compute the mean family size generated by a newborn woman. We then analyse the mean family size across selected time periods and perform a cross-country comparison to understand differences in family sizes generated by different female populations. (Back)

Efficient inference for differential equation models without numerical solvers

Alexander Johnston
Queensland University of Technology

Parameter inference is essential when interpreting observational data using mathematical models. Standard inference methods for differential equation models typically rely on obtaining repeated numerical solutions of the differential equation(s). Recent results have explored how numerical truncation error can have major, detrimental, and sometimes hidden impacts on likelihood-based inference by introducing false local maxima into the log-likelihood function. We present a straightforward approach for inference that eliminates the need for solving the underlying differential equations, thereby completely avoiding the impact of truncation error. (Back)

The role and benefit of heterogeneity in migratory animal populations

Stuart Johnston
The University of Melbourne

Long-distance annual migrations are a key part of many animals' lifecycles. Migratory populations often exhibit heterogeneity across a range of characteristics and behaviours. This includes the ability to perceive navigational information, the ability to communicate that information with conspecifics, and social standing within the population. However, it is unclear which heterogeneous features benefit navigational performance for the population as a whole. Here we explore this question via agent-based modelling in the context of long-distance whale migration. We determine which features benefit population migration, while simultaneously maintaining cohesion within the migratory population. (Back)

Towards geometry of aesthetic shapes: Klein geometry, integrability and self-affinity

Kenji Kajiwara, Shun Kumagai
Kyushu University

Starting from the log-aesthetic curve (LAC), a family of planar curves identified among the curves that car designers regard as “aesthetic”, we consider the extension of LAC from the viewpoint of the symmetry called “self-affinity” and Klein geometry. LAC has been identified as the similarity geometry analogue of Euler's elastica in Euclidean geometry in the sense that they are shape-invariant curves of the integrable deformations.

The LAC also has the following property: Take an arbitrary subcurve of a given planer curve and change the scales arbitrarily (there are variations of this property according to the scales to be changed). The obtained curve coincides with the original curve by a suitable affine transformation. Researchers in industrial design pointed out that such “self-affinity” is a characteristic property of “aesthetic” curves. We reconsider the self-affinity of plane curves and show that the quadratic curves have a certain self-affinity in the framework of equiaffine geometry ($SL(2, R)$ Klein geometry). Our result may imply that there is another family of “aesthetic curves” including the quadratic curves in equiaffine geometry. Together with the previous results on LAC under similarity geometry, it suggests that the two families of aesthetic curves may be unified under the framework of Möbius geometry, where “geometry of aesthetic shape” might be developed. (Back)

Detecting communities in temporal networks with the inflated dynamic Laplacian for graphs

Gary Froyland, **Manu Kalia**, Peter Koltai
Freie Universiteit Berlin

Complex time-varying networks are prominent models for a wide variety of spatiotemporal phenomena. The functioning of networks depends crucially on their connectivity, yet reliable techniques for determining communities in spacetime networks remain elusive. We adapt successful spectral techniques from continuous-time dynamics on manifolds to the graph setting to fill this gap. We formulate an *inflated dynamic Laplacian* for graphs and develop a spectral theory to underpin the corresponding algorithmic realisations. We develop spectral clustering approaches for both multiplex and non-multiplex networks, based on the eigenvectors of the inflated dynamic Laplacian and specialised Sparse EigenBasis Approximation (SEBA) post-processing of these eigenvectors. We demonstrate that our approach can outperform the Leiden algorithm applied both in spacetime and layer-by-layer, and we analyse voting data from the US senate (where senators come and go as congresses evolve) to quantify increasing polarisation in time. (Back)

Assessing parameter identifiability in age-structured epidemic models with under-reporting

K Kamboj*, JA Flegg, JM McCaw, FM Shearer
The University of Melbourne

Pathogens can disproportionately affect specific age groups due to differences in susceptibility, physiological responses, and social contact patterns. A common hypothesis to explain variations in observed case incidence across age groups is age-dependent susceptibility. However, observed data often underestimates the true number of infections due to under-reporting, driven by factors such as asymptomatic cases, variations in reporting behavior, and surveillance limitations. Incorporating an observation layer that accounts for the probability of reporting in an age-structured model adds complexity and can introduce challenges related to parameter identifiability. In this study, we use a simulation/re-estimation framework with Bayesian inference to evaluate whether age-dependent susceptibility and reporting parameters can be simultaneously inferred from age-specific incidence data. We explore different scenarios, corresponding to distinct functional form of reporting probabilities, and assess the robustness of inference and parameter identifiability for ODE based models. (Back)

Viscoelastic drop spreading: Cox−Voinov theory with normal stress effects

Minkush Kansal, Vincent Bertin, Charu Datt, Jens Eggers, Jacco H Snoeijer
UNSW Sydney

The dynamics of slowly spreading drops is dictated by the contact line motion. In Newtonian fluids, the classical Cox-Voinov theory links the macroscopic contact angle to the microscopic contact angle and the contact line velocity. Here, we investigate the effects of viscoelastic normal stresses on wetting dynamics. We first analytically derive an asymptotic expression for the radius of a spreading drop, and find the existence of two qualitatively different regimes. For weak viscoelasticity, the contact line dynamics follows a modified Cox-Voinov theory, where the microscopic contact angle is now replaced by an apparent microscopic angle dependent on the magnitude of viscoelasticity. By contrast, at larger values of viscoelasticity, the wetting dynamics, although affected by viscoelasticity, is independent of the microscopic properties, as had been previously anticipated in the case of complete wetting. We then discuss the intricate differences between spreading and retraction dynamics in the presence of viscoelasticity. (Back)

Resilience in the evolution of cooperation: measuring the effect of inequality

Maria Kleshnina
Queensland University of Technology

In this talk, we explore the resilience of cooperation in linear public good games, focusing on how asymmetries in endowments (ability to contribute) and productivities (effectiveness of contributions) affect the stability of cooperative behavior. While direct reciprocity often assumes symmetry, real-world settings typically involve unequal allocations. We analyze how endowment distributions can support full cooperation under adverse conditions, showing that resilient cooperation is best achieved through unequal allocation−more productive individuals should receive higher endowments. This focus on resilience contrasts with efficiency-driven approaches, emphasizing stability over fairness. Through analytical models and simulations, we demonstrate that maintaining cooperation in the face of inequality is crucial for the long-term survival of collective action. (Back)

Learning transfer operator dynamics on latent spaces

Kevin Kühl*, Gary Froyland
UNSW Sydney

The transfer operator method allows us to convert complex, nonlinear dynamical systems into linear representations that are simpler to analyse. While the spectrum of these operators may contain important insights into system predictability and emergent behaviour, approximating transfer operators from data can be challenging. We address this problem through the lens of general operator and representational learning, in which we approximate the action of transfer operators on infinite-dimensional spaces using tractable finite-dimensional forms. Specifically, we machine learn orthonormal, locally supported basis functions that are tailored to the system dynamics. These learned basis functions and dynamics then serve to compute accurate approximations of the transfer operator's eigenpairs. Our approach offers a promising direction for robust approximation of transfer operators, particularly in high-dimensional systems where traditional numerical methods may become computationally intractable. (Back)

Effect of contact structure on the realised generation intervals of an outbreak

Pratyush Kollepara*, Chiara Poletto, Joel Miller
La Trobe University

The reproduction number is a critical measure of the severity of an infectious disease epidemic. The generation interval, defined as the time taken by an infector to create another infection from its time of infection, is crucial for estimating the basic reproduction number. However, the generation intervals observed, 'realised generation intervals', change over time depending on the dynamics of the epidemic. These time varying distributions are well understood for homogeneous populations, and can be obtained using the intrinsic generation intervals and simple aggregate observations of the epidemic. For heterogeneous populations, the state-of-the-art method relies on the use of expensive simulations and data analysis. We simplify this process by developing exact expressions for simple structured populations. (Back)

Optimising chemotherapy for high grade serous ovarian cancer

Cristina Koprinski*, Georgio Hawi
The University of Sydney

Ovarian cancer is the deadliest gynaecological cancer and eighth leading cause of cancer deaths in women. High grade serous ovarian cancer (HGSOC) accounts for 75% of cases, and chemotherapy resistance and relapse occur in 85% of patients, leading to a 5-year survival of below 30%. Currently, the literature lacks comprehensive immunobiological models of HGSOC, and developing such models could provide critical insights into the disease's underlying mechanisms and interactions within the tumour microenvironment. We address this using delay differential equations to model immune cells including CD4+ and CD8+ T cells, dendritic cells, macrophages, damage-associated molecular patterns, NK cells, and pro-inflammatory and immunosuppressive cytokines. The model consists of two compartments − the tumour site and the tumour-draining lymph node and incorporates phenomena including DC and T cell migration, the priming of T cells with cancer antigen, and T cell proliferation. We use experimental data to estimate the initial conditions and parameter values of the model, incorporating deconvolution of bulk RNA-sequencing data from the TCGA OV. Finally, we optimize the standard chemotherapy regimen of carboplatin and paclitaxel for locally advanced HGSOC, focusing on maximising efficacy, minimising toxicity, and improving treatment efficiency. (Back)

Model reduction and analysis: a case study of a malaria control model

Maame Akua Korsah*, Stuart T Johnston, Kathryn Tiedje, Karen Day,
Camelia R Walker, Jennifer A Flegg
The University of Melbourne

Malaria's rising cases have prompted a concerted effort to control its transmission, utilizing various mathematical models to support the Roll Back Malaria agenda. Despite their thoroughness and specific modifications, many existing models exhibit rigidity, limiting their application to different datasets and their usefulness in solving diverse questions. This study addresses this limitation by employing reduction and approximation techniques on a comprehensive malaria control model to derive a simplified system that preserves the essential dynamics of the original system. We validate the accuracy of the reduced model through model-to-model fitting analysis using least squares and Bayesian MCMC fitting tools. Basing on simulation study and sensitivity analysis, we compare the two models and show that the reduced system exhibit similar transmission characteristics as the original model. Our results demonstrate that the reduced model effectively captures the essential behavior of the comprehensive model, while providing flexibility and computational efficiency, making it a valuable tool for evaluating and implementing malaria control strategies. (Back)

Phase resetting and the geometry of isochrons

Bernd Krauskopf
University of Auckland

Phase resetting is an experimental tool, originally from neuroscience, for the study of oscillatory systems. Given an underlying stable periodic orbit Γ parametrised by its 'old' phase $\theta_{\mathrm{o}} \in [0, 1)$, the classical phase transition curve (PTC) records the 'new' phase θ_{n} after the system has relaxed back to Γ following a perturbation of a given amplitude A in a given direction $\mathbf{d}$. Phase resetting is closely related to the concept of isochrons, which are submanifolds consisting of all points that converge to Γ with the same phase. The isochrons foliate the basin of attraction, and the PTC is determined by which isochrons are 'hit' when the periodic orbit Γ is shifted as a whole by A in the direction $\mathbf{d}$.

We consider the resetting map to the new phase θ_{n} more globally, not only as a function of θ_{o} but also of $\mathbf{d}$ and A. Its graph is a hypersurface that encodes all possible phase resets. By employing recently developed advanced numerical tools, we compute phase resetting surfaces as suitable slices of this graph. Moreover, our computational approach allows us to determine the foliations by isochrons in two-dimensional sections of a higher-dimensional phase space. As will be illustrated with examples, a crucial ingredient for understanding the overall geometric picture are singularities due to perturbations beyond the basin of attraction of Γ.

This is joint work with Peter Langfield, Kyoung Hyun Lee and Hinke Osinga. (Back)

A stochastic model of biological tissue growth in confined spaces

Shahak Kuba*, Matthew J Simpson, Pascal R Buenzli
Queensland University of Technology

The growth of biological tissues in confined spaces is strongly influenced by the surrounding geometry and by the mechanical relaxation of the cells composing the new tissue. Experimental observations of tissue growth in 3D-printed scaffolds and in bone pores show that the progression rate of the tissue depends on the curvature of the tissue substrate. Newly formed tissue is deposited at the tissue interface and comprises extracellular matrix and embedded cells. Previously, we developed an individual-based model that simulates the evolution of the tissue interface during growth through the deposition of extracellular matrix and mechanical interactions between cells. While this model can explain the curvature dependence of tissue growth rate observed experimentally, it focuses on the evolution of the interface and does not model bulk properties of the newly formed tissues, such as the density of embedded cells and of other tissue inclusions. In this contribution, we extend this model to incorporate cell proliferation, cell death, and cell embedment into the growing tissue as stochastic processes. The consideration of these cellular processes enables us to model bulk properties of the tissue. It allows us to compare tissue cell densities with experimental data and shows that stochasticity may be responsible for part of the variability in growth patterns seen for example in bone pore filling. (Back)

Modelling T cell expansion in immune cell-mimicking scaffolds for adoptive cell therapy

Mason Lacy*
Queensland University of Technology

T cells are immune cells that are known to be effective at killing cancer cells, however in normal immune responses there are often not enough tumour-specific T cells to eliminate the cancer or control its growth. Adoptive cell therapy involves activating and expanding T cells outside of the body and injecting them back into the body to effectively employ their cancer-killing functions. This activation and expansion is often achieved by facilitating interactions between T cells and artificial particles that mimic the activating functionality of other immune cells. As a promising example, antigen-presenting cell-mimetic scaffolds (APC-ms) consist of micro-rods that efficiently imitate immune cells and form fluid scaffolds for cell interaction. In my talk, I will present a stochastic agent-based model (ABM) of T cell expansion in APC-ms, with biologically accurate interactions between T cells and micro-rods. The continuum limit of this ABM is used to examine the expected behaviour of T cells within these scaffolds under varying scaffold parameter regimes. These models reveal the underlying processes that drive observations from experimental results, and suggest alterations to these micro-rods that will likely improve the speed and efficiency of T cell expansion for adoptive cell therapy. (Back)

Gradient recovery based on a biorthogonal system

Bishnu P Lamichhane, Muhammad Ilyas
The University of Newcastle

Gradient recovery approach is often used to improve the property of the gradient of a finite element solution. The gradient of the finite element solution is computed and then projected back to the finite element space to improve the approximation. Our projection is based on a biorthogonal system. Working with a biorthogonal system, the projection is computed in a very efficient way. We will also show an efficient boundary modification technique. Numerical examples will be presented. (Back)

The coordinate-independent geometric singular perturbation toolbox: model reductions of chemical reaction networks

Timothy Earl Figueroa Lapuz*, Martin Wechselberger
The University of Sydney

Geometric singular perturbation theory (GSPT) has been employed in many models that exhibit two-or-more time-scales. The typical approach has been to rely on the disparate scales that variables evolved on. More recently, tools were developed so that a scale splitting based on variables is no longer necessary i.e. a coordinate-independent approach.

