Australasia Astrobiology Meeting

PROGRAM AND ABSTRACTS

13-15th June 2023

Photo by Ethan Soh on Unsplash

Welcome!

Since humankind evolved, we have been fascinated by the stars, planets, and cosmos. Is there life, even intelligent life, out there, or are we alone? The attempt to search for life in the Universe touches on fundamental hopes and concerns. It goes to the heart of what it is to construct a theory, grasp a concept, and have an imagination.

With the hope that intelligent life exists somewhere in the Universe, we welcome you to join us and be a part of the Australasia Astrobiology Meeting (AAM) 2023. We will explore Prebiotic Chemistry & Origins of Metabolism, Geology & Geochemistry of Early Earth & Mars, Space Exploration & Technology, as well as Science Communication, Outreach & Engagement at UNSW Kensington campus, Sydney.

This event will bring together experts and students interested in Astrobiology to cultivate and exchange ideas on how life could originate and endure in the Universe.

We are excited to host you at AAM2023, and to provide a supportive platform for students, especially to present their work and build networks within the collaborative and interdisciplinary Astrobiology research community. Just as life itself is a synergistic process in the sense that life's biological, physical, and chemical properties are intertwined, we wish AAM2023 to do the same.

We hope you enjoy the meeting!

Organising Committee Members:

Albert Fahrenbach	Brendan Burns	Martin Van Kranendonk
Anna Wang	Joshua King	Soumya Kanti De
Lauren Lowe	Dev Chauhan	Arslan Siddique
Clare Fletcher	Quoc Phuong Tran	

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AUSTRALIAN CENTRE *for* ASTROBIOLOGY

LOCATION

The Australasia Astrobiology Meeting 2023 will be held at UNSW Kensington Campus.

All oral presentations will be held in the Ritchie Theatre in the John Niland Scientia Building, marked with a green star on the map below in grid reference G19.

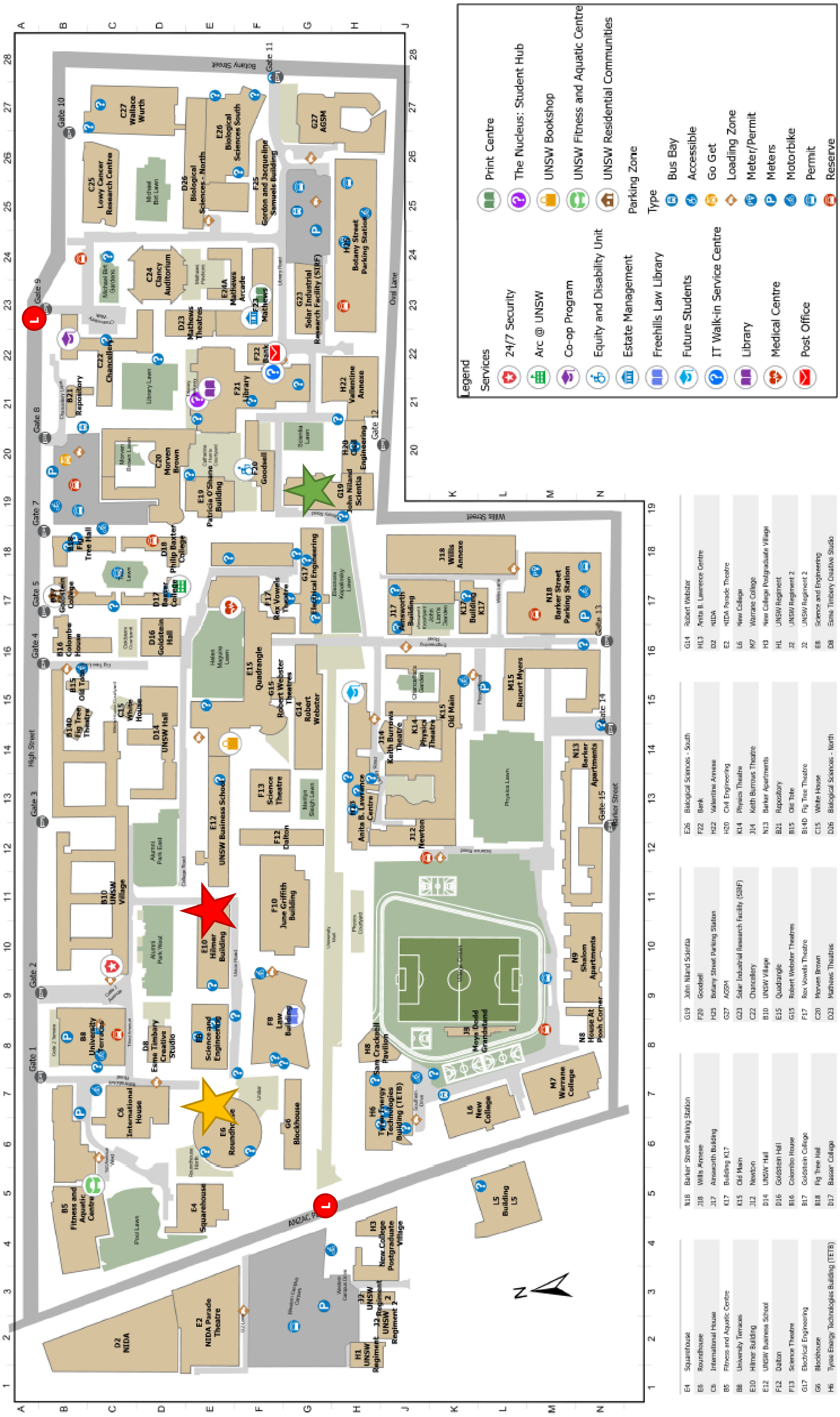
The poster session will be held in the Michael Crouch Innovation Centre in the Hilmer Building, marked with a red star on the map below in grid reference E10.

The optional conference dinner will be held in the UNSW Roundhouse, marked with a yellow star on the map below in grid reference E6.

If you are driving to UNSW, there are many places to park your car marked on the map below with a white letter 'P' in a blue circle. If you are instead catching public transport, the L2 and L3 light rail services stop on High St near Gate 9, and Anzac Pd near the Main Walkway respectively. These light rail stops have been marked with a white letter 'L' in a red circle.

A larger copy of this map will also be provided on the website.

MAP



E4	Squarehouse	N18	Barker Street Parking Station	G19	John Niland Scientia	E26	Biological Sciences - South	G14	Robert Webster
E6	Roundhouse	J18	Willis Annexe	F20	Goodsell	F22	Bank	H13	Anita B. Lawrence Centre
C6	International House	J17	Ainsworth Building	H25	Botany Street Parking Station	H22	Valentine Annexe	D2	NIDA
B5	Fitness and Aquatic Centre	K17	Building K17	G27	AGSM	H20	Civil Engineering	E2	NIDA Parade Theatre
B8	University Terraces	K15	Old Main	G23	Solar Industrial Research Facility (SIRF)	K14	Physics Theatre	L6	New College
E10	Hilmer Building	J12	Newton	C22	Chancellery	J14	Keith Burrows Theatre	M7	Warrane College
E12	UNSW Business School	D14	UNSW Hall	B10	UNSW Village	N13	Barker Apartments	H3	New College Postgraduate Village
F12	Dalton	D16	Goldstein Hall	E15	Quadrangle	B21	Repository	H1	UNSW Regiment
F13	Science Theatre	B16	Colombo House	G15	Robert Webster Theatres	B15	Old Tote	J2	UNSW Regiment 2
G17	Electrical Engineering	B17	Goldstein College	F17	Rex Vowels Theatre	B14D	Fig Tree Theatre	J2	UNSW Regiment 2
G6	Blockhouse	B18	Fig Tree Hall	C20	Morven Brown	C15	White House	E8	Science and Engineering
H6	Tyree Energy Technologies Building (TETB)	D17	Basser College	D23	Mathews Theatres	D26	Biological Sciences - North	D8	Esme Timbery Creative Studio
H8	Sam Cracknell Pavilion	D18	Philip Baxter College	F23	Mathews	C27	Wallace Wurth	J8	Moya Dodd Grandstand
N8	House At Pooh Corner	E19	Patricia O'Shane Building	E24A	Mathews Arcade	C25	Lowy Cancer Research Centre		
N9	Shalom Apartments	F21	Library	C24	Clancy Auditorium	F8	Law Building		
M15	Rupert Myers	L5	Building L5	F25	Gordon and Jacqueline Samuels Building	F10	June Griffith Building		

AAM2023 SCHEDULE OVERVIEW

Time	Day 1 13/06	Day 2 14/06	Day 3 15/06
8:30	Registration	Registration & Networking	Registration & Networking
8:40	Opening Remarks (Dr Albert Fahrenbach)		
8:50			
9:00	Prebiotic Chemistry & Origins of Metabolism	Geology & Geochemistry of Early Earth & Mars	Prebiotic Chemistry & Origins of Metabolism
9:10			
9:20			
9:30			
9:40			
9:50			
10:00			
10:10			
10:20			
10:30		Break	Break
10:40	Break		
10:50			Space Exploration & Technology
11:00	Space Exploration & Technology	***Keynote - Professor Steven Benner***	
11:10			
11:20			Prebiotic Chemistry & Origins of Metabolism
11:30			
11:40			Lunch
11:50	Lunch		
12:00		Lunch	
12:10			
12:20			
12:30			
12:40			
12:50			
1:00			

1:10			Geology & Geochemistry of Early Earth & Mars
1:20	Space Exploration & Technology		
1:30		Posters	
1:40			
1:50			
2:00			
2:10			Break
2:20			
2:30			Geology & Geochemistry of Early Earth & Mars
2:40			
2:50			
3:00	Break		
3:10			
3:20			
3:30	Science Communication, Outreach & Engagement		
3:40			Closing Remarks (Dr Anna Wang)
3:50			
4:00		End Day 2	End Day 3
4:10			
4:20			
4:30			
4:40			
4:50	End Day 1		
6:30	Conference Dinner (Optional)		

AAM2023 DETAILED SCHEDULE

<table>
<tr><th>Time</th><th>Day 1 13/06</th><th>Day 2 14/06</th><th>Day 3 15/06</th></tr>
<tr><td>8:30</td><td>Registration</td><td rowspan="3">Registration & Networking</td><td rowspan="3">Registration & Networking</td></tr>
<tr><td>8:40</td><td rowspan="2">Opening Remarks (Dr Albert Fahrenbach)</td></tr>
<tr><td>8:50</td></tr>
<tr><td>9:00</td><td rowspan="3">Professor Jim Cleaves</td><td rowspan="3">Professor Andy Tomkins</td><td rowspan="3">Dr Nick Green</td></tr>
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<tr><td>9:20</td></tr>
<tr><td>9:30</td><td rowspan="2">Lauren Lowe</td><td rowspan="2">Dr Joseph Michalski</td><td rowspan="2">Quoc Phuong Tran</td></tr>
<tr><td>9:40</td></tr>
<tr><td>9:50</td><td rowspan="2">Professor Anthony Poole</td><td rowspan="2">Emeritus Professor Simon George</td><td rowspan="2">Professor Rowena Ball</td></tr>
<tr><td>10:00</td></tr>
<tr><td>10:10</td><td rowspan="3">Associate Professor Matthew Baker</td><td rowspan="2">Qiannan Xu</td><td rowspan="2">Shotaro Tagawa</td></tr>
<tr><td>10:20</td></tr>
<tr><td>10:30</td><td rowspan="3">Break</td><td rowspan="2">Break</td></tr>
<tr><td>10:40</td><td rowspan="2">Break</td></tr>
<tr><td>10:50</td><td rowspan="3">Dr Chris Hansen</td></tr>
<tr><td>11:00</td><td rowspan="3">Dr Laura McKemmish</td><td rowspan="6"><u>Keynote - Professor Steven Benner</u></td></tr>
<tr><td>11:10</td></tr>
<tr><td>11:20</td><td rowspan="2">Dr Soumya Kanti De</td></tr>
<tr><td>11:30</td><td rowspan="2">Professor Martin Van Kranendonk</td></tr>
<tr><td>11:40</td><td rowspan="9">Lunch</td></tr>
<tr><td>11:50</td><td rowspan="9">Lunch</td></tr>
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<tr><td>1:10</td><td rowspan="2">Professor Penny King</td></tr>
<tr><td>1:20</td><td></td></tr>
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1:30	**Professor Gretchen Benedix**	Posters	
1:40			**Dr Joshua Hedgepeth**
1:50	Associate Professor Kate Poole		
2:00			
2:10	Dr Eriita Jones		Break
2:20			
2:30	**Dr Ben Montet**		**Dr Indrani Mukherjee**
2:40			
2:50			
3:00	Break		Ema Nersezova
3:10			
3:20			Khushi Daga
3:30	Associate Professor Carol Oliver		
3:40			Closing Remarks (Dr Anna Wang)
3:50	Dr Cobi Calyx		
4:00		End Day 2	End Day 3
4:10	Juan C. Zapata Trujillo		
4:20			
4:30	Rabeea Abdul Rasheed		
4:40			
4:50	End Day 1		
6:30	Conference Dinner (Optional)		

LIST OF ABSTRACTS: DAY 1, TUESDAY 13TH JUNE

ORAL PRESENTATION – INVITED SPEAKER

Analysis of Complex of Reaction Networks

Professor Jim Cleaves[1]

[1]Blue Marble Space Institute of Science

Prebiotic chemistry concerns itself with the transition from abiotic to biological chemistry. While the definition of life remains slippery, a hallmark of evolving living systems is that they find novel molecular solutions for their propagation via the complex interactions of natural selection acting on an extremely large phase space, thus it is difficult to predict what evolving living systems will become, "retrodict" their prior states, or ultimately determine how they began given their present state. The nature of this problem is presented here, as is a novel method for exploring complex reaction networks that may give rise to life.

ORAL PRESENTATION

Modulating the lipid packing and solute permeability of model protocells.

Lauren Lowe[1,2], Rifah Riyadh[1,2], Dr Anna Wang[1,2]

[1]School of Chemistry, UNSW, Sydney, NSW 2052, Australia, [2]Australian Centre for Astrobiology, UNSW Sydney, NSW 2052, Australia

This project is part of efforts to build a propagating minimal synthetic cell (model protocell). A core feature of this synthetic cell that enables membrane growth to occur is the presence of enzymes required for phospholipid synthesis. For a high yield of phospholipid synthesis, an external feedstock of nutrients is required, and these nutrients need to be able to permeate the membrane (1). The growing membrane could have a range of lipid compositions depending on gene expression levels, but it is not yet understood how this range of lipid compositions could impact membrane permeability. Improving the permeability of membranes of mixed lipid composition to the nutrients required for phospholipid synthesis will help ensure that membrane growth and subsequent division can occur successfully.

Electrical impedance spectroscopy and a shrink-swell assay were used to monitor lipid packing and the permeability of bilayers composed of a mixture of lipids. We found that vesicles composed of a blend of POPC and POPG were permeable to glycerol and glucose but impermeable to larger sugars such as sucrose. Blended POPC and POPG bilayers were permeable to glycine, but impermeable to slightly more complex amino acids such as lysine. We also found that these membranes were impermeable to a range of other solutes including AMP, ATP and NaCl, likely owing to their charged nature or size. Cataloguing the permeability of blended membranes to solutes such as these helps us tune gene expression levels to improve bilayer permeability to nutrients vital to the function of the synthetic cell. This will help us build a propagating synthetic cell that can grow and divide using the simplest components possible, helping us understand how these processes evolved throughout life's history.

(1) Eto, S., Matsumura, R., Shimane, Y., Fujimi, M., Berhanu, S., Kasama, T., & Kuruma, Y. Phospholipid synthesis inside phospholipid membrane vesicles. Commun Biol, 5 (2022) 1–11.

The origin of DNA – early or late?

Professor Anthony Poole[1]

[1]School of Biological Sciences, University of Auckland, Auckland, New Zealand

All life on earth depends on ribonucleotide reduction for the production of DNA building blocks (deoxyribonucleotides), required for genome replication. In ribonucleotide reduction, deoxyribonucleotides are derived from ribonucleotides (RNA building blocks), suggesting that the evolution of modern DNA-based genomes was from RNA-based genomes. The nature of the reaction is such that it appears ribonucleotide reductases (RNR) evolved only after the evolution of the genetic code as the reaction appears to only be available to protein-based enzymes. However, some researchers have speculated that ribonucleotide reduction replaced an earlier route for deoxyribonucleotide synyhesis. This proposed route is called the reverse deoxyriboaldolase (reverse DERA) pathway, and is still used in cells but for salvage (recycling) of surplus DNA building blocks. We were interested to know whether a bacterial line could be created that completely lacks ribonucleotide reduction and, if so, would the reverse DERA pathway compensate for its absence. To this end, we created an Escherichia coli line where the genes for all three RNRs were deleted from the genome. We next evolved our line under conditions where DNA building blocks were in short supply to see whether the reverse DERA pathway may compensate for loss of ribonucleotide reduction. We report that, instead of compensation, we observe mutation in a key gene in the DERA pathway. These mutations render the pathway inactive. Interestingly, such mutations are also found in the small number of bacterial endosymbionts and parasites that have lost ribonucleotide reduction and are instead dependent on their hosts for DNA building block production. We conclude that pathway loss provides a short term benefit as preventing recycling avoids the loss of building blocks in short supply. Finally, we will present preliminary data indicating that because our lines cannot synthesise deoxyribonucleotides they are prone to incorporation of ribonucleotides in their genomes. We will discuss the significance of our results within the context of the origin of DNA.

Ask the ancestors: resurrecting and re-evolving the bacterial flagellar motor.

Associate Professor Matthew Baker[1]

[1]UNSW

The flagellar motor is one of the canonical molecular complexes, ~40 nm in diameter but capable of rotating at 1000 Hz, self-assembling in the membrane and changing rotational direction in milliseconds. Recent new structures revealed that the 'engine' of this motor, the stator complex, is itself a rotating nanomachine powered by ion flow. Our recent work on the flagellar motor used directed evolution to explore how the motor adapts to new power sources. We combine phylogenetics, ancestral reconstruction, directed evolution and synthetic biology to examine key aspects of the origins of motility. We have initially focussed on the stator complex as this represents a key exaptation of ion channels to drive the motor that 'got life going' and powered early motility. Our next work will look at the role of the propellor in the origins of motility, to answer questions such about what is the minimal functional flagellar motor, and how has it optimised for microbial propulsion over billions of years.

Ridone, P., Ishida, T., Lin, A., Humphreys, D.T., Giannoulatou, E., Sowa, Y., and Baker, M.A.B. (2022).

The rapid evolution of flagellar ion selectivity in experimental populations of E. coli.

Science Advances 8, eabq2492. 10.1126/sciadv.abq2492.

Beyond Phosphine on Venus: How do we know if we have found aliens?

Dr Laura McKemmish[1]

[1]UNSW

In late 2020, astronomers announced the detection of phosphine - a well-known biosignature - on Venus and vigorous debate exploded. Was there life on Venus? Was it a telescope error? Or just sulfur dioxide?

As a computational quantum chemist specializing in producing molecular spectroscopy data for astronomers, I was keenly aware of the lack of suitable spectral data necessary for meaningful remote follow-up studies of initial biosignature detections both on Venus and in future studies of planets within and beyond our solar system. It turned out that astronomers are completely unable to detect any phosphorus-bearing molecules except phosphine and diatomics because they did not know their spectra, meaning the reaction networks that produce and destroy phosphine cannot be remotely probed. Though this data paucity is more acute for phosphorus-bearing molecules (which are often solids), more generally, less than 100 molecules have sufficiently accurate spectral data to allow remote detection in the infrared or visible spectral regions - the only detection method for molecules on exoplanets.

The ability to detect molecules and understand the limitations of these detections, including potential misidentifications, is crucial to the future scientific search for extraterrestrial life. My group takes two complementary and critical approaches. First, very high-accuracy predictions of the spectroscopy of small molecules by combining and experimental results to produce sub-cm-1 accuracy spectral cross-sections. Second, high throughput quantum chemistry methods to determine approximate spectroscopy of thousands of molecules. Together, ongoing method development and new research using both these approaches will provide the spectral data required to support future astrobiology needs.

LifeSpringsMars: A new Australian-led sample return mission to search for life on Mars

Professor Martin Van Kranendonk[1]

[1]UNSW

LifeSpringsMars is a new, multi-national sample return mission to search for signs of ancient life in digitate nodular opaline silica hot spring deposits of the Columbia Hills, Gusev crater, Mars. Discovered by NASAs Spirit rover, the hot spring deposits represent the best materials to investigate for signs of life, on account that they are morphologically identical to digitate nodules from terrestrial hot springs where their form is mediated by microbes, that hot spring silica entombs microbial fossils and preserves them for billions of years, and because hot springs are now widely regarded as the most likely site for the origin of life on Earth.

A novel, low-cost, mission architecture, purposely designed to be 'light and nimble', outlines sample return via a single launch aimed for 2032. If successful, LifeSpringsMars could provide the first sample return material from the red planet. Australia is leading this initiative, in collaboration with scientists and engineers from Japan, the US, and New Zealand.

"Cheap" Sample Return from Mars using Machine Learning

Professor Gretchen Benedix[1]

[1]Curtin University

Planetary science is the study of the planets and moons in our solar system and the processes that formed them. Understanding the geological history of another world has an importance of its own, but there is a larger significance beyond that. Our solar system shows us the many different pathways geological bodies can evolve along over time and therefore provides a template for understanding planet formation and evolution not just here, but throughout the universe. If we understand habitable zones in our solar system, we can apply that knowledge across the galaxy.

Finding the source craters of the martian meteorites has been a topic of interest since these meteorites were first hypothesised to be from Mars. It's been a mystery with the samples providing tantalising clues pointing to where they might have formed on Mars. The major clues are around the ages of the meteorites - we use radiometric dating to determine the crystallisation age, a re-heating event age and even an impact event age (the one that launched the sample into space towards the Earth). To map these ages to the surface of another planet takes either extreme patience or a leap in technology.

My team at Curtin focussed on developing the latter - using new machine learning techniques, we have been able to unravel the surface history of Mars by counting all craters > 100m in diameter. We have also used our algorithm to count craters smaller than that size, but the data are not complete. This devlopment has also be timely because of the availability of very high resolution (cm/pix) imagery of Mars.