In this talk, we discuss the advantage of using this coordinate-independent GSPT toolbox. Using the well-known Michaelis-Menten (MM) chemical reaction network as an example, we highlight that the GSPT approach may be employed for the common assumptions invoked, such as the standard quasi-steady-state approximation (QSSA), the reverse QSSA, the total QSSA and the partial equilibrium approximations (PEA). No coordinate transformations are required at any point and, irrespective of which approximation is appropriate, the same steps are taken to arrive at a model reduction.

Furthermore, this GSPT approach naturally leads to a geometric classification of the model reductions of the MM chemical reaction network, based on the underlying critical manifold and fast fibre orientation. (Back)

Simulating emergency animal disease outbreaks and response

Thao P Le, Isobel Abell, Sarita Rosenstock, Chris Baker
The University of Melbourne

Potential outbreaks of animal diseases such as Lumpy Skin Disease (LSD) in Australia pose a significant risk to animal populations and livestock industries. Outbreaks would impact trade and livelihoods, have negative animal health and welfare, and affect food security. We are collaborating with policy makers to design modelling tools aimed to give decision makers the information they need to quickly and effectively respond to such outbreaks. To test these tools, we will be running simulation exercises, which simulate animal disease outbreaks and provides decision-makers the opportunity to use forecasting tools as part of their simulated decision-process. Accompanying the simulation exercises will be qualitative research to ensure that these models are useful to policymakers. This talk will present a trial simulation workshop, simulating a disease outbreak in cattle in NSW. Come along ready to participate in the mock decision-making process! (Back)

When therapeutic intervention is destined to fail

Noa Levi*, Adrianne Jenner, Robyn Araujo
The University of Melbourne

Mathematics plays a crucial role in advancing our understanding of biological systems and developing effective therapeutic strategies. In this talk, I will explore the connection between the regulatory mechanisms that govern biological systems and their impact on treatment outcomes. Specifically, I will compare two key regulation strategies−robust perfect adaptation (RPA) and bistability−and demonstrate how even small adjustments to regulatory mechanisms can significantly alter the system's response to treatment. By highlighting the importance of identifying the regulatory mechanisms underlying disease-promoting networks, I emphasise the value of this approach for biomedical research and therapeutic development. (Back)

Reading the shark's bar-code

Angus Lewis, Hilary Lewis
The University of Adelaide

Basically all shark conservation is based off of age-growth estimates and further, generation lengths (time between generations). But the problem is that shark age estimates are whack [sic] the 'bands' that were first discovered in 1921 and are currently used to age sharks, are being proven as inaccurate time recorders. In this project I am collaborating with experts in sharks and marine chemistry in the Research School of Earth Sciences at ANU to work out better ways to age sharks. Better age estimates will ultimately be used to better-inform conservation efforts. My collaborators are using fancy modern techniques (LA-MC-ICP-MS) to analyse the elemental composition of shark vertebrae and collect a multivariate time-series inside of which a chronological history of the shark is recorded. My job is to determine a way to extract this history, if it is even possible. We hope to shed light on the accuracy of the current band ageing technique and, if there is evidence that the bands are inaccurate, we hope to determine a better way to age sharks. We are also looking for any other important ecological/ontogenetic information in the data which can help us better understand the shark's life-history and better-inform population management to save the sharks from extinction! (Back)

An off-lattice discrete model to characterise filamentous yeast colony morphology

Kai Li*, Edward F Green, Hayden Tronnolone, Alexander KY Tam, Andrew J Black,
The University of Adelaide

We combine an off-lattice agent-based mathematical model and experimentation to explore filamentous growth of a yeast colony. Under environmental stress, Saccharomyces cerevisiae yeast cells can transition from a bipolar (sated) to unipolar (pseudohyphal) budding mechanism, where cells elongate and bud end-to-end. This budding asymmetry yields spatially non-uniform growth, where filaments extend away from the colony centre, foraging for food. We use approximate Bayesian computation to quantify how individual cell budding mechanisms give rise to spatial patterns observed in experiments. We apply this method of parameter inference to experimental images of colonies of two strains of S.cerevisiae, in low and high nutrient environments. The initial nutrient concentration and a forking mechanism for pseudohyphal cell proliferation are the key features driving colony morphology. Simulations run with the most likely inferred parameters produce colony morphologies that closely resemble experimental results. (Back)

The mathematics of collapse: geometric singular perturbation theory and rate-induced tipping phenomena in multiple-time-scale ecological models

Matthew Lim*
The University of Sydney

'Rate-induced tipping' or 'R-tipping' − a dramatic and often irreversible transition due to exceeding a critical 'rate' of change − is an elusive and commonly overlooked tipping mechanism in ecology or, more broadly in any dynamical system. While bifurcation-induced tipping ('B-tipping') points have been extensively studied, the role of critical rates in driving system collapse has remained largely overlooked. In this talk, R-tipping is examined through the lens of Geometric Singular Perturbation Theory (GSPT).

We demonstrate the power of GSPT methods by analysing food chain models with two respectively three distinct timescales and environmental system parameters evolving on the slowest timescale. In particular, we will show that R-tipping can be understood as the consequence of special solutions, called canards, forming transient tipping-threshold manifolds in such multiple timescale problems. Analysis of a tritrophic predation model allows for these transient tipping-thresholds to be linked with key geometric objects known as 'folded singularities' in three-time-scale problems, revealing a new phenomenon termed "R-double-tipping." We also identify novel tipping-phenomena such as a purely rate-induced change in stability regime and a paradoxical rescue mechanism that occurs along the R-double-tipping boundary. These findings aim to further establish R-tipping as one of the most consequential and robust dynamical phenomena to emerge from multiple-time-scale systems. (Back)

PDE models for the spatial spread and evolutionary dynamics of heterogeneous cell populations

Tommaso Lorenzi
Politecnico di Torino

In this talk, PDE models for the spatial spread and evolutionary dynamics of heterogeneous cell populations will be considered. In these models, a continuous structuring variable captures intercellular variability in proliferation and migration rates. Analytical and numerical results summarising the behaviour of the solutions to the model equations will be presented, and the insights generated by these results into the mechanisms that underpin collective cell migration will be briefly discussed. (Back)

Utility indifference approach for option pricing

Xiaoping Lu
University of Wollongong

This talk explores option pricing using the utility indifference approach. While it offers the integration of investor risk preferences as a key advantage over traditional models like the Black-Scholes framework, the utility indifference approach also presents limitations, including computational complexity, sensitivity to utility function specifications, and difficulties in pricing short call options, due to their potential for unlimited losses and extreme risk exposure. The talk will discuss both the advantages and limitations of this approach in option pricing, drawing on our experiences. (Back)

Stokes’ phenomenon in complex solutions to nonlinear PDEs

Christopher Lustri
The University of Sydney

A decade ago, there was a spark of interest in studying PDE solutions by analytically continuing the solutions into the complex plane and studying the formation and dynamics of singularities, and the Stokes’ Phenomenon that this created. Interesting results were obtained, but the technical challenge of these methods for nonlinear problems slowed progress. Recently, new asymptotic methods have been devised to study these singularities. I will show some recent results in this area on solutions the regular and fifth-order KdV equations. This is joint work with Scott McCue and Jon Chapman. (Back)

Modelling chytridiomycosis transmission in frogs

Michael Lydeamore, Claire Miller, Anthony Waddle, Lee Berger, Lee Skerratt,
Jennifer Flegg, Patricia Campbell
Monash University

Chytridiomycosis is a fungal disease that has spread worldwide, driving at least 90 amphibian species to extinction, and severely affecting hundreds of others. We constructed a dynamic model of chytridiomycosis transmission in frogs that accounts for the progression of infectious load in the frogs, and the effect of novel sunlight-heated artificial refugia. This model was fit using approximate Bayesian computation to experimental data where frogs were separated into cohorts based the amount of heat the refugia received.

Our results show that the effect of heating the refugia reduced infection in frogs by 2.5 times. Further, frogs that were infected and recovered had significant protection, with subsequent infections occurring at 20% of the rate of naive frogs. (Back)

Many ODEs (and PDEs and an ABM) to a wound healing mechanism

Matthew Mack*
University of South Australia

When the body sustains an injury, body cells die and release actin into the extracellular system (which includes the bloodstream). To prevent toxicity from the build up of actin, the body's scavenging system uses Gelsolin to break down actin filaments into extractable pieces. Flightless (Fli-I) has been identified as a protein that can interfere with the process by preventing gelsolin's functions, and thus reducing the body's capability to heal from the injury. In this talk I will present my current work which aims to model these interactions through a system of ODEs with an accompanying PDE derivation. I'll also present a sketch of an agent-based model (ABM), and outline intended further analysis and directions. (Back)

Topology optimisation for soft robotic grippers

Connor Mallon
Queensland University of Technology

Soft robotic grippers are widely recognized as the standard solution for handling complex, delicate, and deformable objects. However, designing a universal gripper capable of grasping general objects remains a challenging problem due to the complex design space and the need to meet multiple performance criteria. This work introduces a topology optimization approach to design soft grippers, resulting in a set of designs that demonstrate effective performance for various common objects. We also discuss the extension of the work to next generation soft grippers with self-sensing capabilities for force detection. (Back)

Floquet theory and stability analysis for Hamiltonian PDEs

Robert Marangell
The University of Sydney

I will discuss some applications of Floquet theory to the stability and instability of periodic traveling waves in Hamiltonian PDEs. I will present several examples of such PDEs, including the generalized KdV and BBM equations (third order), the nonlinear Schrdinger and Boussinesq equations (fourth order), and the Kawahara equation (fifth order). The characteristic polynomial of the monodromy matrix inherits symmetry from the underlying PDE, and by employing the Floquet discriminant, one can determine properties of the essential spectrum along the imaginary axis including bifurcations of the spectrum. (Back)

A MCMC framework for differentially-private synthetic data generation

Harry McArthur*, Peter Taylor, Kate Smith-Miles, Joseph Chien, Chris Mann
The University of Melbourne

We present a novel framework for data generation and publication that preserves privacy while maintaining utility. Our approach generates synthetic datasets with privacy guarantees, offering an alternative to traditional methods that rely on adding noise to individual queries. We prove our method is differentially-private for an important class of queries and provide tight bounds for special cases of the algorithm. Our method produces a synthetic dataset using a MCMC approach, defining a Markov chain with a state space on the set of feasible databases. The chain converges to a carefully designed stationary distribution, which can be flexibly chosen. We show empirically that selecting a stationary distribution that places higher probability mass on databases closer to the original dataset (in a chosen metric) provides an effective balance in the privacy-utility tradeoff. We propose a novel metric to bound the noise introduced to queries, and pair it with a stationary distribution inspired by the geometric distribution. Through computational experiments across various MCMC implementations, we demonstrate the effectiveness of our method as a privacy-preserving data generation technique. (Back)

How immune dynamics shape multi-season epidemics: a continuous-discrete model in one dimensional antigenic space

James M McCaw, Roslyn I Hickson, Mick G Roberts
The University of Melbourne

Respiratory viral illnesses, caused by pathogens such as influenza, typically cause regular seasonal epidemics in temperate climates. Taking influenza as a case study, infection stimulates the human immune system, and in particular elicits a strain-specific antibody immune response, that contributes to the resolution of infection and provides long lasting strain-specific protection such that subsequent exposure is unlikely to result in a productive infection.

Strong strain-specific immunity, combined with the inherent erroneous replication of the virus drives viral evolution, selecting for immune-escape variants. In consequence, for influenza and many other viral infections, while strain-specific immunity is long (perhaps even life-long), protection against the circulating viral strains may be short lived.

Here we extend a previously published model for the dynamics of a single strain of an influenza-like infection. The model incorporates waning acquired immunity to infection and punctuated antigenic drift of the virus, employing a set of coupled integral equations within a season and a discrete map between seasons. The long term behaviour of the model is demonstrated by examples where immunity to infection depends on the time since a host was last infected, and where immunity depends on the number of times that a host has been infected. The first scenario leads to complicated dynamics in some regions of parameter space, and to regions of parameter space with more than one attractor. The second scenario leads to a stable fixed point, corresponding to an identical epidemic each season. We also examine the model with both paradigms in combination, almost always but not exclusively observing a stable fixed point or periodic solution.