I'll present some of the nuts and bolts of the machine learning language, but will focus on the outcome, which are the locations on Mars that we can confidently say we have sampled.

Force sensing ion channels in human cells modulate cellular adaptations to microgravity

Associate Professor Kate Poole[1]

[1]UNSW

The evolution of life on Earth has occurred under the persistent impact of Earth's gravitational field. Life can be sustained in reduced gravity environments, including microgravity, however Earth-based organisms undergo adaptive changes under these conditions. While many changes in human physiology are relatively well described (including bone and muscle wastage, changes in immune system function and the development of anaemia), there are many open questions regarding the molecular and cellular mechanisms that underpin these changes. We have investigated whether force sensing ion channels modulate cellular adaptations when isolated human cells are treated with simulated microgravity, using a random positioning machine. Deletion of a force sensing ion channel (ELKIN1) from melanoma cells led to a reduction in the microgravity-induced changes in cell attachment and cell morphology, a reversal in the microgravity-induced modulations in focal adhesion structure and a loss of alterations in the localisation of the transcriptional co-activator, YAP1 that are all observed in wild type cells. These observations stem from experiments conducted on flat tissue culture substrates. When clusters of cells were embedded in three dimensional gels formed from collagen I, simulated microgravity reduced the ability of wild type cells to break from the cell cluster and invade the surrounding matrix. However, this reduction in invasion was delayed in ELKIN1 knockout cells. These data suggest that force sensing ion channels play a role in cellular adaptations to a reduction in gravitational loading. Future studies will investigate whether similar impacts are noted when additional force sensing ion channels are disrupted and will address the question of how the function of these molecular force sensors is altered under conditions of microgravity.

Initial Development of a Planetary HYdrothermal eNvironment Detector (PHYND)

Dr Eriita G. Jones[1], Associate Professor Katarina Miljkovic[1], Dr Joshua E. Hedgepeth[1], Hely C. Branco[1]

[1]School of Earth and Planetary Sciences, Space Science and Technology Centre, Curtin University

Hydrothermal systems on Earth can sustain diverse chemosynthetic microbial communities due to their warmth, mineral-rich fluids and complex chemistry. On other planets, hydrothermal systems can have high astrobiological significance. They can occur where a heat source and fluid source intersect in the subsurface. This type of environment, and the ecosystems they may sustain, have been studied on Earth in a variety of settings, such as: hydrothermal vents along the ocean floor, where upwelling magma heats seawater in fissures in the oceanic crust; hot springs, where subsurface magma or deep geothermal heated crustal rocks superheat groundwater; and impact-generated hydrothermal systems. In impact-generated hydrothermal systems, the shocked pressures and temperatures of the impact event heats, melts and fractures target materials containing water, thereby both heating fluids and generating fluid pathways. Given that impact cratering is a common geologic process in the Solar System, locating hydrothermal systems on other planets is of great importance in the search for sites with the potential for supporting past, or even present day, habitable environments in the subsurface. In this work, we present the initial development of a comparative planetology approach for a Planetary HYdrothermal eNvironment Detector (PHYND) using multi- and hyper-spectral satellite imagery across visible and infrared wavelengths, namely Sentinel-2, ASTER, CRISM, THEMIS, CTX and HiRISE data. Early work in developing the PHYND on terrestrial and martian impact craters will be shared. The future development of the detector and the pseudo-validation of any positive detections via comparison to impact modelling (fluid pathways and heat distribution mapping, see Hedgepeth et al. abstract, same meeting) and in-situ terrestrial sampling will be discussed.

The Search for Habitable Exoplanets

Dr Ben Montet[1]

[1]UNSW

The NASA Kepler and TESS missions have revolutionised our understanding of many aspects of planetary systems, ranging from their demographics and the occurrence of Earth-sized planets to the role of their active host stars in enabling habitable environments. As we move closer to a new generation of large telescopes, which planets should we prioritise in the search for biosignatures? How will we distinguish true signs of life from false positives? And how much does the host star matter? In this talk, I will give an overview of our understanding of nearby planetary systems and our limits in detailed characterisation, highlighting some of the opportunities that will present themselves in the coming years.

Astrobiology Virtual Field Trips in higher education settings: Moving from explanation to exploration

Associate Professor Carol Oliver[1,2]

[1]UNSW, [2]Australian Centre for Astrobiology

Hot springs are considered a potential site for the origin of life, and an essential piece of the narrative in second year university astrobiology courses. In 2022, a collaboration was initiated to leverage the combination of a unique immersive laptop-delivered VFT authoring tool at UNSW and the hot spring expertise at the University of Auckland. An initial run of the hot springs VFT occurred in astrobiology classes in both universities with a common problem arising – the students did not understand the reasons for undertaking a VFT. As a result, we modified the hot springs VFT to move it from a 'sage on the stage' approach typical of university teaching to 'education through exploration,' with the aim of moving students from lower order thinking of 'remembering' to higher order thinking of 'understanding' requiring critical thinking and problem solving that occurs in discovery. Students will now explore the VFT embedded with samples with no explanatory text. They will use a handwritten field notebook for their virtual field experience, an approach proven over six years of testing in another astrobiology VFT. Students will be provided with questions to prompt discovering the differences between an alkali chloride and acid hot spring environment. They will then use the field experience to consider hydrothermal systems on Mars and potentially Jupiter's moon, Europa. In this paper we demonstrate the difference between a 'show and tell' and 'exploratory' VFT - from teaching astrobiology as a body of facts, to how astrobiologists see this dynamic and highly visual discipline.

ORAL PRESENTATION

Choosing Australia's first plants in space

Dr Cobi Calyx[1]

[1]UNSW

Australia recently invested in astrobotany with the new ARC Centre of Excellence for Plants in Space, but informal science organisations have already been moving forward with Australian plants in space. Golden wattle seeds were sent to the International Space Station in 2021 by the One Giant Leap Australia Foundation and the Japan Aerospace Exploration Agency (JAXA). The NASA-affiliated Growing Beyond Earth project has launched in Australia in partnership with Royal Botanic Gardens Victoria. This has involved public discussion about plans for schools to experiment with Australian native plants in growth chambers designed for space.

Given the wide range of Indigenous knowledges and uses of Australian native plants, there are many communities with potential but non-exclusive rights to free, prior and informed consent about using species associated with traditional knowledge. Are there paths forward in which these rights could be respected? Plants like warrigal greens and purslane have long histories of use in Australia given the edibility and flexibility of growing conditions that would make them good candidates for astrobotany. Could they one day be cosmopolitan to space as they are to coastlines here? Do their ethnobotanical histories on Earth matter for this future?

What could benefit sharing in astrobotany look like? How could NASA's standard open data policy coexist with principles of Indigenous data sovereignty? How does astrobotany relate to the democratisation of space? Are there ways we can move forward with taking Australian plants into space that don't replicate the inequities and injustices that continue to shape how we live on Earth?

Involving Senior High School Students in the Scientific Search for Outer Space Life

Juan C. Zapata Trujillo[1]

[1]UNSW

The search for molecular species, especially biosignatures, in exoplanet atmospheres is an intriguing topic that can inspire high-school students to engage in scientific research. This exploration provides students with the opportunity to learn about molecular spectroscopy, computational chemistry, data science, and programming in Python, while gaining a deeper understanding of how researchers look for molecules in gaseous environments.

During this talk, I will share my experience mentoring senior high school students in research, while developing biosignature-themed educational resources to facilitate their engagement and research experience. I will discuss my involvement as a lead mentor (2021-2023) in designing, developing, and delivering the Spectra project within the SciX@UNSW summer school, which is a week-long research-integrated-learning experience for senior high school students in New South Wales, Australia (unsw.to/scix). Specifically, I will describe our strategy for designing guided workshops and Jupyter Python notebooks that are accessible and interesting to this audience, promoting skill development in an exciting research environment.

High school students greatly benefit from involvement and exposure to this field, as it offers them with a pull of learning outcomes that can leverage their experience and equip them with essential skills for future scientific pursuits. Most notably, quotes from former Spectra students highlight how their scientific thinking and networking is enhanced throughout the week, e.g., they "enjoyed learning new chemistry" and "getting their research project working and making new friends", and how they become more confident about programming in Python (confidence rate increases by 2 points by the end of the summer school).

Astrobiology Roadmap of Pakistan–Education and Outreach activities

Rabeea Abdul Rasheed[1]

[1]Blue Marble Space Institute of Science

Introduction:

A tough module of astrobiology was started in October 2017 to Grades 6th and 7th at Lahore Grammar School. This module is the first to be taught at the secondary school level in Pakistan. More than 4000 students are now familiar with Astrobiology 101. Furthermore, there are more than 600 students enrolled in the next session of Astrobiology. While the first session was only a 6 months long course, the subject proved to be of such great interest to the school management and pupils that the next session's duration got increased to be 1 year long.

Objective:

Astrobiology is evolving rapidly and it should be accessible to every student. It considers the possibility of life beyond Earth while keeping in mind what life is on Earth and how it evolved. These are important and essential questions for which students should get a chance to reflect on and search for answers.

Summary:

The introduction of Astrobiology on the secondary school level is important because astrobiology integrates several areas of knowledge and gives students a thorough outlook of the Cosmic perspective. The impact of astrobiology is visible now students who took the course in 2017 and onwards are working on astrobiology-related projects independently at national and international levels.

ORAL PRESENTATION – INVITED SPEAKER

Meteorites and micrometeorites on Mars: Potentially micro-fossil preserving sites with enhanced availability of limiting nutrients

Professor Andy Tomkins[1]

[1]Monash University

NASA's strategy in exploring Mars has been to follow the water, because water is essential for life, and it has been found that there are many locations where there was once liquid water on the surface. Now perhaps, to narrow down the search for life on a barren basalt-dominated surface, there needs to be a refocusing to a strategy of "follow the nutrients". We have investigated meteorites and micrometeorites on the Nullarbor Plain in Australia to explore their utility in the search for life on Mars. Meteorites and micrometeorites are more useful to chemolithotrophic life than typical Martian basaltic crust. They are rich in reactive reduced forms of common limiting nutrients that can be used as sources of chemical energy via oxidation reactions, such as P, S, Fe in phosphides, sulfides and FeNi alloys. Dense micrometeorites are abundant in a range of desert environments, and are concentrated by aeolian processes into specific sites that would be easily investigated by a robotic rover. Meteorites and micrometeorites are currently far more abundant on the surface of Mars than on Earth, and given the far greater abundance of water and warmer conditions on Earth and thus much more active weather system, this was likely true throughout the history of Mars. Our studies of meteorites found on the Nullarbor show that they preserve microbe microfossils and DNA from active microbial colonies, they protect microbes from ionising radiation, and they are well suited to preserving isotopic evidence of microbial activity.

ORAL PRESENTATION

Geological diversity and astrobiological potential of lakes and seas on Mars

Dr Joseph Michalski[1]

[1]The University of Hong Kong

Hundreds of ancient lake basins detected on Mars via orbital remote sensing represent rare oases of hydrosphere-atmosphere-lithosphere interaction with great astrobiological potential. Most martian paleolakes date to the Noachian (>3.7 billion years ago, b.y.a.) and likely lasted ~102-106 years, representing only a small fraction of the ~400 million years of Noachian time. Noachian lacustrine deposits contain detrital Fe/Mg-rich clay minerals as well as authigenic Fe/Mg-carbonates, sulphates, silica, chlorides and clay minerals, which likely preserve characteristics of the ancient atmosphere and climate. While martian paleolakes are undeniably among the popular targets for future surface exploration and sample return, many questions surrounding prospects for biogenesis and biological productivity in short-lived lakes and transient warm climates on an otherwise cold planet remain: How would the faint young sun, Mars' greater distance from the sun, a dusty atmosphere or the planet's lack of a magnetic field affect possible evolution of photosynthesis and our concept of biosignatures in martian lakes? In the absence of land plants to stabilize the surface, and with slower settling of suspended sediment in lower gravity, would martian lakes have been murky with a very shallow photic zone? How would the lower gravity and impact-fractured crust affect compaction of lake sediment and seepage of lake water to regional groundwater systems? The oldest lacustrine deposits on Earth (2.77 b.y.a.) are nearly a billion years younger than most of the known lakes on Mars. Lost from the Earth's geological record is evidence for subaerial hot springs, fresh water and fluid mixing zones where life is thought by many to have originated on this planet c.a. 3.8-4 b.y.a.. Martian lakes from this time period, some of which contain evidence for hydrothermal settings, fluid mixing and wet-dry cycles, can thus provide an invaluable window into early prebiotic processes, climate and potentially life's origins on Earth.

ORAL PRESENTATION

Massive manganese carbonate deposits had a major effect on biogeochemical carbon cycling during the Cryogenian interglacial period

Emeritus Professor Simon George[1]

[1]Macquarie University

Manganese-rich deposits in the lower member of the Datangpo Formation (DTP) (ca. 663–654 Ma) in South China formed in the aftermath of the Cryogenian Sturtian glaciation. The Mn in the DTP occurs dominantly as rhodochrosite and Ca-rhodochrosite. Detailed reports on the formation mechanisms of micro-scale (<2–5 μm) ooid-like Mn carbonates in the DTP have rarely been published. Systematic petrography and geochemical analyses in this study demonstrate the coexistence of two types of micro-scale ooidal-like Mn carbonates formed through two distinct mechanisms, either dominated by microbially-mediated or physiochemically-forced pathways. The Type I Mn carbonate has relatively larger grain size of 2–5 μm and exhibits a radial-concentric microfabric that shows signs of growth banding in the form of alternating light and dark laminae, which mainly express variation in Ca and Mn concentrations. The initial precipitation phase of the Type I Mn carbonate is interpreted to be Mn oxide/hydroxide, based on positive Ce anomalies and selective enrichments of particular trace elements. Multiple roles of organic matter in Mn carbonate formation have been established: (1) catalysed Mn-redox cycling; (2) trapping and transportation of initial mineral precipitates to sediments; (3) serving as a carbon source; (4) regulating the morphology of the Mn carbonate. As a key link for understanding Cryogenian carbon and Mn cycling, specific formation pathways for the DTP Mn-carbonates are likely to have been controlled by given atmospheric-oceanic compositions (including oxygen level, pCO2, and redox conditions) in response to major geological and biological events during the interglacial period. In turn, massive storage of inorganic carbon and phosphorous in Mn carbonate phases would have had a substantial influence on biogeochemical carbon cycling during the Cryogenian.

Carbon cycle recognition in a marine ecosystem initiated by Milankovitch forcing during the Early Cambrian

Qiannan Xu[1,2]

[1]China University of Mining and Technology, [2]Macquarie University

Organic carbon flux from living biotas transfers through an ocean to marine sediments, causing a shift in the carbon cycle. The organic geological processes that encompass early diagenesis and thermal alteration are key parts of a complete carbon cycle in a marine ecosystem. In this work a set of oceanic sediments from the early Cambrian, which underwent several important bio-events, are used to test the carbon cycle mechanism for early Earth. Organic carbon deposited as organic matter may be consumed or preserved differently depending on the sedimentary area and the geological period. Redox conditions and primary productivity are increasingly recognised as the principle factors governing the rate of accumulation of organic matter in sediments, which has a major effect on the global carbon cycle, but how those sedimentary conditions changed over time is still unclear. The objective of this study was to clarify the roles of external and internal forcing characteristics in the Lower Cambrian formations from the southwestern part of the Yangzi Platform, South China Block. External forcings were determined using frequency analysis of a high-resolution log from a borehole (drilled in Yunnan Province, China). Internal forcings including sedimentary conditions and paleo-climate conditions were determined through geochemical analysis of major elements, trace elements, and rare earth elements. The mutual influence of internal and external forces on organic matter accumulation were also examined through Pearson Correlation analysis to provide evidence for the intensity of alteration of sedimentary conditions and the forces impacting on the organic carbon cycle in the marine ecosystem. The results show that a ~1.2 Myr astronomical cycle had the highest coefficient of correlation with organic carbon contents of all the identified astronomical periods, which also included 2.4 Myr, 405 kyr and 125 kyr intervals. Redox conditions had the highest correlation coefficient with organic carbon alteration. Fluctuations in sea level establish a connection between Milankovitch forcing and changes in sedimentary conditions, thereby providing evidence for the mechanism of organic matter accumulation and the effect of astronomical forcing on the organic carbon cycle.

A More Continuous Geo-Centric Model for the Prebiotic Synthesis of RNA

Professor Steven Benner[1]

[1]Foundation for Applied Molecular Evolution, Alachua, Florida, United States

Many multistep processes proposed to be prebiotically relevant for the abiological formation of polyribonucleic acid (or RNA) on a Hadean Earth are criticized because they could not occur in any geological context without human intervention, or because they are run as "relay syntheses". In a relay synthesis, products of a preceding reaction are not used directly as starting materials for the following reaction in a prebiotic reaction sequence. Instead, a human buys fresh reagents from a chemical supply house to be used as the started materials for following reactions. The constant intervention by human chemists makes such processes unpersuasive to those not prone to persuasion.

We recently proposed a "Discontinuous Synthesis Model" where steps requiring human intervention were highlighted as targets for criticism. Here, photochemically produced one- and two-carbon species could "not not" have reacted with volcanic SO2 to form organic minerals. In the presence of borate minerals, these undergo controlled diagenesis to give borate complexes of five-carbon carbohydrates, such as ribose, the R in RNA. Further, the bases of RNA could "not not" have formed in a post-impact reducing atmosphere. The two can be coupled with condensed phosphates proposed in basaltic glasses.

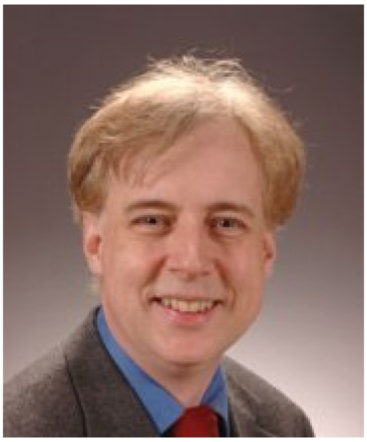
This talk will focus on improving continuity of the model. Here, ribose-borate is converted without intervention to adenosine 2'-(3'-) phosphate in the presence of adenine, Ca++, and diamidophosphate; this process involves a dozen microscopic reaction steps. Surprising, and contradicting expectations that borate might inhibit the process by tying up ribose in an unreactive form, borate was shown to assist. These nucleoside phosphates are near precursors for nucleoside triphosphates that basaltic glass converts to polyribonucleic acid. In addition to these geological conditions having been present on the Hadean surface, they also appear to have been present on Noachian Mars.

ORAL PRESENTATION - KEYNOTE

A More Continuous Geo-Centric Model for the Prebiotic Synthesis of RNA

Professor Steven Benner[1]

[1]Foundation for Applied Molecular Evolution, Alachua, Florida, United States



Biography:

Professor Steven Benner is a Distinguished Fellow at the Foundation for Applied Molecular Evolution, which he founded after serving on faculties at the University of Florida, ETH Zurich, and Harvard. His research has helped initiate several fields, including synthetic biology, paleogenetics, dynamic combinatorial chemistry, and evolutionary bioinformatics. Professor Benner's interests span synthetic, planetary, and systems biology, chemical genetics, palaeogenetics, and the connection between natural history and physical sciences. He has worked with NASA to develop methods for detecting alien genetic material. Professor Benner's group has also worked to identify molecular structures that are universally likely to constitute biosignatures.

Look Before You Leap: Consolidating Astrobiology Theory and Practice to Protect Martian Geoheritage

Clare Fletcher[1,2]

[1]UNSW, [2]Australian Centre for Astrobiology

The search for evidence of life in our solar system is presently focussed on Mars, though exploration of Mars has extended beyond the search for life and towards broader exploration and potential colonisation. The race to get crewed missions to Mars constitutes a second space race, dominated not by nation-States as the first space race was, but by billionaire individuals and private corporations. Increased activity on Mars puts practical astrobiology activities and the search for evidence of life on Mars at risk.

Astrobiologically significant geological sites on Earth have been subject to damage at the hands of professionals, which is detrimental to the continued scientific inquiry of these sites and removes outstanding universal geoheritage value at these sites. The most significant sites on Earth only occur over small scales and are globally rare. The same is true of potential sites of outstanding universal geoheritage value on Mars, such that a single rocket landing has the potential to destroy whole outcrops of astrobiological significance.

Astrobiology is an interdisciplinary field, and therefore understanding current astrobiological activities and how they will be practically translated to Mars exploration is inherently an interdisciplinary task. This means that interdisciplinary knowledge is necessary for the conservation of sites of outstanding universal geoheritage value on Mars to ensure that such sites on Mars do not succumb to the same fate as sites on Earth. In conserving outstanding universal geoheritage values on Mars, science and exploration must not be negatively affected. By taking into account current astrobiology research, practical field methods, geoconservation methodologies, and space policy and law, the search for life on Mars can continue sustainably for future generations without hindering present science and exploration.

Abiotic and Biotic Controls of Digitate Growth: Analogues for Potential Life on Mars

Megan Amos[1]

[1]UNSW

Understanding life's origins and searching for signs of extraterrestrial life remain some of the greatest scientific challenges for humanity. Yet our capacity to understand where life may have started on Earth is limited by its geological record, which preserves very little useful information prior to 3.8 billion years old (Ga). Investigating the geology of Mars, which preserves ancient crust up to 4.2 Ga, may provide a key to understanding life's origins both here on Earth and, potentially, on Mars.

Many terrestrial hot springs from across the world form silica precipitates known as sinter, which can contain textural and molecular biosignatures of microbial life. Indeed, some of the oldest preserved biosignatures have been identified in hot spring deposits in the Dresser Formation of the Pilbara Craton, Western Australia, dating back 3.48 billion years ago. The NASA Mars Spirit rover discovered opaline silica deposits (known as digitates) at Columbia Hills, Gusev Crater, which closely resemble sinter deposits in El Tatio, Chile. These deposits form through the evaporation of silica-rich hot spring fluids, mediated by microbes. A comparison between the morphology of the El Tatio deposits and the digitates found by the Spirit rover led to a case being proposed for the possible presence of a biosignature on Mars.