Our results suggest that if the level of host immunity depends on the elapsed time since the last infection then the epidemiological dynamics may be unpredictable. Given the public health benefit of being able to make more accurate predictions of future epidemic activity, our findings emphasise the need to develop a better understanding of how past exposure(s) shape the immune response. (Back)

Unusual type of thin film rupture

Scott W McCue, Steven A Kedda, Michael C Dallaston
Queensland University of Technology

We consider an idealised model for the evolution of a thin liquid film driven by the thermocapillary Marangoni effect. Numerical solutions show the height of the film decreasing, suggesting the film will undergo an infinite-time rupture at certain points in space. In the lead up to rupture, the local minimum of the film height bifurcates into two minima, leaving a kind of ‘‘satellite droplet’’ in between. Subsequently, each local minimum bifurcates into two more minima, resulting in two much smaller satellite droplets, and these new minima each bifurcate into two more, leaving even smaller satellite droplets, and so on. We will study this fractal-like process in the infinite-time limit and attempt to relate it to a phenomenon call ‘‘discrete self-similarity’’. (Back)

Modelling with differential equations − highlights

Mark McGuinness
Victoria University of Wellington

The last thirty years of my research have been dominated by the use of partial differential equations to solve problems brought to Maths in Industry Study Groups, or to model geophysical processes. I will talk about cooking crispy cereals, freezing sea water in Antarctica, volcanic eruptions in Iceland, volcanic bombs in Tonga, alumina silos on the Shannon Estuary, and microwaving bauxite on conveyor belts. Problem solving and understanding processes provide a common theme in this eclectic reminiscence collection from my own journey in applied mathematics. (Back)

Farauti and Furious: modelling malaria mosquitoes for outbreak prevention

M Mendiolar, B Trewin, N Beeton, R Hickson, A van den Hurk, NW Beebe
CSIRO

Malaria remains one of the deadliest infectious diseases worldwide. In the Southwest Pacific region, *Anopheles farauti* is a primary malaria vector through the region. Mosquito control is the cornerstone of malaria prevention; however, this species has rapidly adapted behaviorally to avoid traditional control methods, such as long-lasting insecticidal nets and indoor residual spraying, reducing their effectiveness. As a result, innovative approaches like genetic vector control methods are gaining attention as promising, durable, and cost-effective solutions. Gene drive, one such method, substantially increases the chances of a specific gene being inherited by offspring. In this context, the introduced genes can be designed to reduce the mosquito’s ability to carry and transmit the malaria parasite.

An. farauti mosquitoes are currently found in coastal areas of northern Queensland and the Northern Territory, with their malaria transmission capacity demonstrated during the last Australian mainland outbreak in 2002. Australia provides an ideal setting to study gene drive interventions of *An. farauti* due to its genetically isolated mosquito populations and fragmented landscapes, facilitating gene target design that would minimise the risk of unintentional export to other regions, even within Australia.

We are using modelling to support efforts to explore testing *An. farauti* gene drives in Australia. We aim to understand where the populations are likely to be found using ecological niche modelling and to estimate mosquito abundance in these areas. These findings will underpin future work to modify and apply an existing spatial process model to simulate the spread of a population-modifying gene drive in *An. farauti across* where it occurs in northern Australia. (Back)

Analytic methods in hydroelasticity

Mike Meylan
The University of Newcastle

Hydroelasticity describes any problem in which fluid and elastic structures interact and has found a wide and ever-growing range of application. This is especially true in the field of marine engineering and polar geophysics, but it has also recently become a significant area of research in wave energy conversion. As always, simple analytic solutions have proven to be of great use to understand complex behaviour such as is exhibited in hydroelastic systems. I will present here some examples involving floating thin plates in which we have been able to find analytic solutions using methods from complex variables and showcase some of the applications. (Back)

The effect of obstacle length and height in supercritical free-surface flow

Hugh Michalski*
The University of Adelaide

Two-dimensional open channel flow past a rectangular disturbance in the channel bottom is considered in the case of supercritical flow, where the dimensionless flow rate is greater than unity. The response of the free surface to the height and length of a rectangular disturbance is investigated using the forced Korteweg-de Vries model. A rich and complex structure of solutions is found as the length of the disturbance increases. As the length of the disturbance is decreased, some solutions approach those of the well-studied point forcing approximation, but there are other solutions that are not predicted by the point forcing model. (Back)

Modelling immune interactions with endometrial cells in endometriosis lesion onset

Claire Miller, Domenic Germano, Alicia Chenoweth, Sarah Holdsworth-Carson
The University of Auckland

Endometriosis is a chronic gynaecological condition affecting one in nine people with a uterus. The disease is characterised by the growth of lesions of endometrial-like cells outside of the uterus, such as in the peritoneum (lining of the abdomen and pelvis). Symptoms include chronic pain and fertility issues. The hypothesised root cause of endometriosis is retrograde menstruation−where menstrual debris is ejected through the fallopian tubes and into the peritoneal cavity rather than out the cervix. However, retrograde menstruation is more common than endometriosis, pointing towards a more complex pathophysiology.

The immune system is responsible for clearing the ectopic (abnormally located) cells in the peritoneal cavity. This leads to two hypotheses for endometriosis onset: 1. Endometriosis patients have an increased amount of retrograde influx, overcoming an otherwise healthy immune system; or 2. Endometriosis patients have an immune system disorder, such as a reduced ability to detect the ectopic cells, or a reduced ability to clear the ectopic cells.

We have developed a compartmental model of the immune cell response to endometrial cells in the peritoneal cavity, focusing on the innate immune system. Altered macrophage and natural killer cell behaviours are the innate immune cells commonly implicated in the literature, and so we focus on these cell types in the model. Using this model, we determine the parameter regimes under which endometrial cells do or do not persist as lesions. We investigate the two hypotheses detailed above and determine that there is no association between increased retrograde influx and disease; and a dysfunction in the immune system's ability to clear the ectopic cells is a stronger driver of disease than a dysfunction in its ability to detect the cells. A bifurcation analysis shows that under both immune dysfunctions considered, the system exhibits hysteresis, indicating a significant improvement in immune function is required to clear disease once onset has occurred. (Back)

The ethical implications of the SIR epidemic final size relation

Joel Miller
La Trobe University

The final size relation predicts the population fraction infected in an SIR epidemic as a function of the Basic Reproduction Number R_0. It is a convex function of R_0. An important prediction of the final size relation is that as the vaccinated fraction increases, the probability an unvaccinated individual will be infected drops. This effect is known as herd immunity. The derivative of the final size relation can be interpreted as the expected number of infections prevented by giving one individual a perfect vaccine. As the vaccinated fraction increases, the convexity of the final size relation implies that the derivative increases. Thus vaccination provides an example of increasing marginal returns at the population scale, even as the individual benefit from vaccination decreases.

This has surprising ethical implications. In a single population it implies that the overall benefit of vaccination is highest when the direct benefit to the recipient is lowest. When there is limited vaccine in a population of multiple subgroups, individuals in smaller groups or groups that are at lower risk will tend to be prioritized.

I will discuss scenarios where the existence of ethical dilemmas can be inferred easily from the shape of the final size relation and how the resulting ethical dilemmas might be resolved. (Back)

Thermal performance curve models calibrated to ecological data using sequential Monte Carlo sampling: an application to Antarctic moss photosynthesis

Elise Mills*, Eliza Domann, Diana King, Alicia Perera-Castro, Krystal Randall,
Sharon Robinson, Matthew Adams
Queensland University of Technology

A range of moss species form the primary terrestrial vegetation inhabiting the Antarctic continent. Moss growth is driven by photosynthesis, which is highly responsive to its microclimate. Photosynthesis models incorporating a dependence on both light and temperature could provide valuable information about how cumulative stressors affect moss survival, growth and species distribution; existing models typically depend on only one of these quantities.

We have therefore formulated four thermal performance curve models with biologically relevant parameters. Two types of model formulation were used: Liebig's law of the minimum, and a multiplicative approach. Each of the four models were calibrated to laboratory data (six moss species, taken from two different locations in Antarctica) using Sequential Monte Carlo sampling. We then considered the performance of the different models and model formulations, as well as the identifiability of the model parameters, which in turn drove the model selection.

We demonstrate that all models can estimate key parameters of moss photosynthesis, and that these parameters are identifiable and consistent with previous studies. Our preliminary results indicate that key parameters can differ vastly between moss species, and there appeared to be a preference for specific model formulations based on species location. It is intended that the models, fully calibrated including rigorous quantification of uncertainty, have utility in forecasting the responses of these unique Antarctic plants to climate change. (Back)

Quantifying biological heterogeneity in nano-engineered particle-cell interaction experiments

Ryan J Murphy, Matthew Faria, James M Osborne, Stuart T Johnston
The University of Melbourne

Nano-engineered particles are a promising tool for medical diagnostics, biomedical imaging, and targeted drug delivery. Fundamental to the assessment of particle performance are in vitro particle-cell interaction experiments. These experiments can be summarised with key parameters that facilitate objective comparisons across various cell and particle pairs, such as the particle-cell association rate. Previous studies often focus on point estimates of such parameters and neglect measured heterogeneity. In this study, we develop an ordinary differential equation-based mechanistic mathematical model that exploits the routinely measured heterogeneity. Connecting this model to data using approximate Bayesian computation parameter inference and prediction tools, we reveal the significant role of heterogeneity in parameters that characterise particle-cell interactions. We then generate predictions for key quantities that are challenging to observe by experimentation alone, such as the time evolution of the number of particles per cell. Finally, we systematically explore how the choice of experimental time points influences estimates of key quantities. Overall, our results suggest that it is critical to consider heterogeneity even when interpreting the simplest of particle-cell interaction experiments. (Back)

Solving for railway deformations using Weeks' method and undetermined coefficients

Josiah Murray*
The University of Newcastle

As we increase the demands we put on our rail systems, we naturally increase the rate at which they deteriorate. To aid in the development of strategies for improving the resilience of our infrastructure, we would like a good understanding of the behaviour of mathematical systems which model railways. A standard section of track can be modelled as an infinite Euler-Bernoulli beam on a viscoelastic foundation and has well-known solutions and solution techniques. If we wish to model transition zones−which are places along the track where the foundation properties change abruptly−we are obliged to change the model. In doing so, many of the solution techniques are no longer applicable. Transition zones cause a negative feedback loop, where short-term deformations feed into long-term plastic settlement, and over all accelerate track degradation. As a step towards a model which can accurately capture this behaviour, we present a solution technique using the Laplace transform and undetermined coefficients to solve for the deformation of an Euler-Bernoulli beam on a piecewise constant viscoelastic foundation. The system can be solved analytically up to the Laplace inversion, which has to be performed numerically. In particular, we apply Weeks' method and comment on its suitability to the problem. (Back)

A mathematical model for smooth muscle cell phenotype switching in atherosclerotic plaque

Joseph P Ndenda, Michael G Watson, Ashish Misra, Mary R Myerscough
The University of Sydney

Smooth muscle cells (SMCs) play a fundamental role in the development of atherosclerotic plaques. SMCs may ingest lipids (mostly cholesterol) in a similar way to monocyte-derived macrophages (MDMs) in the plaque. This stimulates SMCs to undergo a phenotypic switch to a macrophage-like phenotype. However, these SMC-derived macrophages (SDMs) are ineffective in clearing lipids and apoptotic cells from the lesion microenvironment, and they have a reduced phagocytic capacity compared with classical immune cells. Failure to remove lipids and apoptotic cells from the atherosclerotic plaque via phagocytosis leads to secondary necrosis and an inflammatory necrotic core. The stability of the fibrous cap, which is essential for plaque maintenance, is directly related to the number of SMCs it contains. A thin fibrous cap with fewer SMCs increases the risk of plaque rupture, potentially leading to thrombosis and clinical complications such as heart attack and stroke.

Despite its importance, the mechanisms underlying phenotypic switching, cap formation, and plaque stability are not fully understood. We use this model to explore the effect of SMC phenotype switching on plaque fate, and use sensitivity analysis to identify key biological parameters associated with plaque stability. We find that when SMCs switch to a macrophage-like phenotype, the total lipid contained in cells in the plaque increases. Additionally, removal of SMCs from the plaque via phenotype switching reduces the fibrous plaque cap, increases the lipid in the necrotic core, and increases plaque inflammation. This makes the plaque more vulnerable to rupture, which can lead to heart attacks and strokes. When SDMs are highly proliferative and resistant to cell death, the plaque grows rapidly and becomes highly pathological. The model suggests that plaque dynamics, driven by the switch of SMCs to a macrophage-like phenotype, may drive the development of unstable, vulnerable and pathological plaques. (Back)

A coupled agent-based and PDE model for angiogenesis applied to endometriosis

Cecilia Olivesi*, Claire Miller, Alys Clark
The University of Auckland

Endometriosis is a gynaecological disease, affecting 1 in 9 women of reproductive age, where endometrial-like tissue grows outside the uterus, forming lesions. Vascularisation, more particularly angiogenesis, is one of the main events regulating their implantation and development. Angiogenesis is the formation of new blood vessels from a pre-existing vasculature. Once the lesions are vascularised, they receive the hormones and nutrients necessary for their survival and growth.

We developed an agent-based model of angiogenesis for endometriotic lesions. This model has also application to tumour lesions as a similar angiogenesis process is observed. We used an overlapping spheres method to describe the movement, interactions and division of blood 'cells' (we use the term cell here to describe a segment of a whole blood vessel). We considered two types of cells which are subjected to different forces: tip cells start and end the vessel; and stalk cells form the body of the vessel. Tip cells can divide, according to a probability, into either a stalk cell (lengthening the vessel), or into another tip cell (creating a new sprout). Moreover, the lesion releases growth factors regulating the direction of the cells' movement and favouriting the creation of new sprouts. We describe the concentration of those factors using partial differential equations.