My project investigates the contributions that both abiotic and biotic factors have on the growth and morphology of the digitate structures. This involves creating synthetic digitates under varying physicochemical conditions, such as pH, temperature and salt concentration and other environmental factors, such as splashing and evaporative wicking. The results of these experiments will be useful in determining the viability of nodular silica structures on Mars as potential biosignatures of ancient life.

Peptide Synthesis Catalysed by Ribonucleotides under Prebiotically Plausible Hot Spring Conditions

Yaam Deckel[1]

[1]UNSW

Current hypotheses for the origins of life on Earth suggest the abiotic emergence of genetic and catalytic polymers that could self-replicate prior to the advent of enzymes. The RNA world hypothesis suggests that RNA could have been the original molecule that arose abiotically, ignoring the role of amino acids and peptides, which compared to RNA, are much more readily synthesised prebiotically and were likely abundant on early Earth. Investigation of the RNA-peptide world, where co-evolution of these two polymers occurs, may provide a fuller picture of life's origins. Moreover, supporting this RNA-peptide world, protein synthesis occurs in the ribosome through a series of 3´-peptidyl tRNA intermediates, i.e., RNA-peptide conjugates.

Previous studies show wet/dry cycle reactions inducing peptide polymerisation with the implementation of strategies such as salt induced peptide formation (SIPF), mineral catalysis, and ester-mediated peptide bond formation improving kinetics and yields. This project aims to support the RNA-peptide world hypothesis through combining adenosine 5′-monophosphate (AMP) and glycine under wet/dry conditions, potentially showing the formation of RNA-peptide conjugates which, as analogous to the ribosome, can catalyse amino acid oligomerisation.

Wet/dry cycles are thought to have commonly occurred on early Earth in the context of hot springs with dehydration and rehydration stages occurring over varying time cycles. The Taupō Volcanic Zone (TVZ) in New Zealand's North Island provides a modern analogue to early Earth geothermal fields with various springs containing diverse pH, temperature values, and ionic compositions providing a possible environment for favourable interactions between RNA and amino acids. Overall, this project investigates interactions between RNA and peptides within synthetic hot spring conditions and on relevant mineral surfaces, potentially mimicking the way peptides are synthesised in the ribosome in an early Earth context.

Investigating the Impact of Membrane Composition on Fluidity

Katelyn La[1]

[1]UNSW

To study the principles of early life, scientists are attempting to reconstruct artificial cells to better understand their self-propagating nature [1]. In previous attempts involving an artificial cell that makes its own phospholipid membrane [2], only minimal growth in the membrane was observed. Therefore, an investigation into how intermediates of phospholipid synthesis, namely lyso-PC and oleic acid, can affect membrane fluidity is important to ensure that they are not compromising reaction rates within the membrane. Understanding how the membrane composition can influence fluidity is crucial as adequate fluidity is required for membrane-bound reactions to occur.

To study the fluidity of a simple phospholipid membrane system, a membrane-sensitive fluorescence probe called Laurdan is added to generate an emission spectrum that changes as a function of membrane polarity. This can be quantified by calculating generalised polarisation (GP) [3] which gives an indication of the membrane fluidity. Our study using a 10% combined addition of lyso-PC and oleic acid in 1:1 POPC/POPG phospholipid vesicles shows that membrane fluidity increases with both increasing lyso-PC and decreasing oleic acid. Our other study using 1% to 50% oleic acid and no lyso-PC revealed decreasing membrane fluidity with increasing oleic acid.

Although the addition of lyso-PC causing increased membrane fluidity is expected, oleic acid does not display the same trend. This finding is rather unexpected as the addition of simple single-tailed, unsaturated fatty acids is expected to make the membrane more fluid due to increased gaps in the lipid packing. The reason for this trend is currently being looked into, with investigations on the effects of different pHs being studied. Understanding the relationship between membrane composition and fluidity may provide insights into how fluidity is important to self-propagating cells and hint at the possibilities of the emergence of primitive cells near the origins of life.

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Radiolytic synthesis of Aminooxazolines: Intermediates of Pyrimidine Ribonucleotides

Jiazheng Cao[1]

[1]UNSW

The RNA world hypothesis theorises that RNA proliferated before DNA and was taking on both the roles of proteins and DNA by catalysing reactions and encoding genetic information in the protocell.

To demonstrate that this is possible, simple organic materials have to react to form ribonucleotides under prebiotically plausible conditions. The Sutherland group presented an interesting approach by synthesising the sugar and pyrimidine nucleobases concurrently then phosphorylating the pyrimidine ribonucleoside to make the nucleotide.

Inspired by the Sutherland group the Fahrenbach group proposed a less restrictive one pot synthesis method using radiolysis as its driving force. It uses HCN as its only organic feedstock and produces sugar through Kiliani-Fischer synthesis and 2 amino oxazole from wet-dry cycling.

This project further examines one of the key intermediates proposed by the pathway – the pentose aminooxazolines, which were detected in minimal quantities. Upon further investigation it was discovered that this is caused by cyanohydrin formation from the reaction between cyanide and glyceraldehyde which inhibits aminooxazoline formation. While dry-down removes the cyanide from the cyanohydrin the cyanohydrin would also undergo cyclisation and form aldonic acids.

Thus far, the experiments have shown that the pentose aminooxazolines formation and cyanohydrin cyclisation happens concurrently during and after drydown. The rate of formation is observed to be affected by the pH and temperature of the reaction, higher pH during drydown strongly favours cyclisation.

As such, there is a need to investigate the reaction and formation of cyanohydrin and sugar acids to optimise the reaction for pentose aminooxazoline production. The next step in this study would be incorporating the reaction into a radiolysis project which would synthesize the pentose aminooxazolines starting from HCN in the one pot system.

POSTER PRESENTATION

Viewing RNA-peptide interactions from a supramolecular chemistry perspective

Anika Moller[1]

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RNA's role in the body is largely dictated by its ability to interact with a variety of other biomolecules, namely proteins, lipids, and sugars. These four classes of molecules constitute the four major macromolecules responsible for life. It has been well established that non-covalent interactions between RNA molecules and proteins are responsible for a variety of cellular functions by biologists, such as the regulation of protein synthesis and formation of liquid-liquid phase separated structures (membraneless organelles).

The 'RNA world hypothesis' posits tha the catalytic properties and ability to code information of RNA implicate it as a potential stepping stone in the development of early life, preceeding the DNA/RNA/Protein world we inhabit today. The other biomolecule suspected to be responsible for the formation of early life is peptides, while having strong catalytic properties lack the potential of self-replication or information storage. Many researchers are somewhat sceptical of the RNA world hypothesis, due to RNA's complexity preventing it from arising prebiotically, its inherent instability, and its catalysis being rare and limited. Hence, modern hypotheses examine the complimentary interactions of peptides and RNA together as a mechanism for the evolution of pre-biotic life.

My research involves the use of short peptides (7-10 amino acids) and RNAs (5 nucleotides) to investigate how these interactions occur on the molecular level by the use of supramolecular analysis techniques such as Isothermal Titration Caloritmetry (ITC) and NMR. This is to investigate these fundamental interactions on the molecular level. By varying peptide and RNA structure and measuring how this affects binding thermodynamics with ITC, it is possible to see which motifs in each molecule promote binding. I have shown that increasing positive charge in the peptide promotes binding, and that there is some preference for certain nucleotides. I plan to use NMR to confirm binding constants, and to use 2D experiments such as NOESY to better understand the binding mechanism.

Creating a proton gradient in encapsulated RNA-peptide coacervates

Alisha O'Brien[1]

[1]UNSW

Life on Earth is a product of evolution, and the Origin of Life remains one of the biggest mysteries in biology. In recent years, there has been growing interest in the study of coacervates as model systems in Astrobiology. Coacervates are dense, liquid-like droplets that can form spontaneously when biomolecules - including RNA and peptides, are mixed together. These droplets have demonstrated a myriad of emergent properties, including the ability to encapsulate other molecules and to undergo metabolic-like reactions. Additionally, due to the ability to concentrate pre-biotically relevant reaction sequences, coacervates have been proposed as supramolecular precursors to Life. However, the lack of an energy source remains a major challenge in understanding how coacervates could have become self-sustaining, self-replicating and adaptable.

One possible solution begins with the creation of a proton gradient across a liposomal membrane. This gradient could ultimately drive the production of ATP and GTP. To test this hypothesis, an RNA-peptide mixture will be encapsulated within a liposome and a pH gradient established. A buffer solution will be added to the outside of the coacervates, thereby creating a proton concentration gradient across the liposomal membrane. Either ionophores or the flippase ATPase class of proteins will be added to the buffer medium in order to facilitate the movement of protons (H+) across the lipid bilayer.

If it is indeed possible to create a proton gradient across the liposomal membrane encapsulating RNA-peptide coacervates with ATP/GTP synthesis activity, similar structures may have played a role in the emergence of metabolic processes in early life.

By examining the behaviour of coacervates in controlled environments, this research hopes to identify conditions that could have supported the emergence and evolution of life. In addition, the role of proton gradients in coacervates – which are essential for energy production in modern cells, may be further quantified.

POSTER PRESENTATION

Mechanical Properties of Fatty Acid Bilayers with Varying Protonation States and Counterions: Insights into Prebiotic Membrane Systems

Dr Joshua J. Brown[1]

[1]UNSW

The emergence of cell-like structures with lipid bilayers is considered a crucial step in the origins of life. Fatty acid (FA) bilayers, in particular, are believed to have played a pivotal role in the transition towards more complex lipid bilayers, as they represent simpler, more accessible building blocks that could spontaneously self-assemble in prebiotic environments.[1] These features along with the high permeability of nutrients across FA membranes make them favorable for model artificial and protocells.[2]

Distortion and shape changes in vesicles due to different external stimuli or encapsulated contents is postulated to be correlated with different cellular functions such as membrane budding prior to division.[3] Additionally it is known that small changes in the structure of FAs can lead to dramatic change in self-assembly properties and a basis of fundamental understanding for the interplay of chemical structure and supramolecular packing/ordering on FAs assembles is sort.[3]

This study implements molecular dynamics (MD) simulations to investigate the resultant change in mechanical properties of a FA bilayer as a function of amphiphile chain length, lipid protonation % and subsequently counterion type (Na^+, K^+, Mg^{2+} or Ca^{2+}) to gain insights in the properties of prebiotic membrane systems. Here, FA bilayer structures are composed of either octanoic, lauric, and oleic acid modelled with CHARMM36 lipid force field with explicit treatment of long-range dispersion (C36/LJPME) in the GROMACS software suite.

Our results provide an understanding of how the afore mentioned features contribute the MD predicted bilayer properties of; area per lipid, bending modulus, membrane density profiles, and lateral diffusion of lipids are affected by tail length, counterion and protonation % of the bilayer.

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Excitation Spectra of Indene and Fluorene Cations in comparison to the Diffuse Interstellar Bands

Jay Mendham[1]

[1]UNSW

Light that passes through the space between stars emerges on the other side marked with various absorption and scattering features attributed to, as of yet, largely unknown molecules. The diffuse interstellar bands (DIBs) refer to ~500 of these absorption features in UV, visible and IR light, observed through all lines of sight within the interstellar medium (ISM). Since their discovery in 1919, and with the systematic research that began in 1936, only one DIB carrier has been identified: ionised buckminsterfullerene (C60+) accounting for 4 bands within the IR region. This discovery supports the theory that DIB carriers consist largely of polycyclic aromatic hydrocarbons (PAHs) and other possible large carbonaceous molecules.

These molecules may play an integral role in theories on the evolution of life, with the ISM being rich in chemistry that may provide the chemical inventory necessary to account for prebiotic chemistry for early Earth and elsewhere in the universe.

The two molecules of interest in my experiment are fluorene and indene, which both are fragments of C60+. They both form resonance stabilised radicals, and thus their cations are more likely to be formed within the interstellar environment. This environment will be replicated in my experiment with the use of a jet-cooled gas-phase molecular beam within a vacuum chamber. The molecules contained within this beam will be studied using resonance-enhanced multi-photon ionisation (REMPI), which uses multiple lasers to excite and ionise the molecule, producing an excitation spectrum of the cation that can be compared to the DIBs. This poster will present a detailed methodology of my experiment, an unprecedented technique for recording the excitation spectra of cations, and preliminary data for both indene and fluorene DIB comparisons.

Simple Coacervates as a Model for Prebiotic Cell Formation

Grace Maynard[1]

[1]UNSW

One of the biggest challenges facing prebiotic chemistry is the transition from spatially separated and dilute chemicals into organised, functional cells. Liquid-liquid phase separation has been proposed as a method of chemical organisation which may have facilitated the formation of the earliest model cells. Liquid-liquid phase separation is a spontaneously occurring process where groups of molecules separate into distinct chemical environments – a dilute phase and a concentrated. Concentrated phase environments, commonly referred to as coacervates or condensates, retain solute from the dilute phase – most commonly water.

The process is often divided into two types: simple coacervation and active coacervation. Simple coacervation occurs when changes to the dilute phase chemical environment (such as pH, salt, and temperature) induce coacervation; whereas complex coacervation is triggered by active associative phase separation with another type of molecule and is driven by electrostatics, pi-pi interactions, pi-cation interactions and more. Liquid-liquid phase separation is a known a method of organisation for biochemical reactions in modern cellular biology. This discovery precipitated the investigation of coacervates as a method to chemical reactions for non-enzymatic membraneless biological catalysis.

Building on established methods of cellular organisation, my research is investigating the use of micro-RNA and small peptides as a simple model for driving prebiotic catalysis; and sequence dependency on coacervate formation and catalysis. The advantage of using micro-RNA and short peptides is that their simplicity makes them a viable candidate for prebiotic synthesis as previous research has studied the ability of these short polymers to form in situ in model primordial pool systems. This investigation has systematically studied the factors that lead to prebiotically plausible coacervation by utilizing the simplest available biopolymers to form a range of coacervates which can respond to environmental changes such as pH and concentration.

Genome analysis of evolved thymidylate synthase knockout strains reveals mutations affecting the machinery replication.

Appoline Dubois[1], Alannah M. Rickerby[1], Professor Anthony M. Poole[1]

[1]School of Biological Sciences, University of Auckland, Auckland, New Zealand

The de novo synthesis of deoxyribonucleotides components of DNA is present and necessary in almost all organisms on Earth. Early life on Earth likely had RNA genomes instead of the DNA genomes in modern organisms. One theory is that the transition from RNA to DNA genomes occurred in two stages. The first step was the transition from an RNA genome to an intermediate DNA genome with uracil and the second step was the replacement of uracil by thymine.

To study this possible intermediate genome, we set up an evolution experiment using a mutant strain of the bacterium Escherichia coli. This strain lacks key genes required for the synthesis of thymidine. In brief, we knocked out: the thymidylate synthase gene (responsible for the synthesis of thymidine), the tRNA (m5U54) methyltransferase gene (involved in posttranscriptional modification to produce thymine in tRNA) and the uracil-DNA glycosylase gene (involved in the removal of uracil in the genome). We next performed an evolution experiment where we progressively decreased the thymidine (dT) supplementation in the culture medium, which we expect to drive uracil accumulation in the genome. Following 55 transfers, our knockout lines were able to grow without dT supplementation in the media.

The genomes of these lines were fully sequenced to understand how the lines adapted to the inability to produce thymidine. We expect to see adaptations for the uptake of dT into the media and/or the accumulation of uracil into the genome. The sequencing data revealed numerous non-synonymous mutations in genes responsible for transcription, replication, and DNA repair. Some were found in the DNA polymerase III, the primary enzyme responsible for DNA replication in prokaryotes, with the ability to correct replication errors. Ongoing analysis of these mutations indicates significant impacts on the machinery of replication. Future objectives will be to determine the extent of uracil incorporation into the genome.

Protein structures as time capsules: Unravelling viral evolutionary history through structural phylogenetics

Desiree B. Langer[1], Asher J. Malik[2,3], Associate Professor Jane R. Allison[1], Professor Anthony M. Poole[1]

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Tracing the early evolution of life on Earth often focuses on cellular lineages, but viruses likely played a role in early evolution as well. Thus is worthwhile to examine the evolutionary relationships between viruses.

Comparing virus coat architectures has revealed the presence of a common jelly-roll fold in viruses infecting all three domains of life and found in both RNA and DNA viruses. However, these similarities are observed at the structural level rather than in protein sequences, making traditional sequence-based tools impractical for building viral evolutionary trees. To overcome this, our lab developed a novel method for constructing evolutionary trees based on protein structure, which can trace deep relationships even with low sequence similarity. Protein structures retain evolutionary signals over longer timescales, so have the potential to uncover deeper relationships than detectable through sequence alone. Traditionally, structural phylogenetics approaches lack statistical methods for assessing the robustness of these relationships. To address this, a molecular dynamics-based bootstrap-like method was developed to show the potential for adding statistical support to structure-based phylogenies.

The jelly-roll fold consists of two main architectures: the single jelly roll (SJR) fold and the double jelly roll (DJR) fold plus, a rare third variant, the triple jelly roll. Studies suggest that the DJR motif arose via ancient gene duplication, but the timing of this event remains unclear.

We report the results of using structural data for reconstructing the evolutionary history of viruses. Our results also shed light on the evolution of the diverse jelly roll architectures. Our research highlights the value of using structural phylogenetics to probe viral evolutionary history.

Primordial Evolution by Linking Sequence Information and Vesicle Reproduction

Akiko Baba[1]

[1]Tohoku University

The linkage of sequence information of nucleic acids or proteins and the proliferation of vesicles potentially enables evolution, which is a major milestone in the origin of life. Evolution are changes shifted towards greater fitness over time, where fitness is a measure of proliferation ability, such as the rate of replication. The fitness of individual organisms is determined by proteins. This is because genetic information is passed on via an amino acid sequence. In modern sophisticated living systems, the relationship between genotype (sequence information) and phenotype (hence fitness) is so complex that it is difficult to understand. In contrast, in the early stages of living systems, the relationship is expected to have been simple. Studying such systems may reveal the physical underpinning of the relationship.

On early earth, fatty acids formed a precursor structure of the cell membrane called a vesicle. In the primordial soup, the fatty acid vesicles are thought to coexist with many primitive molecules such as nucleotides, amino acids, and peptides. Therefore, we have investigated the growth and division of fatty acid vesicles in the presence of each primitive molecule as a model primordial evolution system. Specifically, the relationship between the amino acid sequence of the peptide and the growth rate of fatty acid vesicles as a measure of fitness has been examined using dipeptides and tripeptides. We identified the following properties of peptide-fatty acid vesicle systems: 1) they have specific sequences that promote vesicle growth, 2) these specific sequences maintain their effects independent of the peptide length, and 3) there is epistasis, where the effect of one amino acid replacement on the fitness depends on the rest of the amino acid sequence in the peptide. Our findings suggest that the evolution of protocells occurred at a very early stage in the primordial soup.

Impact of vesicle confinement on prebiotic reaction networks

Dev Chauhan[1,2]

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The compartmentalisation of several biochemical reactions within a membrane-bound aqueous environment serves as a crucial initial step in understanding the origin of life on early Earth. Fatty acid vesicles have been considered as a model compartment, and have a semipermeable membrane potentially allowing nutrient exchange (nutrient uptake and waste removal). People have demonstrated a few prebiotic reactions within the confined environment of fatty acid vesicles by encapsulating the substrate molecules inside the vesicle. However, sustaining the reaction inside the system requires continuous nutrient exchange through the semipermeable membrane with the surrounding environment. Thus far, there have been few methods for tuning membrane permeability to take advantage of fatty acid vesicle semipermeability for encapsulated prebiotic chemistry reactions.

I will provide an overview of previous attempts to perform prebiotically plausible chemical reactions within the confined vesicles and explore how membrane permeability can be tuned to improve the nutrient exchange to sustain the chemical reactions. With the addition of unsaturated fatty acid molecules to the preformed vesicles, it is predicted that there will be an increase in membrane permeability due to changes in membrane packing. Incorporating/adding the different carbon chain-length unsaturated fatty acids (e.g., C12-14) molecules to the preformed vesicle (e.g., C18) to alter the membrane permeability could enable increased nutrient exchange with the environment. This, in turn, can help sustain the reaction inside the vesicle. This is possibly due to the formation of transient pores in the membrane, facilitating nutrient transport across the membrane.

This approach has the potential to address the key challenge of ensuring the fatty acid vesicle has continual access to the nutrients and subsequent waste removal to sustain the prebiotic reaction network. Such a transfer of nutrients is critical not only for getting nutrient substrates for primitive metabolic processes but also for the removal of inhibitory side products.

Inducing Cryptobiosis state in Tardigrades in Cyanobacteria Synechococcus elongatus For effective preservation

Souvak Manna[1]

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Cryptobiosis is a dormant state where all measurable metabolic activities are at a halt, allowing an organism to survive in extreme conditions like low temperature (cryobiosis), extreme drought (anhydrobiosis), etc. This phenomenon is observed especially in tardigrades that can retain this state for decades depending on the abiotic environmental conditions. On returning to favorable conditions, tardigrades re-attain a metabolically active state. In this study, cyanobacteria as a model organism are being chosen to induce cryptobiosis for its effective preservation over a long period of time. Preserving

cyanobacteria using this strategy will have multiple space applications because of its ability to produce oxygen. In addition, research has shown the survivability of this organism in space for a certain period of time. Few species of cyanobacterial residents of the soil such as Microcoleaceae , are able to survive in extreme drought as well. This work specifically focuses on Synechococcus elongatus, an endolith cyanobacteria with multiple benefits. It has the capability to produce 25% oxygen in water bodies. It utilizes carbon dioxide to produce oxygen via photosynthesis and also uses carbon dioxide as an energy source

to form glucose via the Calvin cycle. There is a fair possibility of initiating cryptobiosis in such an organism by inducing certain proteins extracted from tardigrades such as Heat Shock Proteins (Hsp27 and Hsp30c) and/or hydrophilic Late Embryogenesis

Abundant proteins (LEA). Existing methods like cryopreservation are difficult to execute in space keeping in mind their cost and heavy instrumentation. Also, extensive freezing may cause cellular damage. Therefore, cryptobiosis-induced cyanobacteria for its transportation from Earth to Mars as a part of future terraforming missions on Mars will save resources and increase the effectiveness of preservation. Finally, Cyanobacteria species like Synechococcus elongatus can also produce oxygen and glucose on Mars in favorable conditions and holds the key to terraforming Mars.