In this talk, I will highlight the impact of the lesion's growth factors on the resulting vascularisation. (Back)

Competing mechanisms for the buckling of an epithelial monolayer identified using multicellular simulation

James M Osborne, Phillip J Brown, J Edward F Green, Benjamin J Binder
The University of Melbourne

In this talk we will use the recently developed Rigid Body Multi-Cellular Framework (RBMCF) to investigate the mechanisms that drive the buckling of an epithelial monolayer. Specifically, the deformation of a monolayer of epithelial cells which are attached to a basement membrane and the surrounding stromal tissue. The epithelial monolayer, supporting basement membrane, and stromal tissue are modelled using two separate vertex dynamics models (one for the epithelial monolayer layer and one for the basement membrane and stromal tissue combined) and interactions between the two are considered using the RBMCF to ensure biologically realistic interactions. Model simulations are used to investigate the effects of cell-stromal attachment and membrane rigidity on buckling behaviour. We present simulations that demonstrate that there are two competing modes of buckling, stromal deformation and stromal separation. (Back)

Incorporating thermodynamic constraints into parameter estimation for dynamic models of cell metabolism

Michael Pan
The University of Melbourne

Metabolism is the fundamental process by which cells convert external substrates and nutrients into energy and basic building blocks of life. Mathematical models of metabolism have long been of interest in systems biology, contributing to our understanding of the mechanisms of disease and enabling drug discovery. In recent years, the availability of metabolomics and fluxomics measurements has greatly expanded, making it possible to create dynamic models calibrated to specific cell types. However, it is currently time-consuming to develop these large-scale models. Therefore, a systematic pipeline for constructing and parameterising these models would be immensely valuable in studying metabolism.

This talk outlines some initial work towards this modelling pipeline, focussing on parameter estimation. Large-scale dynamic models of metabolism can be constructed by connecting individual models of enzymes (described by rate laws) in a modular manner. Publicly accessible enzyme databases report k^{cat} and K_M values that can be used to parameterise these models. However, in many cases, these datasets may be incomplete, with measurements of certain parameters absent. On the other hand, reported parameter values may also be inconsistent with each other as thermodynamic constraints introduce dependencies between parameters. To resolve these issues, we apply parameter balancing, an approach based on Bayesian statistics. Through the use of independent species-specific and reaction-specific parameters, parameter balancing ensures that parameters are thermodynamically consistent by construction. In the case where measurements of parameters are missing, parameter balancing can estimate their values through a combination of prior distributions and thermodynamic constraints. This approach results in posterior distributions for model parameters, ensuring thermodynamic consistency while also resembling experimental measurements as closely as possible. We apply this approach to a metabolic network of the tricarboxylic acid cycle in *Leishmania* parasites, using reported values from the BRENDA and eQuilibrator databases. Future directions for calibrating these models to metabolomics data from specific cell types will be discussed. (Back)

Slowly, then all at once: uncovering the dynamics of a catastrophe

Davide Papapicco*
The University of Auckland

Many natural and human complex systems evolve on a slow timescale and are stable with respect to external perturbations. However, these systems can experience sudden rapid departures from their natural equilibrium, known as tipping events, which often bring catastrophic, unrecoverable repercussions. Extreme paleoclimate events, ecosystems’ collapse and economic crises are some examples of dynamical systems evolving slowly around an equilibrium until a tipping point causes a fast critical transition outside the basin of attraction and onto a new, unhealthy state. Given the disruption of natural equilibria and the potential unrecoverability of certain states past the critical transitions, forewarning of these tipping points has been the subject of extensive research for the past 30 years. Characterisation of these events and their early-warning signals starts with a dynamical interpretation of these different regimes and further develops into the realm of stochastic processes and transitional states. Numerous precursors have been hypothesized and statistical measures have been derived as leading indicators of tipping events for simplified and low-dimensional dynamical systems. Despite these efforts several fundamental issues still plague the practical application of early-warning signals in natural timeseries, with their lack of consistency across a broad spectrum of real-world tipping points posing a major shortcoming in their reliability. The purpose of this talk is twofold. In the first part we will address the challenges facing the generalisation of frameworks of tipping events to spatially-extended (high-dimensional) models. Subsequentially we will show how a novel, prototypical approach based on the finite-states probabilistic interpretation of critical transitions can potentially address the fallacies of previously proposed, model-based indicators. (Back)

When does non-stationarity matter for managing threatened ecosystems?

Luz V Pascal*, Iadine Chades, Matthew P Adams, Kate J Helmstedt
Queensland University of Technology

Ecosystems are undergoing shifts in their dynamics due to changes in environmental conditions, for example due to climate change and habitat degradation. These shifts create new challenges for environmental decision-makers, now managing non-stationary ecosystems. First, accounting for changes in ecosystem dynamics increases the decision-space dimensionality, which increases the computational burden of solving such decision-problems. When faced with these computational challenges, managers must then decide if the benefits of modelling these shifts in ecosystem dynamics justify the added effort. Second, decision-makers are often uncertain how ecosystems will respond to environmental change. This uncertainty is usually addressed using adaptive management -an optimization framework to dynamically learn the best strategy based on the ecosystem response to interventions. However, studies using adaptive management have focused on low-dimensional problems, and existing methods become intractable in high-dimensional problems. In this talk, I will show how the value of information theory can quantify the importance of modelling non-stationary dynamics of ecosystems and help practitioners find strategies to manage non-stationary ecosystems with uncertain response to environmental change. (Back)

Global bifurcations in a 4D Lorenz-like system

Juan Patiño-Echeverría*, Hinke Osinga, Bernd Krauskopf
University of Auckland

We study a four-dimensional generalisation of the classical Lorenz system with the property that it can exhibit *wild chaos*, a form of chaotic dynamics unique to vector fields of dimension at least four. We investigate the global bifurcations of the system that could play a role in generating such wild chaos. We focus on the two-parameter plane determined by the Rayleigh number from the classical Lorenz system and a new parameter that introduces rotation around the z-axis. Our analysis begins by extending the bifurcation structure of the classic three-dimensional Lorenz equations to the four-dimensional system by ‘‘switching on’’ this new parameter. A central focus of this talk is on two distinct trajectories that converge to the origin in backward time, forming the so-called one-dimensional unstable manifold of the origin. These trajectories are crucial to the emergence of complex dynamics in the system. The two-parameter plane is divided into different regions by curves of homoclinic bifurcations at which the unstable manifold of the origin returns to the origin. In contrast to the classical Lorenz system, each homoclinic bifurcation is of Shilnikov type, meaning that the return to the origin happens in a spiralling manner. We classify the different regions with a so-called kneading diagram and discuss how this kneading diagram offers insights into regions where wild chaos may occur. We also highlight a specific parameter point that acts as an organising centre for the system's dynamics. (Back)

An analytic solution to a hole opening problem for a bacterial colony

Aidan Patterson*, Alex Tam, Bronwyn Hajek, Judy Bunder
University of South Australia

The zone of inhibition test is a standard method in microbiology to assess the efficacy of antimicrobial agents, where the spatial spread of a diffusing substance forms a visible boundary of reaction. This talk presents an analytic solution to this test through its conceptualization as a hole opening problem, providing a mathematical framework to predict the maximum spread of the inhibition zone and the time at which it is reached. The solution combines the diffusion equation with the Lambert$W$ function to yield precise insights into the dynamics of bacterial growth and inhibition. These results offer potential applications in optimizing antimicrobial testing and understanding diffusion-driven processes in biological systems. (Back)

Numerical methods for approximating the transfer and Koopman operators

Nicholas Peters*
University of New South Wales

The spectrum of the transfer and Koopman operators of a dynamical system reveal useful information about the dynamics of the system, such as identifying cycles and their frequencies. Recently there has been a surge in popularity for methods for approximating these operators from measurement data without necessarily knowing the underlying equations of the system. In this presentation, we look at two such methods for constructing approximations to the transfer operator. Both methods involve several parameters and the accuracy of their output depends on the values chosen for these parameters. For several systems, we compare the results obtained using the two methods and investigate ways of choosing parameter values which yield good results. (Back)

Tsunami waves in a compressible ocean near a step-type topography

Ravindra Pethiyagoda, Santu Das, Mike Meylan
The University of Newcastle

We consider the propagation of tsunami waves generated by ground motion, and their subsequent scattering from a sudden change in bathymetry following linearised water wave theory and a weakly compressible ocean. This talk presents a process of using eigenfunction matching to find solutions for an arbitrary piecewise-constant bathymetry profile and presents solutions showing the propagation of free-surface waves and internal pressure waves. (Back)

New non-Lie non-classical symmetry solutions of a class of reaction−diffusion equations

David Plenty*, Maureen P Edwards
University of Wollongong

Nonlinear one-dimensional reaction-diffusion equations are useful for modelling processes in science and engineering. Non-classical symmetry analysis with a vanishing coefficient of $\frac{\partial}{\partial t}$ is applied to search for non-Lie solutions of a class of nonlinear reaction-diffusion equations. The analysis leads to two non-classical symmetries. Each symmetry gives a solution that cannot be constructed using classical symmetries or non-classical symmetries with a non-vanishing coefficient of $\frac{\partial}{\partial t}$. A solution is applied in a potential model for population growth in biology. (Back)

Directed helical motility of active particles in the zero-Reynolds number limit

Olle Ponten*, Douglas Brumley
The University of Melbourne

Dinoflagellates, a family of unicellular microalgae (5−10 μm in size), are key components of marine ecosystems, and exhibit distinctive helical swimming trajectories driven by transverse and longitudinal flagella. The physical arrangement of their flagella places fundamental constraints on how dinoflagellates can navigate towards nutrient sources of various sizes. While the motility and navigation of smaller bacteria (e.g., E. coli) has been well documented, the capacity for dinoflagellates to navigate by modifying their helical trajectories is less explored. Investigating dinoflagellate motility requires novel modelling approaches at the micro-scale, which extend beyond traditional run-and-tumble frameworks used for smaller bacteria, and experimental validation that can resolve both individual trajectories and interactions with nutrient sources. We have developed reduced-order agent-based models that links information from trajectories to body-local instantaneous forces to be able to follow the transduction of chemical stimuli to flagellar motion. Numerical simulations of flagellar hydrodynamics in the zero-Reynolds number regime, together with simulating cellular signalling allows our simulations to relate instantaneous forces and torques to directed helical motion. This allows us to capture the longer time-scale dynamics of biased helical motility while seeing how it arises from local body motion. Experimental validation spans three scales: flagellar and body hydrodynamics at the microscale and collective motility in suspensions at the macroscale via particle image velocimetry, stereographic imaging of 3D single-cell trajectories at the mesoscale. Our results aim to refine agent-based models for active particles and provide predictive insights into behaviours of helical swimmers. Ultimately, these tools may guide coral restoration strategies and enhance our understanding of other microscale swimmers with analogous locomotion. (Back)

Large-scale vortices in electromagnetically driven horizontal soap films

Andrey Pototsky, Aldo Figueroa, Jose Olvera-Orozco, Misael Alvarez-Jimenez,
Sergio Cuevas, Sergey Suslov
Swinburne University of Technology

We study the conditions under which large-scale vortex flow patterns appear in electromagnetically driven conducting horizontal soap films created between two coaxial cylindrical electrodes and placed in a vertical magnetic field. For large Marangoni and Peclet numbers, the two-dimensional flow in a flat free film is effectively incompressible and the surface concentration of an insoluble surfactant plays the role of the pressure away from the boundaries. If the direct radial electric current flows through the film, the Lorentz force arising in a uniform field drives the azimuthal flow. Its stability is investigated in cases of slip and no-slip boundary conditions at the edges of the film in the limit of a small Hartmann number. Flow stability changes non-trivially depending on the slip length and the flow stabilises for perfect-slip boundaries. In contrast, if the vertical axisymmetric field is strongly non-uniform, the flow may become linearly unstable at much smaller Reynolds numbers than the critical value for no-slip boundaries leading to the formation of large-scale circulation cells. Our experiments conducted using a piecewise constant magnetic field detect the formation of vortex structures that are in qualitative agreement with those predicted by the performed analysis. (Back)

Exploring partial tipping through variation in forcing timescale

Courtney Quinn, Hassan Alkhayuon
University of Tasmania

Many physical systems, particularly those related to weather and climate, experience external forcing across a range of timescales. If this forcing manifests as parameter changes in the model, then the system can be at risk of rate-induced tipping. This is where the system crosses a critical threshold preventing it from tracking a time-varying attractor. When the forcing can have different realisations, such as with periodic or chaotic variation, then the system can undergo extit{partial tipping}. In such cases only a subset of forcing realisations will cause the system to tip.

We explore this phenomenon in a low-order model of ice-age dynamics. The model exhibits bistability between two equilibria in one region of the parameter space, and between an equilibrium and a periodic orbit in another region. When allowing for variation of the parameters within these bistable regions, the solution can undergo either reversible or irreversible tipping between attractors. We find that the timescale of the parameter variation induces resonance-like behaviour in that there exists an optimal timescale for tipping as well as a minimum timescale for the occurrence of tipping. We derive a linearized solution for small periodic variation which also produces damped resonance at particular timescales. To understand the tipping threshold, we explore the crossing of the stable manifold of the time-varying saddle equilibrium through the use of finite-time Lyapunov exponents. (Back)

Understanding complex oscillations in a model of intracellular calcium dynamics

Behnaz Rahmani*, Samuel Jelbart, Vivien Kirk, James Sneyd
The University of Auckland

Oscillations of free intracellular calcium concentration are thought to be important in the control of a wide variety of physiological phenomena, and there is long-standing interest in understanding these oscillations via the investigation of suitable mathematical models. Many mathematical models of calcium dynamics exhibit variables or terms that evolve on vastly different time scales, leading to temporally complex oscillations. This talk describes efforts to use geometric singular perturbation theory and numerical bifurcation analysis to explain complex oscillations observed in a model of hepatocytes (liver cells). (Back)

Convergence rate of the derivative-free VU-algorithm

Thakshila Rajapaksha*
University of Wollongong

The VU-algorithm is a powerful tool for minimizing finite-valued functions in nonsmooth convex optimization, leveraging theVU-space decomposition to address smoothness and nonsmoothness on orthogonal subspaces: the$U$-space and$V$-space. This decomposition enables superlinear con vergence in its classical form. In this presentation, we explore the derivative-free version of theVU-algorithm, which utilizes approximations for subgradients, Hessians, and related components. By systematically investigating the factors that influence superlinear convergence, we reveal how accurate approximations play a pivotal role in maintaining the algorithm's efficiency. Our findings provide insights into the key elements necessary to preserve the convergence behaviour of the classicalVU-algorithm in a deri vative-free setting, opening avenues for broader applicability in challenging optimization problems. (Back)

Modelling amphitheatre gully erosion with coupled hydrology and erosion dynamics in two-dimensions

Llewyn Randall*
Griffith University

Gullies are major contributors to sediment discharge and ecosystem health in the Great Barrier Reef. They evolve over time from linear forms to large amphitheatres that dominate the landscape. These amphitheatre-like gullies, which are nearly as wide as they are long, feature complex internal channels, protruding structures, and multiple active heads, presenting challenges for traditional one-dimensional models like MERGE. To address this, we are developing a two-dimensional gully erosion model that integrates hydrology with erosion dynamics, capturing the non-uniform processes across the gully width. In this talk, I will explore the methods and challenges involved in constructing (and solving) this model. (Back)

ShapleyX – a handy python tool for simulation-specific global sensitivity analysis

Melanie Roberts, Fred Bennett
Australian Rivers Institute, Griffith University

Model sensitivity analysis is an important step in understanding the models we develop, in supporting model parameterisation, and in understanding results from scenario analysis. One-at-a-time (OAT) methods are popular as they provide a simple way to quantify the effect of variations in a parameter, but cannot capture effects of parameter interactions. In contrast, global methods such as a Monte-Carlo style parameter exploration (often visualised with spaghetti plots) allow for parameter interactions, but are often difficult to quantify the sensitivity of an individual parameter. ShapleyX is a newly developed python tool that aims to promote sensitivity analysis as an expected element of model scenario analysis studies by providing a simple, effective way of attributing variations in results to individual parameters. We illustrate the advantages of this approach using the MERGE gully erosion model as an example. (Back)

Constructing accurate multi-continuum micromorphic homogenisations in multi-D space-time

Tony Roberts
University of Adelaide

Homogenisation empowers the efficient macroscale system level prediction of physical problems with intricate microscale structures. Here we develop an innovative powerful, rigorous and flexible framework for asymptotic homogenisation of dynamics at the *finite* scale separation of real physics, with proven results underpinned by modern dynamical systems theory. The novel systematic approach removes most of the usual assumptions, whether implicit or explicit, of other methodologies. By no longer assuming averages the methodology constructs so-called multi-continuum or micromorphic homogenisations systematically based upon the microscale physics. The developed framework and approach enables a user to straightforwardly choose and create such homogenisations with clear physical and theoretical support, and of highly controllable accuracy and fidelity. (Back)

Balancing competing priorities: optimising land use allocation

Grace Robinson*
Queensland University of Technology

Since climate overshoot scenarios have become optimistic how we utilise natural resources has never been more important. The trade-offs between establishing food security, maintaining biodiversity while mitigating emissions are a question of resource management. Quantifying land use allocations impacts on these goals allows this to be formulated into an optimisation problem. Attempts at understanding the trade-offs these goals present implement food production as a constraint on the system, despite production often failing to meet demand, as well as prescribing fine-scale regional solutions based on global level assumptions. We have instead firstly formulated it as a multi-objective optimisation problem. Next, we have developed a novel solution method based on non-dominated sorting genetic algorithms to allow us to determine the Pareto-optimal land use allocations over large scale areas. Lastly, we have included a fourth objective determining the difference between newly generated land use allocations and what is currently present. This will not only allow the solution space to be more adequately identified it will also allow practical solutions to be explored that may result in better outcomes but are often overlooked when we are optimising without thought for the realistic level of changes that can be expected. (Back)

From crowded streets to serene retreats: managing overtourism through mathematics

Mariano Rodrigo
University of Wollongong

Mitigating overtourism is crucial for numerous destinations inundated with visitors, leading to adverse impacts on both the environment and local communities. This talk enhances Butler’s seminal tourism area life cycle model by incorporating culling strategies derived from population ecology, aimed at managing visitor numbers, fostering quality tourism experiences and maintaining sustainability. Both constant-yield and constant-effort strategies highlight the need to customise tourism management as destinations evolve through the life cycle phases. During periods of moderate tourist density, effective compensation mechanisms should be prioritised to support sustainable economic growth. Additionally, acknowledging the negative effects of depensation enables stakeholders to proactively implement strategies to prevent decline. Lastly, incorporating the idea of recovery time accounts for the necessary duration to recover from variations in tourist numbers and aids in developing appropriate policy responses to address shifting tourism patterns. This talk is based on joint work with I Ajala. (Back)

Optimal control theory for climate temperature overshoot: separating mitigation and carbon dioxide removal

Nina Rynne*, Michael Bode, Ryan Heneghan
Queensland University of Technology

Under the Paris Agreement’s 1.5°C temperature target, the world faces a control problem where current warming of 1.3°C makes temporary or permanent temperature overshoot of the 1.5°C target almost certain - creating a rich mathematical question of how to control trajectories that exceed a target before returning below it. This path dependency makes optimal control theory particularly well-suited to analysing these scenarios, as future control choices are fundamentally shaped by past decisions. At the same time, while existing modelling approaches typically combine emissions mitigation and carbon dioxide removal (CDR) interventions into a single abatement strategy, this obscures their fundamentally different roles in managing temperature overshoot. In this presentation, I will outline a novel optimal control formulation that explicitly separates mitigation and CDR strategies and demonstrate how these controls exhibit fundamentally different behaviours, with mitigation constrained by current state variables, while CDR, by operating on cumulative CO2 concentrations, is the essential mechanism for reducing temperature after overshoot. The model provides a framework to systematically examine how varying technological, economic and climate parameters affect optimal overshoot trajectories and their feasibility. This work demonstrates the value of optimal control theory in understanding systems where past trajectories fundamentally constrain future choices. (Back)

Modelling mass transport due to ciliary carpets: Rotlet model

Siluvai Antony Selvan*, Peter W Duck, Draga Pihler-Puzovic, Douglas R Brumley
The University of Melbourne

Ciliary flows are crucial in transporting particulate matter, dissolved substances, and active matter, such as bacteria, in diverse biological systems, including starfish, corals, and airways. While coarse-grained approaches like infinite and envelope models have been widely described the flows of these systems, they fail to resolve the individual ciliary motion, which is critical for understanding nutrient mixing. Our work demonstrates that the steady flow field of a single cilium can be accurately represented using the Rotlet model (Selvan SA, Duck PW, Pihler-Puzovic D, Brumley DR (2023) ‘Point torque representations of ciliary flows’, *Physical Review Fluids*, 8(12):123103) − a point torque framework − which effectively resolves the nutrient transport capabilities of individual cilia. Harnessing this model to investigate ciliated tissues, we incorporate ciliary distribution and alignment calibrated through microfluidic measurements from reef-building corals. We investigate how dissolved and particulate matter are transported in these systems by solving the Langevin model, which simulates the matter as an ensemble of Brownian particles. This comprehensive theoretical framework reveals how physical factors, including nutrient diffusivity, spatial heterogeneity, and ciliary density, shape mass transport by the steady flow fields of ciliary carpets. (Back)

Queuing, even GLUT4 has to do it

Brock Sherlock*, Adelle Coster
University of New South Wales

Mammalian cells regulate their glucose levels by redistributing glucose transporter proteins within the cell. The main insulin activated transporter is Glucose Transporter 4 (GLUT4) − a membrane embedded protein found in fat and muscle cells. Insulin signals the redistribution of GLUT4 from intracellular compartments to the plasma membrane. GLUT4 is constantly recycled throughout the cell. Experimental observation indicates that, on the metabolic timescale, the amount of GLUT4 recycling varies with insulin level; an increase in insulin results in an increase in the amount of GLUT4 recycling up to some saturated level. In the literature, mean-field modelling provides two explanations for the varying recycling amounts that are found: dynamic and static retention. Under dynamic retention, GLUT4 is placed in a slowly cycling compartment that delivers GLUT4 to the plasma membrane with an insulin-dependent rate. Static retention sequesters GLUT4 away from the recycling pathway with the amount sequestered being insulin dependent. Here, we implement a stochastic model, a closed queuing network, to enrich our understanding of the possible biological mechanisms that could act and to capture the variability evident in biological data sets. Using an appropriately scoped distance measure to compare to the experimental data, we investigate the biological plausibility of the dynamic and static retention hypotheses. (Back)

Thomas algorithm in the pricing of American option on coupon paying bond under the CIR interest rate model

Kajanthan Shiyamasuntharam*

University of Wollongong

There have been significant contributions to the valuation of American options on bonds without coupons. This work specifically focuses on pricing American put options on coupon-paying bonds under the Cox−Ingersoll−Ross (CIR) interest rate model. In bond option pricing, the bond's price is not directly available and must be calculated. While there is an analytical formula for determining the price of zero-coupon bonds, this formula does not apply to coupon-paying bonds. To evaluate the price of a coupon-paying bond, we derive a linear bounded Partial Differential Equation (PDE). The American option pricing problem is a moving boundary problem, which we formulate as a Linear Complementarity Problem. As a result, two different PDEs must be solved to obtain the bond price, and the American put option price under the CIR interest rate model. Due to the complexity of obtaining an analytical solution, numerical methods are employed to solve these PDEs. Finite Difference Method (FDM) is applied to discretize the PDE systems and then we used the Thomas Algorithm to improve the solution speed. The numerical results show that the Thomas Algorithm computes the solution implicitly and more quickly. (Back)

Parameter identifiability, parameter estimation and model prediction for differential equation models

Matthew Simpson

Queensland University of Technology

Interpreting data with mathematical models is an important aspect of real-world applied mathematical modeling. Very often we are interested to understand the extent to which a particular data set informs and constrains model parameters. This question is closely related to the concept of parameter identifiability, and in this article we present a series of computational exercises to introduce tools that can be used to assess parameter identifiability, estimate parameters and generate model predictions. Taking a likelihood-based approach, we show that very similar ideas and algorithms can be used to deal with a range of different mathematical modelling frameworks. The exercises and results presented in this presentation are supported by a suite of open access codes that can be accessed on GitHub. (Back)

Intruding into the atmosphere and oceans

Anja Slim

Monash University

Intrusions are the predominantly horizontal flow of fluid of one density into a density stratified ambient fluid. A striking example is a volcanic ash cloud, although they are ubiquitous and important throughout the environment. Surprisingly, despite being a fundamental flow problem with features that appear to lend themselves to asymptotic analysis, no rigorous reduced-order model for intrusions has been developed. I will discuss where existing approaches have failed and the progress we have made towards a new and reliable model. (Back)

Information spreading on real and imaginary networks

Michael Small

The University of Western Australia

In this talk I will describe some of our recent work concerning spreading processes on networks. Transmission of contagion on a network remains both obvious and topical. It turns out that the geometric properties of complex networks, when spreading is restricted to transmission between neighbours, yields some rather nice analytic results which differ from those that one obtains under the well mixed hypothesis. Moreover, such ideas have real practical benefit − from justifying Western Australia's isolationist policy during COVID, to designing an efficient allocation of resources for hospital emergency departments. (Back)

Fokas diagonalisation

Dave Smith

The University of Newcastle

Classical spectral theory establishes that Fourier transforms ‘‘diagonalize’’ differential operators. This means we can use separation of variables, Sturm-Liouville theory, and expansions in bases of eigenfunctions, known in combination as a spectral transform method, to solve initial boundary value problems for the classical equations of mathematical physics, such as the heat equation and time dependent linear Schrödinger equation. But what happens when a spectral transform method fails? For example, the prototypical third order dispersive equation, $u_t = u_{xxx}$, with some natural boundary conditions, does not have a basis of eigenfunctions. We explore how a weak form of diagonalization can still be used to make a spectral transform method work even in such a situation. We develop a general theory for two point problems and present applications to problems of high spatial order, with nonlocal boundary conditions, with interface conditions, with mixed partials, and on semiinfinite domains. (Back)

Reconciling neutralising antibody titres across assays

Eva Stadler, Francesca Mordant, Siddhartha Mahanty, Kanta Subbarao,
Miles Davenport, David Khoury