Quantifying vesicle loading following osmotic bursting events

Lan Tran[1]

[1]UNSW

Fatty acid vesicles are used as model primitive cells for research into possible avenues in the emergence of cellular life[1]. These vesicles can form different self-assembled structures and occasionally burst depending on their chemical compositions and that of their environments.

Digital holographic microscopy (DHM) is a quantitative imaging technique that relies on light scattering rather than the use of fluorescent or radioactive tracers[2]. DHM has been used in astrobiology to track or detect microorganisms, but it can also be used to measure features in the image such as the refractive index or solute density of an object. Thus, the motivation of the present work is to demonstrate the utility of DHM in quantifying the robustness of these vesicles to dilution into environments that could lead to vesicle bursting.

This study implemented DHM to quantify the retained sucrose concentration of a vesicle following a bursting event via the change in refractive index across the vesicle. The osmotic pressure across the vesicle was modulated by 500, 250, 0 mM glucose buffer in the solution. An imbalance of osmotic pressure between the solute and solution led to influx of water, which was anticipated to increase membrane tension due to swelling, from which a bursting event then relieved the tension on the membrane.

The vesicles encapsulated with 500mM sucrose solute surrounded by 500, 250, 0 mM dilutions of buffer medium were seen to result in significant sucrose concentration reduction of 17.2%, 50.5%, 56.2% respectively. It is notable that not all the sucrose was lost, even in the most extreme case.

From these findings, we can infer that DHM has the capacity to enable us to look further into the behaviour of vesicles of various solute loading in different chemical environments, and consequently how they can withstand bursting.

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POSTER PRESENTATION

Enhancing the Search of Molecules in Exoplanet Atmospheres Using High-throughput Quantum Chemistry

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Identifying molecular species in exoplanet atmospheres is a challenging task that heavily relies on the availability of high-resolution molecular spectroscopic data. Unfortunately, however, the generation of such data is a time-consuming and resource-intensive process, usually spanning months to years per molecule, even for the smallest molecular systems. To date, only a limited number of molecules (<100) have high-resolution spectroscopic data available, significantly restricting the scope of new molecular detections.

Here, we present a complementary high-throughput approach to rapidly generate approximate vibrational spectral data for thousands of molecules of astrochemistry interest using routine quantum chemistry calculations (median errors of 10 cm-1 in the calculated frequencies). While our data is not accurate enough to enable definitive molecular detections in exoplanet atmospheres and is not intended to replace the need for high-resolution molecular spectroscopic data, it has powerful applications in identifying potential molecular candidates responsible for unknown spectral features. For instance, we explore this application in the atmospheric spectrum of WASP-39b, focusing on the 4.56 micron (2192 cm-1) unknown feature and listing potential molecular species responsible for this spectral line. Further applications of our data also include identifying molecules with strong absorption features that can be detectable even at low abundances, and recognising potential molecular ambiguities in spectra.

Emerging data from the James Webb Space Telescope (JWST) is currently providing extraordinary opportunities to deepen our understanding of the molecular inventory of exoplanet atmospheres. Our rapidly generated quantum chemistry big data will play a crucial role in supporting this understanding by giving directions into possible initial detections of the more unusual molecules to emerge, advancing our understanding of exoplanet atmospheres and their potential for habitability.

POSTER PRESENTATION

Light as a molecular fingerprint: How do quantum chemists help find the molecules that make sugars and proteins space?

Maria Pettyjohn[1]

[1]UNSW

The space between stars – the interstellar medium – is not empty but filled with the building blocks of future stars and planets. Over astronomical timescales, with the diversity of temperatures, densities and radiation levels, a variety of complex chemistries can arise. Of particular interest is the expected formation of prebiotic molecules, including the building blocks of sugars and proteins, that form the seeds of life.

Spectroscopy is used to analyse the unique frequencies of light emitted or absorbed by molecules in interstellar gas clouds, allowing researchers to identify specific molecules based on their spectral fingerprint. With the increasing discovery of new molecules and more gas cloud surveys, definitive identification requires more data to avoid misidentification.

We explore the use of high-throughput medium accuracy computational quantum chemistry to predict molecular fingerprints for thousands of prebiotic molecules. We find that rotational spectroscopy, typically used for studying the interstellar medium, makes far higher demands on accuracy to be helpful than vibrational spectroscopy – most common approach for studying exoplanet atmospheres. Nevertheless, approximate data could be helpful in identifying potential ambiguities in astronomical signals if rotational constants can be verified.

SciX: Scalable and sustainable authentic research experiences for high-school students

Dr Laura McKemmish[1]

[1]UNSW

In NSW, the new Yr 12 HSC Science Extension course recommends students find university mentorship to support their individual research projects. The SciX high-school outreach program (unsw.to/scix) has been developed and refined to meet this demand in an equitable, sustainable, scalable, effective and quality-controlled way.

SciX centres around an intensive one-week authentic research experience with online pre-work and post-summer-school Q&A sessions. High school students select a research area and are placed in small groups led by SciX mentors, usually paid PhD researchers. Students are taught disciplinary research topics and tools then supported to develop their individual hypothesis and conduct their research. Qualitative and quantitative surveys show that students really enjoy the experience and develop crucial transferable and scientific skills.

As SciX mentors, PhD students are supported in developing important professional skills, e.g. in supervising, mentoring, teaching and management. Project development and delivery is carefully scaffolded with training, structured support and regular reviews. Time expectations are clearly set and reasonable to avoid interfering with PhD progression.

In recruitment, the program is clearly addressing equity, diversity and inclusion goals, with typical enrolments 63% female, 40% fee-waiver positions and 26% regional or rural. The program's success in implementation is most clearly demonstrated by preliminary data showing that students' science identity increases during the program, particularly for girls (3.8/7 to 5.1/7 for girls, 5.1/7 to 5.4/7 for boys). Science identity is known to correlate with aspiration and perseverance in STEM careers.

This talk will be targeted at those interested in supporting research for high-school and/or undergraduate (pre-Honours) research students through supervision and/or program design. As inspiration for how you might deliver this enriching student experience, I will describe how SciX has addressed key challenges, specifically careful project design, program design appropriate to the local context, securing funding and developing a scalable team structure.

Simulating the Thermodynamic Landscape of Hydrogen Cyanide Derived Polymers

Siddhant Sharma[1]

[1]University of Delhi, India

Hydrogen Cyanide (HCN) is a ubiquitous and reactive species present in many environments ranging from the interstellar medium to comets, asteroids, and planetary atmospheres. HCN, and HCN polymers have a proposed key role in the abiotic origin of life and are suspected to be an essential prebiotic building block for the synthesis of nucleobases, amino acids, and a large variety of polymers. HCN is, for example, generated in large amounts by the atmospheric photochemistry of Saturn's moon Titan. Despite many decades of research, the complex nature of products derived from HCN polymerization experiments remains largely unknown.

We describe how quantum chemical calculations and simulations can garner insight into the possible prebiotic synthesis of macromolecules and polymers. Our evaluation covers several molecules and oligomers, most of which have been discussed in the literature, and ranks them based on thermodynamic preference. We sidestep the complexities of experimental reaction mixtures by computationally exploring individual candidate prebiotic molecules and polymers in solution. A method for conformational sampling is combined with Density Functional Theory (DFT) to predict the thermodynamic stability of most HCN-based structures considered in the literature.

Our enumeration of thermodynamically plausible reaction products and the reaction routes for the abiotic formation of organic macromolecules starting from simple units of HCN offers extensive insights into the chemical and physical limitations of suspected key prebiotic processes. Some structures and reactions suggested in the literature are here proven unviable on thermodynamic grounds. However, most HCN-self reactions are found to be spontaneous. Polyaminoimidazole, and the nucleobase adenine, are computed to be the most thermodynamically favored products that can form from HCN. The presented thermodynamics of HCN polymerization coupled with predictions of closely competing reaction kinetics have several consequences for interpreting HCN reactivity in various astrochemical environments and may help explain experimental observations of complex reaction mixtures.

POSTER PRESENTATION

Evaluating Potential Trace Metal Biosignatures in Fossilised Hydrothermal Siliceous Sinter Deposits

Barbara Lyon[1], Dr Michael Rowe[1], Professor Kathleen Campbell[1], Andrew Langendam, Dr Diego Guido

[1]University of Aukland

Siliceous sinters are promising targets in the search for evidence of early life on Earth and possibly Mars. Terrestrial hot springs harbour extremophiles that may be preserved in life-position by rapid silicification from the cooling and evaporation of the thermal discharge. Despite their high preservation potential, hot spring deposits form in dynamic geological environments and consequently undergo numerous changes over time (e.g., changes in fluid chemistry, fluctuation of the water table), often leading to the alteration or destruction of microfossils and biomediated fabrics and the loss of organic components. In the absence of clear organic signatures, the biogenicity of trace metals is increasingly scrutinized as supporting evidence of early life. Ongoing investigations have highlighted the correlations between trace metals and microbial material. However, it is unclear how these geochemical tracers are preserved/modified in the 'deep time' geologic record. This study uses x-ray fluorescence microscopy at the Australian synchrotron to examine the potential trace metals to fingerprint biogenicity as an independent assessment of evidence of life. The fossilised Ohakuri hydrothermal system (~16 ka), in the Taupo volcanic zone, New Zealand, represents an excellent stepping stone back into geologic time. Sinter textures record varying states of preservation of microbial textures and carbonaceous material. Trace metals (Ga, Fe, Mn, Cr, As, Ti, Ba, W, Ca, Zn) in samples representing high and low-temperature microbial biofacies record a complex relationship. Gallium and Fe show strong spatial correlations to microbial textures, typically enriched in the silicified sheaths around the microbial trichome portion of preserved filaments. However, acidic overprinting also modifies trace element abundances, and textures that otherwise appear to be well preserved do not always record trace metal enrichments. Ongoing investigations into silica phase mineral transformations may provide critical insights into links between diagenesis, silicification, and the preservation potential of trace metal biosignatures.

ORAL PRESENTATION – INVITED SPEAKER

Investigating Formamide as a Medium for Potentially Prebiotic Amino Acid Derivative Synthesis

Dr Nick Green[1]

[1]University of Otago

Amino acids are central to the development of sophisticated, organised and functional chemical processes that we recognise as biological. I will discuss recent work implicating formamide as an essential component of the prebiotic milieu, because of its role in the synthesis of dehydroalanine and other amino acid derivatives, which may have a played a critical supporting role to nucleic acids in the rise of biology.

ORAL PRESENTATION

Biomolecule Synthesis meets Nonlinear Dynamics - Integrating Ribonucleotide Precursor Synthesis with the Autocatalytic Formose Reaction

Quoc Phuong Tran[1]

[1]UNSW

How protometabolism emerged from prebiotic chemistry has remained a topic of intense debate in the scientific community. It is hypothesised that biomolecule synthesis intertwined with nonlinear dynamics may provide a potential clue. Using the formose reaction as a model for prebiotic autocatalysis, we added other feedstocks proposed to be present on early Earth to investigate their effects on the kinetics and product distributions of the resulting reaction network. In one case study, cyanamide was shown to inhibit the formose reaction by reacting with formose sugars to form aminooxazole derivatives while also forming tetrose and pentose aminooxazolines, precursors for TNA and RNA synthesis. Implications regarding chemical evolution and future work involving microfluidics will also be discussed.