UNSW Sydney

Neutralising antibodies (nAbs) are a known correlate of protection against SARS-CoV-2 and other viral infections. However, there are several different neutralisation assays that can yield different estimates of the nAb titre. For example, assays can use either the authentic virus or a pseudovirus, the assay readout can be different types of evidence for virus infecting or killing cells, and the format of the assay can be a reduction of viral killing by 50% (‘per virion’ neutralisation) or neutralisation of all virions in 50% of wells (‘per well’ neutralisation). In this interdisciplinary collaboration, we aimed to compare three different neutralisation assays and the estimated nAb titres to determine which factors drive differences in the estimated nAb titres. All assays were performed in the same laboratory and we analysed the raw data to estimate the nAb titre for each assay using statistical methods and model fitting. We found that neutralisation titres are strongly correlated between all assays and the use of live virus and pseudovirus yields comparable titre estimates in two assays with the same format. The assay format, i.e., ‘per virion’ neutralisation or ‘per well’ neutralisation, however, leads to approx. 20-fold differences between nAb titres. Based on the estimated ‘per virion’ neutralisation and the number of virions per well, we predict the ‘per well’ neutralisation. This prediction agrees well with the estimated ‘per well’ neutralisation and indicates that the assay format is a key factor influencing differences between nAb titres. (Back)

Navigating the maze: a synthesis of dynamic conservation planning methods for a changing environment

Tace Stewart*, Matthew Adams, Kate Helmstedt
Queensland University of Technology

Antarctica faces unprecedented environmental change, challenging the effectiveness of its static protected area system. This research explores dynamic conservation planning methods to address this challenge, offering a synthesised comparison of approaches found in the literature. We analyse various methods, examining their required inputs, mathematical frameworks, and outputted recommendations. This work provides a critical foundation for informed decision-making in conservation planning, enabling practitioners to select the most suitable methods for incorporating environmental change into dynamic conservation strategies. (Back)

The complex stability landscape for drawing of holey fibres

Yvonne Stokes, Jonathan Wylie, Nazmun Papri
The University of Adelaide

Isothermal drawing of thin solid fibres, where the effect of surface tension is negligible, is unstable above a critical value $D_{\mathrm{crit}} \simeq 20.21$ of the draw ratio, i.e. where the pulling speed exceeds the feed speed by the factor D_{crit} (Matovich and Pearson, Industrial & Chemical Fundamentals 8, 1969). However, practical fibre drawing sees the successful use of draw ratios well in excess of this value, raising questions of how inertia, temperature, surface tension and other parameters affect draw stability. Moreover, the manufacture of ‘holey’ fibres, which has revolutionised the use of optical fibres in modern technologies since the 1980s, has added the questions of how draw stability is affected by air channels in a fibre and their possible pressurisation. Using an asymptotic model of fibre drawing and linear stability analysis, we investigate these questions and show a complex stability landscape. (Back)

Approximating solutions of the Chemical Master Equation using neural networks

Augustinas Sukys, Kaan Öcal, Ramon Grima
The University of Melbourne

The Chemical Master Equation (CME) provides an accurate description of stochastic biochemical reaction networks in well-mixed conditions, but it cannot be solved analytically for most systems of practical interest. Although Monte Carlo methods provide a principled means to probe system dynamics, the large number of simulations typically required can render the estimation of molecule number distributions and other quantities infeasible. In this talk, I will discuss how we can leverage the representational power of neural networks to approximate the solutions of the CME and propose a framework for the Neural Estimation of Stochastic Simulations for Inference and Exploration (Nessie). Our approach is based on training neural networks to learn the distributions predicted by the CME from relatively few stochastic simulations. Using Nessie, I will demonstrate on biologically relevant examples that simple neural networks can capture highly complex distributions across parameter space, thereby accelerating computationally intensive tasks such as parameter exploration and inference. (Back)

Vortices in electromagnetically driven films: physical nature and bifurcation characteristics

Sergey A Suslov, Andrey Pototsky
Swinburne University of Technology

This talk will continue discussing the physical nature and nonlinear characteristics of flow structures arising in thin films driven by the action of Lorentz force (introduced in Andrey Pototsky' presentation). Specifically, we will look into the type of instability that leads to the vortex formation and show that the commonly assumed Kelvin-Helmholtz mechanism is not necessarily the main player and may be even absent completely. We will also look at the types of bifurcations resulting in the experimentally observed instabilities and demonstrate that, depending on the geometry of the film and on the spatial distribution of the driving force, it can be either super- or subcritical. Time permitting, we will briefly overview the main features of past-bifurcation states. (Back)

Accidental and regulated cell death in yeast biofilms

Daniel Netherwood, **Alex Tam**, Edward Green, Campbell Gourlay,
Vladimir Jiranek, Benjamin Binder
University of South Australia

The yeast species *Saccharomyces cerevisiae* (the budding yeast) is one of the most widely studied model organisms in molecular and cell biology. Budding yeast can form biofilms, in which cells reside in a self-produced extracellular matrix. Biofilm formation makes yeasts highly resistant to antimicrobial therapy and is a key reason for the major health burden of yeast infections. Lab-grown biofilms provide a way to study the mechanisms of growth relevant to pathogenic yeast species.

A central feature of yeast biofilms is cellular demise, which occurs by one of two independent mechanisms: accidental cell death (ACD) or regulated cell death (RCD). In this talk, we describe a reaction−diffusion equation (RDE) model for the nutrient-limited growth of a yeast biofilm, including the effects of ACD and RCD. The model consists of a coupled system of four non-linear RDEs for the yeast cell density, nutrient concentration, and two species of dead cells. Numerical solutions of the governing equations reveal that cell death due to RCD occurs in a localised annular region, which propagates with the biofilm as it expands. In contrast, ACD occurs in a circular region, which trails the expanding annular region of RCD cells. These numerical predictions provide good qualitative agreement with experiments. (Back)

A preconditioner of iterative domain decomposition methods based on a multigrid strategy

Daisuke Tagami
Kyushu University

A Balancing Domain Decomposition (BDD) method is originally proposed by Mandel (1993), and is regarded as the preconditioner of linear iterative solvers for artificial boundary problems appearing in Domain Decomposition Methods (DDM) based on finite element methods; see, for example, Glowinski, et al. When using BDD method, we need to set a coarse space, which includes the kernel of the coefficient matrix of resultant linear system derived from a corresponding artificial boundary problem. In case of a mixed finite element method for magnetic field problems, the number of the Degrees Of Freedom (DOF) of the coarse space is equal to the number of nodal points of triangulation. This fact leads BDD methods for magnetic field problems cannot reduce their computational costs. Now, to reduce the number of DOF of coarse spaces in BDD methods and their computational costs, a multigrid strategy based on Polytopal Element Methods (PEM; see Di Pietro, et al. (2021)) is introduced, and is used for approximations of the coarse space with Domain-by-Domain methods. Owing to the approximation of coarse spaces, we can expect to reduce computational costs to solve coarse-space problems as well as to keep the condition number of the coefficient matrix of resultant linear system. (Back)

Coordinating a virtual power plant with a decentralised distributed algorithm

Matthew K Tam, **Liam Timms***, Lele Zhang
The University of Melbourne

Power banks present an increasingly accessible and adaptable way to use and store power. Multiple power banks can be coordinated to create a virtual power plant (VPP) that can satisfy larger power demands. However, coordinating a VPP introduces difficulties regarding how individual charging decisions interact. In this talk, we present a model for managing a VPP as a non-cooperative game with individual power banks as agents. To solve this model and find optimal charging schedules, we develop an algorithm based on monotone operator splitting. This algorithm is distributed to reflect the independent agents making up the VPP, and decentralised to avoid the drawbacks of a centrally coordinating agent. (Back)

Metamodelling for geometric Brownian motion using polynomial chaos expansion

Parul Tiwari
Auckland University of Technology

In the presence of inherent and extrinsic noise, Stochastic Differential and Partial Differential Equations (SDEs/SPDEs) are being utilised as a mathematical tool to describe numerous physical, biological, and economic systems. However, solving these equations can be very difficult because of the random elements involved. Stochastic spectral methods are helpful tools that simplify these equations by breaking down the solution into simpler parts using special mathematical functions. These methods allow researchers to better understand and handle uncertainty in various practical problems. In this research, a metamodel for geometric Brownian motion is developed by using stochastic spectral method called Polynomial Chaos Expansion (PCE). Different quadrature rules are applied and the spectrum for PCE coefficients are compared. Actual and PCE evaluated responses are plotted and it is worth mentioning that the results are comparable. (Back)

Multi-strain infection dynamics with an immunity-structured model

Ruarai Tobin*, James McCaw, Freya Shearer
The University of Melbourne

In immunity-structured compartmental models of infectious disease, the population modelled is stratified according to their level of immunity (as described by, e.g., antibody levels). These models allow for individual-scale immune phenomena such as boosting, waning and thresholds of protection to be incorporated into models at the population-scale. Here, I extend an existing immunity-structured modelling framework that considers a single strained pathogen to construct a model of infection dynamics with multiple pathogen strains, where each strain imparts cross-reactive immunity. In this presentation, I will describe the structure of the model with two pathogen strains and briefly present some results. (Back)

Creating a nutrient-based model for cylindrical yeast growth

Aidan Patterson, **Hayden Tronnolone**
Flinders University

The *yeast saccharomyces cerevisiae* is a model eukaryotic organism, so understanding its behaviour provides insight into other eukaryotic cells. Experiments have demonstrated that yeast cells can be grown into cylindrical colonies with a linear increase in colony length over time, rather than the exponential growth seen in other biological examples. Agent-based models have previously explored this, using a prescribed probability for cell proliferation to represent nutrient availability. We extend this approach by modelling both the cells and nutrient diffusion explicitly using agent-based models, and verify that this does provide a plausible mechanism for the observed behaviour, while also giving greater insight into the behaviour within the colony. (Back)

Levy flight search in 2-D geometries

Justin Tzou
Macquarie University

Levy flight models of diffusion describe many systems that traditional Brownian motion cannot. The models typically involve the fractional Laplacian operator - the Levy flight analog of the Laplacian. However, methods and frameworks for handling the fractional Laplacian are few and less developed compared to those of the regular Laplacian. We provide remedies and apply them to reveal insights into the classic problem of stochastic searches for small targets. We focus on 2-D geometries for which methods and results are especially rare. (Back)

Modelling spike frequency adaption through higher-order fractional leaky integrate and fire model

Yash Vats*
The University of Queensland

Spike frequency adaptation is a key characteristic of spiking neurons. To examine this form of adaptation, we introduce a higher-order fractional leaky integrate-and-fire model. In this model, the exponent of the fractional derivative can range from one (representing an ordinary first order derivative) to two. In this regime, the impact of the past membrane potential on the present potential is inhibitory leading to spike frequency adaptation. We also analyzed spike frequency adaptation in response to noisy input and show that spike frequency adaptation is reinforced as the intensity of noisy input increases. (Back)

Calibrating mathematical models when data is limited: how to use non-empirical observations for parameterisation

Sarah Vollert*, Christopher Drovandi, Cailan Jeynes-Smith, Matthew Adams
Queensland University of Technology

Many of the systems we model are data-limited, due to the costs, time constraints, invasiveness or untrustworthiness of data collection. Yet, experts studying these systems often have rich knowledge of their behaviours and functions that are often not considered as “data”; for example, typical system behaviours, responses to specific changes, observed phenomena, physical limitations, and other non-empirical observations. When modelling highly uncertain systems, this knowledge should be incorporated into our forecasts, without adjusting the underlying mechanistic understanding of the model. This work introduces a framework for incorporating expert knowledge of expected model outputs within Bayesian model calibration, to avoid manually adjusting models or parameters to remove impossible model behaviours. We demonstrate the method using case studies in applied mathematical ecology and biology. (Back)

A viscoplastic deposit on an oscillating plate

Matthew Walker*, Jesse Collis, John Sader, Douglas Brumley, Edward Hinton
The University of Melbourne

Viscoplastic fluids are non-Newtonian fluids that do not flow until the magnitude of the internal stress exceed a threshold ‘yield stress’. Geophysical, industrial and household materials such as mud, magma, concrete, toothpaste and mayonnaise exhibit such behaviour. We consider a thin volume of a viscoplastic fluid on a transversely oscillating plate, which causes the volume to spread laterally. Unlike in the Newtonian case, this viscoplastic current slumps asymptotically towards a final, arrested state. This arrested state is the same as that attained by a viscoplastic deposit on an inclined plane, for a specific inclination angle that may be expressed in terms of the plate oscillation parameters. At late times, separable solutions are obtained for the free surface evolution, and are shown to decay algebraically to the arrested state. Three dimensionless groups govern the flow physics, and distinct early-time behaviours are observed for different flow regimes. The evolution of the ‘yield surfaces’ which partition the fluid-like and solid-like regions characterise by the qualitatively different regimes, illuminated by interesting topological features unique to inertial viscoplastic flows. (Back)

A Bayesian hierarchical framework for capturing experimental variability in flow cytometry data

Xiangrun Zhu, Thomas Steele, Ryan J Murphy, Stuart T Johnston, Scott A Sisson,
Matthew Faria, Alexander P Browning, **David J Warne**
Queensland University of Technology

Targeted therapeutics, rely on precise drug delivery to specific molecular targets, necessitating advanced analytical techniques for assessing therapeutic efficacy. Flow cytometry, a powerful tool for single-cell analysis, offers insights into traits of each cell at a point in time. However, heterogeneity in flow cytometry data, stemming from biological, technical, and experimental factors, poses challenges for accurate data interpretation. To address this, we propose a Bayesian hierarchical framework coupled with ordinary differential equation models for individual cell dynamics and perform parameter inference. This framework aims to capture heterogeneity across multiple levels, including cell-to-cell variability, replicate variability, and experimental condition variability. Using simulated synthetic datasets, we demonstrate the effectiveness of the proposed approach for accurately estimating model parameters, even in the presence of outliers or significant variation between experimental conditions. Our findings underscore the potential of hierarchical modelling techniques to enhance the reliability and robustness of flow cytometry data analysis, thereby advancing our understanding of cellular processes crucial for targeted therapeutics and disease treatment. (Back)

A moving-boundary model of lesion growth in multiple sclerosis

Georgia Weatherley*, Michael Dallaston, Adrianne Jenner
Queensland University of Technology

Often, biological populations are modelled using reaction-diffusion systems with the assumption that their behaviours play out on a nice, uniform domain. In patients with multiple sclerosis, immune cell populations misbehave within the brain to create areas of damage called lesions. Through time-series MRI data, clinicians observe heterogeneous lesion geometries that evolve across the patient's disease course. Here, we describe a local contest at the lesion edge between harmful immune activity and the brain's innate ability to heal, giving scenarios of lesion worsening (expansion) or recovery (recession). Using ideas from the Stefan problem, typically defined in the context of phase change of a material, we explicitly model the lesion boundary subject to local immune activity. We describe the migration and proliferation of the immune cell population as a reaction-diffusion process. By disregarding the brain's microstructure to assume linear diffusion of the cell population, we will present preliminary numerical work towards ultimately examining whether local cell densities alone can explain the lesion geometries observed in the brains of MS patients. (Back)

Parallel level set-based optimisation of three-dimensional piezoelectric materials

Zachary J Wegert*, Anthony P Roberts, Vivien J Challis
Queensland University of Technology

Owing to their ability to generate voltage under deformation and vice versa, piezoelectric materials are utilised in several industrial applications including for sensing, actuating, and energy harvesting. Recent advancements of fine-scale additive manufacturing techniques have prompted the design of state-of-the-art heterogeneous piezoelectric meta-materials that exhibit exotic or enhanced properties. Optimisation of such materials can be achieved computationally using a mathematically motivated technique called topology optimisation. This is a class of PDE-constrained optimisation that seeks to minimise functionals that depend on the underlying domain and the solutions to PDE constraints.

In this talk we will discuss computational techniques and results for memory-distributed topology optimisation of three-dimensional piezoelectric materials and structures using the level-set method. In the first part of the talk we will introduce parallel level set-based topology optimisation. Following this we will discuss homogenisation of periodic piezoelectric materials and consider preconditioning the coupled discretised linear system resulting from the finite element method. We use the developed techniques to design high-resolution piezoelectric meta-materials with enhanced properties that yield new insights into material design for sensing and hydrophone applications. (Back)

Broadband capture of ocean wave energy: a 3D model

Amy-Rose Westcott*, Luke Bennetts, Nataliia Sergiienko, Benjamin Cazzolato
University of Adelaide

Wave energy converters are devices that are designed to generate power from ocean waves. They need to be deployed in arrays for commercial viability, which creates opportunities for more effective energy capture than would be offered by the same number of devices acting independently.

We generate a strategy to obtain broadband power capture over a targeted band of wavelengths (142 to 429 m) covering two thirds of useable ocean wave frequencies, by arranging the devices in a 3D array into rows, and gradually changing the resonant properties of successive rows. The mathematical model of the array is developed based on linear wave theory in the frequency domain, and semi-analytical methods are used to solve for the hydrodynamic interactions.

Over 90% of the incident wave energy is captured over the target frequency range by an array with six rows (approximately half the length of the longest wavelength) using linear spring-damper power take-off mechanisms. This high absorption is sustained for incident wave angles between approximately $\pi/8$ and $7\pi/8$, and can be improved by increasing the number of rows. (Back)

Layout and parameter optimisation of a wave energy park in an irregular sea

Ben Wilks
The University of Newcastle

The task of developing the technology to harness the energy in ocean waves is an important challenge for the renewable transition. This talk describes a linear model of an array of cylindrical wave energy converters. The model is then used to construct an optimisation problem, in which both the device parameters and the locations of the wave energy converters are variables. Some preliminary optimisation results obtained using a genetic algorithm will be presented. (Back)

Using neural networks for inference problems in genetic epidemiology

Thomas Williams*, Alexander E Zarebski
The University of Melbourne

Phylogenetic trees, reconstructed from pathogen genomes, are used to estimate the reproduction number and the prevalence of infection over time. However, current inference methods are computationally expensive and usually rely on strong simplifying assumptions. To overcome these limitations, we developed a computational framework for the analysis of phylogenetic trees using neural estimators. In our approach, we use simulated data to train a neural network to estimate epidemiologically important quantities from phylogenetic trees.

Once pre-trained, such models can readily be adapted to novel settings, providing a versatile and computationally efficient approach to likelihood-free inference. We demonstrate that a neural network, trained to estimate parameters for one epidemic model (e.g. in which there is surveillance across the whole epidemic), can rapidly be fine-tuned to estimate parameters from other epidemic models (e.g. in which surveillance is constrained to a limited window of time). We show that fine-tuning can reach practically the same accuracy as fully trained estimators, but in an order of magnitude less computational time. (Back)

Fractional advection−diffusion modelling in fluid dynamics with spatially varying diffusion coefficients

Benchawan Wiwatanapataphee, Yong Hong Wu
Curtin University

This study presents a computational model for analysing fractional advection-diffusion processes in fluid dynamics, focusing on two-dimensional domains with spatially varying diffusion coefficients and memory effects. The model employs fractional calculus to extend traditional diffusion equations, integrating the Mellin Transform and its inverse for efficient numerical solutions. The evolution of concentration profiles, initiated with a Gaussian-like distribution, is simulated under the combined effects of advection and diffusion. Spatial heterogeneity in the diffusion coefficient is modelled through sinusoidal variations, reflecting realistic fluid dynamics scenarios. Analytical solutions in the Mellin domain are derived and transformed back to the spatial domain for detailed temporal analysis. The results reveal the critical influence of fractional orders and spatial variability on fluid transport dynamics, providing insights into complex anomalous diffusion phenomena in biological fluids. This approach demonstrates significant potential for advancing fluid dynamics modelling in biomedical engineering contexts. (Back)

Fractional Black−Scholes model for pricing derivatives in the Australian energy market

Doungporn Wiwatanapataphee*, Yong Hong Wu
Curtin University

The Australian energy market is characterized by high volatility, price spikes, and non-linear dynamics stemming from supply-demand imbalances, renewable energy integration, and regulatory interventions. These features challenge traditional models like the Black-Scholes framework, which fail to account for long memory, heavy tails, and volatility clustering inherent in energy prices. The Fractional Black-Scholes Model overcomes these limitations by incorporating fractional derivatives, which capture memory effects and anomalous diffusion, offering a robust framework for modeling price dynamics and valuing derivatives. By leveraging fractional time derivatives to model long memory and fractional space derivatives to address heavy-tailed behavior, this approach improves the valuation of electricity options and enhances risk management strategies under conditions of volatility clustering, price spikes, and non-Gaussian price behavior. This study calibrates the model to Australian energy market data and demonstrates its capability to address key challenges in derivative pricing and hedging strategies, with a focus on practical applications and the mathematical formulation of the model. (Back)

An efficient statistic for bounding the spectrum of data-driven operators

Caroline Wormell
The University of Sydney

Least-squares estimation from data is a very popular way of approximating operators, such as Laplacian operators for manifold visualisation, or Koopman operators for pattern identification in dynamics. These operators are typically interesting because of their spectrum, but there is typically huge variation between eigenvalues as to how much data sampling perturbs, or even swamps, them. It is consequently often unclear whether an data-driven eigenvalue reflects the true operator, or is simply a numerical artefact.

In this talk I will introduce a numerical test that allows us to answer this question by computing a pseudospectrum-like statistic that restricts the location and number of true eigenvalues. This statistic has many very useful properties: it is completely agnostic to function norm, it requires no extra information beyond that used to construct the operator, and it provides efficient rigorous bounds with limited data. This makes it a very useful tool in studying data-sampled operators in applications. (Back)

Stochastic limit cycles in the Togashi−Kaneko model of an autocatalytic system

Jeremy Worsfold, Richard G Morris
University of New South Wales

At finite system sizes,$O(1/\sqrt{N})$ fluctuations whose magnitude depends on the system's state can be essential to understanding non-trivial emergent phenomena. Such noise-induced behavior − where the peak of probability distributions do not coincide with fixed points of deterministic dynamics − have been used to explain collective motion of fish and ants, evolutionary dynamics and opinion formation. In the context of molecular biology, these notions were popularized by Togashi and Kaneko, and their eponymous model of autocatalytic chemical reactions in a cell. While this and other examples of noise-induced switches have been studied extensively, the analysis is invariably limited to systems with a fixed or fluctuating system size. However, this is rarely true in cells, due to active, energy consuming processes, such as secretion, uptake, synthesis and/or degradation of molecules. In this talk, we revisit the Togashi-Kaneko model and relax the assumption that the molecular species migrate in and out of the cell at identical rates. By doing so, we reveal the existence stochastic limit cycles, characterized by stochastic switches between states of almost total dominance by a single species, one of which grows and the other decays. We employ a Piecewise Deterministic Markov Process approximation of the system to enable the characterization of the dynamics and stationary distributions. Our methodology allows us to study models exhibiting switching behavior in the typical mesoscopic limit while allowing for dynamic, state-dependent fluxes in and out of the system. (Back)

Patient movements in the Victorian hospital system: does time matter?

David Wu
Monash University

In Victoria, we observe both established and novel strains of AMR organisms. These persist in our hospital system and have the potential to spread between facilities via colonised patients. An understanding of how patients move between facilities in the healthcare system may help in the design of more effective and reliable control measures for AMR. Most existing work on modelling inter-institutional spread of AMR in hospital systems uses static networks that imply patients move directly between hospitals, but neglect considerations of the timing and duration of patient admissions. Here, we propose that modelling other temporal dynamics, such as long periods between admissions, better captures important temporal patterns in patient movement. We test this by simulating patient movement on various network representations of the hospital system with differing levels of temporal fidelity and demonstrate that there are measurable differences in the timings of the spread of colonised individuals. This highlights the importance of considering temporal dynamics of patient movement when seeking to understand observed patterns of AMR spread. (Back)

Resolving the hydrodynamics of non-spherical microswimmers

Xinyi Yang*, Douglas Brumley, Jesse Collis, Hailong Guo
The University of Melbourne

The squirmer model is a canonical model for spherical microswimmers (e.g., ciliated microorganisms and Janus particles) in Stokes flow, where propulsion is driven by a surface slip velocity. Due to its simplicity and versatility, the squirmer model is a popular tool for modelling the collective dynamics of microswimmers. However, many microorganisms are not spherical in nature, limiting the applicability of this model. In this work, we extend the squirmer framework by connecting two spherical squirmers fore-and-aft in a dumbbell configuration and express the resultant flow field in terms of a twin multipole expansion. Using a boundary collocation method, we resolve the hydrodynamics of this "dumbbell squirmer" with high efficiency and accuracy. Ultimately, this framework permits investigation of systems involving non-spherical microswimmers at a range of length scales, from single-particle to collective dynamics. (Back)

Enhancing Monte Carlo simulation efficiency through optimal computing budget allocation for network reliability analysis

Wei-Chang Yeh
National Tsing Hua University

While Monte Carlo Simulation (MCS) remains a powerful tool for analyzing complex systems that defy analytical solutions, its effectiveness is often limited by substantial computational overhead and lengthy execution times, particularly when striving for high-precision estimates with minimal variance. This paper introduces an innovative approach to MCS that leverages Optimal Computing Budget Allocation (OCBA) principles to strategically distribute computational resources. The proposed methodology, termed SA-MCS (Self-Adaptive Monte Carlo Simulation), employs a dynamic sampling strategy that intelligently adjusts simulation intensity based on intermediate results. By continuously evaluating the potential value of additional samples and allocating computational effort to the most promising scenarios, SA-MCS achieves superior efficiency compared to conventional MCS approaches. Theoretical analysis demonstrates the method's improved convergence properties and reduced variance, while extensive empirical testing on complex binary-state network reliability problems validates its practical advantages. The results show significant reductions in computational requirements while maintaining or improving estimation accuracy. (Back)

Classification of streamline topology of vortex flows in doubly periodic domains

Tomoo Yokoyama
Saitama University

This talk presents a classification theory for the topological structure of orbits in Hamiltonian flows on the torus $\mathbf{T}^2$, a mathematical model for 2D incompressible and viscous flows. Building upon this theory, we extend the framework for converting the topological structure of Hamiltonian flows into a rooted planar tree, called a *partially Cyclically-Ordered rooted Tree (COT)*, and its string expression (COT representation), so that it can be applied to that for the flat torus $\mathbf{T}^2$. Applying the conversion algorithm to snapshots of 2D free-decaying turbulence and enstrophy cascade turbulence, we demonstrate that complicated flow patterns can be effectively represented as trees and letter sequences. This approach facilitates the extraction of coherent vortex structures from a topological perspective. Furthermore, the conversion algorithm addresses the challenge of accurately identifying such vortex structures in intricate flow patterns. This development opens up new possibilities for studying the dynamics and statistical properties of 2D turbulence in doubly periodic domains, offering new insights into the numerical analysis of turbulent flows from a topological viewpoint. (Back)

Numerical analysis of a coupled thermoelastic diffusion plate model

Neela Nataraj, Ricardo Ruiz-Baier, **Aamir Yousuf***
Monash University

We investigate the well-posedness of a coupled hyperbolic-parabolic system modeling diffusion in thermoelastic plates, consisting of a fourth-order hyperbolic c{pde} for plate deflection and second-order parabolic cp{pde} for the first moments of temperature and chemical potential. The unique solvability is established via Galerkin approach, and the additional regularity of the solution is also obtained under the appropriately strengthened given data. For numerical approximation, we employ the Newmark method for time discretization and a (C0-IP) c{dg} scheme for the spatial discretization of displacement. For the first moments of temperature and chemical potential, we use the Crank--Nicolson method for time discretization and conforming cp{fe} for spatial discretization. The convergence of the fully discrete scheme with quasi-optimal rates in space and a quadratic rate in time is established. Several numerical examples are presented to validate the theoretical findings. (Back)

Theoretical and mathematical models of cell fate

Adriana Zanca
The University of Melbourne

How pluripotent cells give rise to progressively more specialised cells over multiple cell divisions, known as cell fate, remains one of the mysteries of life. During development, it is of the utmost importance that cells uphold certain division regimes for an organism to survive. Beyond development, cell fate perturbations can result in cancer and other pathological conditions. The theoretical and mathematical biology community has been making contributions to our understanding of cell fate including by quantifying Waddington’s seminal landscape using dynamical systems, performing statistical trajectory inference on single-cell sequencing data, or considering geometric and algebraic approaches to cell fate. In this talk, I will present a collection of theoretical frameworks for describing cell fate and will introduce new perspectives and potential avenues for further exploration, among other things. (Back)

Pricing knock-out options with transaction costs

Xiaoping Lu, **Xinyi Zhang***
University of Wollongong

Barrier options are options that automatically become worthless, or activated when the underlying asset price hits a prescribed price, the barrier. Although barrier options are extensively studied in the literature, the pricing of such options with transaction costs is less investigated. Our project focuses on the pricing of knock-out barrier options in both European-style and American-style with proportional transaction costs based on a discrete hedging strategy. Taking transaction costs into account makes the pricing governing equations non-linear, thus, an implicit finite difference scheme is used to obtain the numerical solutions. Our results show the effects of transaction costs on option prices for the holder and the writer and the optimal exercise price for American-style options. (Back)

Clone wars: modelling tumour resistance in CAR-T cell therapy

Thomas Cummings, **Yang Zhao**
The University of Melbourne

Chimeric antigen receptor (CAR)-T cell therapy is a revolutionary immunotherapy that engineers T cells to target cancer cells more effectively, and has shown significant efficacy in blood cancers. Despite its success, variability in patient responses and the emergence of tumour resistance are not well understood. Clonal tracing data from mouse experiments show that the clonal composition of a relapsed tumour changes sharply as the initial CAR-T dosage is increased. This is reminiscent of bistability in dynamical systems.

Compartment modelling provides a framework for exploring different hypotheses of resistance development. By treating sensitive and resistant tumour cells as separate compartments, we investigate the possible long-term resistance patterns. Under simplifying assumptions, we analytically determine the stability of certain steady states to evaluate their biological viability. This allows us to hypothesise parameter regimes that support observations of bistability.

In reality, the observed switch-like behaviour may not necessarily be explained by bistability, but the extinction of certain clones at small cell numbers, which cannot be adequately described by deterministic continuous-state models. A preliminary investigation reveals that the switch-like behaviour can be reconstructed by considering a population to be extinct when its size drops below a threshold. (Back)

Counting sheep ... or counting parameters in transmission models

Zhao Mei Zheng*, Anthia Le, Domenic Germano
The University of Sydney

In George Martin's 2001 textbook 'Counting: The Art of Enumerative Combinatorics,' the abstract opens up with 'Counting is hard.' A wide variation in complexity of transmission models exists. This might be due to the context, purpose and decisions around the formation of models. Complex models are associated with more parameters and require a greater level of computation power. Do more parameters correspond to a 'better' model? In this study, we examine how we can classify and count parameters in the context of transmission models to quantify the number of parameters used. This can serve as a metric to describe and possibly evaluate the complexity of a model. (Back)

Major-minor mean field game of stopping: an entropy regularisation approach

Xiang Yu, Jiacheng Zhang, Keyu Zhang, **Zhou Zhou**
The University of Sydney

We study a major-minor mean-field stopping game in discrete time. We look for a relaxed equilibrium which is formulated as a fixed point of a set-valued mapping. Due to the presence of the major player, the set-valued mapping may not be convex, and thus the argument for the existence of a fixed point may not be directly applied. To overcome this difficulty, we consider an auxiliary problem by adding an entropy regularization term in the major player's problem. We show the existence of an equilibrium by the Kakutani-Fan-Glicksberg fixed-point theorem for the entropy regularized mean-field game. Next, we prove that this equilibrium converges as the regularization parameter tends to 0, and the limit is an equilibrium for the original problem. (Back)

9. Conference Delegates (as of 24 January 2025)

Name	Affiliation
Isobel Abell	The University of Melbourne
Matthew Adams	Queensland University of Technology
Ishraq Ahmed	The University of Sydney
Tristram Alexander	The University of Sydney
Sami Al-Izzi	UNSW Sydney
Lamees Alasmari	The University of Newcastle
Afnan Aldosri	The University of Newcastle
Rehab Aljabri	The University of Newcastle
Tharindi Amarathunge Achchige	University of South Australia
Md Nurul Anwar	The University of Melbourne
Karina Arias Calluari	The University of Sydney
Zayed Asiri	Flinders University
Aleksandar Badza	University of New South Wales
Boris Baeumer	University of Otago
John Bailie	The University of Auckland
Christopher Baker	The University of Melbourne
Indu Bala	The University of Adelaide
Weizhu Bao	National University of Singapore
Agnese Barbensi	The University of Queensland
Matthew Berry	University of New South Wales
Samuel Bolduc-St-Aubin	University of Auckland
Mitchell Bonham	The University of Newcastle
Jared Bronski	University of Illinois Urbana-Champaign
Kaitlyn Brown	Queensland University of Technology
Alexander Browning	University of Oxford
Douglas Brumley	The University of Melbourne
Pascal R Buenzli	Queensland University of Technology
Judith Bunder	University of South Australia
Obi Carwood	Queensland University of Technology
David Ceddia	The University of Melbourne
Pierluigi Cesana	Kyushu University
Vivien Challis	Queensland University of Technology
Rebecca Chisholm	La Trobe University
Radu Cimpeanu	University of Warwick
Simon Clarke	Monash University
Robert Cope	University of New England

Adelle Coster	University of New South Wales
Barry Cox	University of South Australia
Jessica Crawshaw	Queensland University of Technology
Richard Creswell	The University of Melbourne
Thomas Cummings	The University of Melbourne
Michael Dallaston	Queensland University of Technology
Siwen Deng	Macquarie University
Rodney Dharma	University of Melbourne
Jiahao Diao	The University of Melbourne
David Groothuizen Dijkema	University of Auckland
Heath Dimsey	University of Tasmania
Sam Doak	The University of Auckland
Steffen Docken	UNSW Sydney
Celia Dowling	The University of Melbourne
Oliver Eales	The University of Melbourne
Edoardo Fabbrini	Kyushu University
Alistair Falconer	The University of Queensland
Muhammad Asim Farooq	The University of Sydney
Luke Filippini	Queensland University of Technology
Jennifer Flegg	The University of Melbourne
Mark Flegg	Monash University
Brendan Florio	Murdoch University
Yong See Foo	The University of Melbourne
Larry Forbes	University of Tasmania
Daniel Fraterman	The University of Adelaide
Gary Froyland	UNSW Sydney
Domenic Paul Joe Germano	The University of Sydney
Liam Gibson	University of Canterbury
Cecilia González-Tokman	The University of Queensland
Patrick Grant	Queensland University of Technology
Catheryn Gray	University of New South Wales
Michael Groom	CSIRO
Hritika Gupta	The University of Melbourne
Bronwyn Hajek	University of South Australia
Lucy Ham	The University of Melbourne
Ashley Hanson	The University of Melbourne
Tianxiao Hao	The Kids Research Institute Australia
Georgio Hawi	The University of Sydney
Andreas Heinecke	The University of Newcastle

Kate Helmstedt	Queensland University of Technology
Daniel Herr	CSIRO
Roslyn Hickson	CSIRO and James Cook University
Edward Hinton	The University of Melbourne
Nam Ho-Nguyen	The University of Sydney
Graeme Hocking	Murdoch University
Alexandra Hogan	UNSW Sydney
Matthew Holden	The University of Queensland
Jordan Holdorf	Griffith University
Mahdi Jalili	RMIT University
Thisaakhya Jayakody	The University of Melbourne
Adrianne Jenner	Queensland University of Technology
Alexander Johnston	Queensland University of Technology
Stuart Johnston	The University of Melbourne
Zlatko Jovanoski	University of New South Wales Canberra
Sunghwan Jung	Cornell University
Kenji Kajiwara	Kyushu University
Manu Kalia	Freie Universiteit Berlin
Kartik Kamboj	The University of Melbourne
Minkush Kansal	UNSW Sydney
Kevin Kühl	UNSW Sydney
Paul Kew	Charles Sturt University
Maria Kleshnina	Queensland University of Technology
Pratyush Kumar Kollepara	La Trobe University
Maame Akua Korsah	The University of Melbourne
Bernd Krauskopf	University of Auckland
Shahak Kuba	Queensland University of Technology
Mason Lacy	Queensland University of Technology
Bishnu Lamichhane	The University of Newcastle
Timothy Earl Figueroa Lapuz	The University of Sydney
Thao P Le	The University of Melbourne
Noa Levi	The University of Melbourne
Angus Hamilton Lewis	The University of Adelaide
Kai Li	The University of Adelaide
Matthew Lim	The University of Sydney
Tommaso Lorenzi	Politecnico di Torino

Xiaoping Lu	University of Wollongong
Christopher Lustri	The University of Sydney
Michael Lydeamore	Monash University
Matthew Mack	University of South Australia
Connor Mallon	Queensland University of Technology
Robert Marangell	The University of Sydney
Harry Ros McArthur	The University of Melbourne
James McCaw	The University of Melbourne
Scott McCue	Queensland University of Technology
Mark Joseph McGuinness	Victoria University of Wellington
Manuela Mendiolar	CSIRO
Mike Meylan	The University of Newcastle
Hugh Michalski	The University of Adelaide
Claire Miller	The University of Auckland
Joel Miller	La Trobe University
Elise Mills	Queensland University of Technology
Ryan Murphy	The University of Melbourne
Josiah Murray	The University of Newcastle
Mary Myerscough	The University of Sydney
Joseph Ndenda	The University of Sydney
Cecilia Olivesi	The University of Auckland
James Mark Osborne	The University of Melbourne
Hinke Osinga	The University of Auckland
Michael Pan	The University of Melbourne
Davide Papapicco	The University of Auckland
Luz Pascal	Queensland University of Technology
Juan Patiño-Echeverría	University of Auckland
Aidan Patterson	University of South Australia
Vinesha Peiris	Curtin University
Nick Peters	University of New South Wales
Ravindra Pethiyagoda	The University of Newcastle
Ben Petschel	CleanCo Queensland
David Plenty	University of Wollongong
Olle Ponten	The University of Melbourne
Andrey Pototsky	Swinburne University of Technology
Courtney Rose Quinn	University of Tasmania
Behnaz Rahmani	The University of Auckland
Thakshila Rajapaksha	University of Wollongong
Llewyn Randall	Griffith University
Melanie Roberts	Australian Rivers Institute, Griffith University

Tony Roberts	University of Adelaide
Grace Robinson	Queensland University of Technology
Mariano Rodrigo	University of Wollongong
Christopher Rycroft	University of Wisconsin−Madison
Nina Rynne	Queensland University of Technology
Wil Schilders	ICIAM
Sungrim Seirin-Lee	Kyoto University
Siluvai Antony Selvan	The University of Melbourne
Sergiy Shelyag	Flinders University
Brock Sherlock	University of New South Wales
Kajanthan Shiyamasuntharam	University of Wollongong
Harvinder Sidhu	University of New South Wales
Matthew Simpson	Queensland University of Technology
Anja Slim	Monash University
Michael Small	The University of Western Australia
Dave Smith	The University of Newcastle
Eva Stadler	UNSW Sydney
Tace Stewart	Queensland University of Technology
Yvonne Stokes	The University of Adelaide
Augustinas Sukys	The University of Melbourne
Sergey A Suslov	Swinburne University of Technology
Daisuke Tagami	Kyushu University
Alex Tam	University of South Australia
Peter Taylor	The University of Melbourne
Natalie Thamwattana	The University of Newcastle
Liam Timms	The University of Melbourne
Parul Tiwari	Auckland University of Technology
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Monica Torres	University of New South Wales
Hayden Tronnolone	Flinders University
Justin Tzou	Macquarie University
Yash Vats	The University of Queensland
Sarah Vollert	Queensland University of Technology
Matthew Walker	The University of Melbourne
David James Warne	Queensland University of Technology
Simon Watt	UNSW Canberra
Georgia Weatherley	Queensland University of Technology
Zachary James Wegert	Queensland University of Technology
Amy-Rose Westcott	University of Adelaide
Ben Wilks	The University of Newcastle

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David Wu	Monash University
Jean Yang	The University of Sydney
Xinyi Yang	The University of Melbourne
Wei-Chang Yeh	National Tsing Hua University
Tomoo Yokoyama	Saitama University
Aamir Yousuf	Monash University
Adriana Zanca	The University of Melbourne
Xinyi Zhang	University of Wollongong
Yang Zhao	The University of Melbourne
Zhao Mei Zheng	The University of Sydney
Zhou Zhou	The University of Sydney
Ilze Ziedins	The University of Auckland