Fluctuating thermochemical drive for incipient life

Professor Rowena Ball[1]

[1]Australian National University

A longstanding issue in emergence-of-life science concerns the power source. In this presentation I shall describe progress made by my group in validating hypotheses concerning involvement of hydrogen peroxide in fuelling prebiotic processes through its action as a thermochemical redox oscillator.

Simulations of homogeneous pre-biotic reacting systems driven by hydrogen peroxide thermochemical oscillations have shown that normally distributed input fluctuations produce a non-normal distribution of output fluctuations. This result is robust, consistent, and well-supported by theory. It implies that

(I) the potential energy of transient non-Boltzmann populations of internal modes of the active medium can manifest as a non-Maxwell-Boltzmann distribution of molecular kinetic energies,

(II) on average, high activation energy synthesis reactions must be favoured over the reverse, low activation energy, degradation reactions, thus complex processes leading to life are enabled, and

(III) constraints are inherent on environments where it is possible for life to emerge, and on probabilities of its doing so and persisting.

In heterogeneous reaction systems, exothermic reactions which occur in the solid phase with adsorbed hydrogen peroxide can be thermally coupled with endothermic desorption. Thus the heat removal rate has an exponential component due to the Arrhenius temperature dependence of the endothermic reaction rate. The process may be conceptualised as a reciprocally acting couple, for which alternating high and low temperature states are intrinsic. This built-in alternator inevitably operates wherever surface sites can be saturated by active adsorbed species. I shall describe dynamical modelling results on the operation of this process on oxidizable mineral surfaces, and show that the periodic accumulation of potential energy and its release as kinetic energy may have driven prebiotic molecular self-assembly.

Deep-sea supercritical CO2-water environment drives prebiotic nucleoside phosphorylation

Shotaro Tagawa[1]

[1]Tokyo Institute of Technology/Earth Life Science Institute

Phosphorylated organic molecules play crucial roles in the modern biological system yet their origin and source of phosphate are still under debate. Previously, many prebiotic phosphorylation reactions have been demonstrated under simulated terrestrial hot spring condition, where water can escape to the atmosphere leading to dehydration and condensation of dissolved organic molecules. Whereas deep-sea environment is considered water-rich and thus unfavorable for phosphorylation reaction. However, recently the existence of natural CO2 fluid in the deep-sea has been considered as a new and attracting environment for various chemical reactions to occur including condensation-type reaction. Therefore, we have setup a reactor to simulate the water-scCO2 two-phase system to validate the nucleoside phosphorylation. Total of four different nucleosides (adenosine, uridine, cytidine, or guanosine) and two different phosphate sources (sodium phosphate:NaH2PO4 and hydroxyapatite) were prepared as a substrate. Series of reactions have been conducted under various temperatures ranging from 25 to 90℃ with two time points (24 and 120 hours). As a result, nucleoside phosphorylation reaction proceeded above 60℃ only under the presence of scCO2. Also similar to previous terrestrial experiment, addition of urea enhanced the phosphorylation reaching up to 2.5 ~ 15.4% nucleotide yield after 120 hours. Both NaH2PO4 and hydroxyapatite were able serve as a phosphate source, in which acidification of aqueous solution by CO2 likely contributed to dissolve and release phosphate from hydroxyapatite. Furthermore, degradation of urea to ammonia was observed, ~1% yield of carbamoyl nucleoside was constantly detected by LC-TOF MS suggesting the presence of isocyanate intermediate. We are currently investigating the precise reaction mechanism of nucleoside phosphorylation and thus look forward to discussing in details with relevance to the prebiotic phosphorylation on early Earth ocean.

ORAL PRESENTATION – INVITED SPEAKER

Astronomical implications of new H2S photochemistry

Dr Chris Hansen[1]

[1]UNSW

Sulfur is the 10th most abundant element in the universe. It's chemical versatility and abundance in the prebiotic Earth, as its reduced sulfide (H2S), implicate it in the origin of life 3.8 billion years ago where it was also a major source of energy in the first seven-eights of evolution…

Now H2S looks like a simple molecule, however, there are some longstanding contradictions between the abundance of H2S (and other sulfur compounds) predicted by astronomical models and by observations. This seemingly simple compound exhibits strikingly rich vacuum ultraviolet (VUV) photodissociation dynamics that we have studied in unprecedented detail. Using the most advanced (VUV) light source in the world, the Dalian Coherent Light Source (free-electron laser), as well as tabletop lasers in both Dalian and Sydney, we have performed careful ionisation and translational spectroscopy experiments to unravel the rotational and nuclear-spin state dependent photodissociation dynamics of H2S with photoproduct quantum state resolution for 5 photodissociation pathways. This new, textbook understanding of H2S photochemistry revises our understanding of interstellar sulfur chemistry allowing us to address some longstanding issues in astrochemical models and hopefully better understand how it is processed in the interstellar medium.

Carbon dots: an unexplored, multifunctional prebiotic material

Dr Soumya Kanti De[1]

[1]UNSW

The potential introduction of a novel component may have a substantial impact on prebiotic chemistry and the emergence of life. Herein, we propose that a carbon-based fluorescence nanomaterial, specifically carbon dots (CDs), has unexplored potential as a prebiotic material. They can be synthesised using a source of heat and carbon, both of which were available on prebiotic Earth, under a wide range of temperatures. Potential sources include heat from ample hydrothermal activity, and carbon from small organic molecules. [1,2] Therefore, our primary objective is to examine the formation of CDs in laboratory settings that replicate the realistic conditions on early Earth.

CDs have the potential to exhibit multifunctional effects in a prebiotic context. Interactions of the CDs with lipid bilayer membranes could induce deformations in the membrane packing, which eventually alters the mechanical properties, affecting the growth and division. Such deformations in the lipid bilayer may also lead to primitive channel formation for nutrient uptake and waste release for protocells. CDs can also function as photocatalysts by generating electron/hole pairs upon exposure to light, contributing to the production of reactive species that lead to subsequent photocatalytic events. [3] CDs are composed of reactive surface groups such as -COOH, -OH, and -NH2, which have been found to facilitate various synthetic organocatalysis processes.[4] Additionally, recent reports have also indicated that CDs can exhibit enzyme-mimicking activity, which could be effective in a prebiotic setting in the absence of biological enzymes. [5] Finally, the unique optical feature of CDs can be used to protect important biomolecules from UV light in prebiotic environments, especially when there is high intensity UV light.

Consequently, we hypothesise that the participation of CDs in the study of prebiotic chemistry has the potential to revolutionise the way researchers tackle the origins of life, and perhaps even played a crucial role in the emergence of life itself.

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Gas-solid reaction drivers for the mineralogy & atmospheric chemistry on Mars

Professor Penny King[1], Tim Hunt[1], Emily Oborski[1], Andrew Palm[1], Chris Renggli[1], and Sarah McIntyre[2]

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Reactions between gases and solids are not something that we learned about in university and they don't come up in most geology textbooks. Nonetheless, hot gas-solid reactions are common on Earth and occur at volcanoes today. Our group has documented these reactions in the 2018 ash eruptions at Kilauea volcano and in the sub-surface of volcanoes. The reaction products are consistent with the results of our recent experiments and thermochemical models showing that hot gases react rapidly and efficiently with common silicate minerals and glasses to produce predictable products. In addition, impact events release gases into the atmosphere and they may subsequently react to form new gases and solids.

In this talk, I will examine the hypothesis that high temperature reactions between gases and solid surface materials, early in the history of Mars, provide a framework to explain its broad surface and atmospheric features. I will argue that these reactions demonstrably influenced Mars's surface (e.g., salts and amorphous phases) and effectively "scrubbed" the reactive gases like water out of the early atmosphere, leaving behind carbon dioxide.

Hydrothermal conditions in Martian impact craters: implications for habitability

Dr Joshua Hedgepeth[1], Associate Professor Katarina Miljkovic[1], Dr Eriita G. Jones[1], Hely C. Branco[1]

[1]School of Earth and Planetary Sciences, Space Science and Technology Centre, Curtin University

Mars could have had habitable environments as early as the Noachian on its surface and/or in the subsurface throughout the Amazonian. Impact craters, a common geological process across the Solar System, provide a case study for habitability as an environment with energy, resources, and possibly liquid water. They also serve as a mechanism by which evidence of past or ongoing subsurface life may be exposed.

In this work, we consider the habitability of the Martian crust by investigating evidence of hydrothermal systems formed within and/or exposed by impact craters. The Martian surface exhibits widespread evidence suggestive of hydrothermal processes, but it remains unclear whether the signatures around impact craters are formed by impact processes and/or excavated by the impact. Our project investigates: a) to identify the threshold diameter below which the excavation depth is insufficient to reach potential cryospheric depths (order of kms), where water may have been (or still is) preserved, and b) to determine if/where impact-induced hydrothermal mineralisation is most likely to be found.

We use the iSALE shock physics code to reproduce complex impact crater morphologies on Mars, the associated thermal anomalies, and the depths in the crust affected by the cratering process (fracturing, excavation, change in stratigraphy). Here we present initial results from simulating Toro crater, a crater with evidence of hydrothermal activity, which was used to validate the model parameters against observations (see Jones, E. et al., AAM 2023). We use the predicted thermal anomaly to model the movement of fluids (if any) within the system as the anomaly evolves using HYDROTHERM. We predict the most likely pathways for hydrothermal biproducts to reach the surface by cross-referencing the fractures and faults formation with the region heated by the crater formation. This work is to be continued for the entire range of complex craters on Mars.

Unlocking the Secrets of Life's Preservation on Earth: The hunt for Biosignatures

Dr Indrani Mukherjee[1]

[1]UNSW

Key insights into critical biological milestones in Earth's history rely on our ability to interpret the rock record. Post Ediacaran, the macroscopic nature of fossils and their traces aid in interpretation of their habitat, past geochemical environments and evolutionary history. However, prior to the Ediacaran, the microfossil record presents challenges, owing to the small size and poor preservation of fossils. Permineralization of microscopic fossils may further complicate our assessment of biogenicity. Therefore, we rely heavily on a multitude of microanalytical geochemical techniques to ascertain biosignatures. Obtaining such information not only helps trace records of ancient life on Earth, it also informs strategies to search for life on Mars.

This presentation will discuss a method to test the biogenicity of putative fossil structures in the rock using the abundance, and spatial distribution of bio-essential trace elements of known fossils. Detailed petrography using reflected light microscopy and Scanning Electron Microscopy (SEM) can help with analyzing textural variation (biotic and abiotic) in the samples. Combined elemental and electron backscatter diffraction (EBSD) mapping of the microfossils can be used to investigate changes in crystal structure, crystal size, and crystal orientation and determine correlation with trace element distribution. Additionally, imaging of microfossil structures using LA-ICP-MS for nutrient elements (e.g., Ni, Mo, Zn), can aid with investigation of the distribution of trace element pathways and help ascertain biogenicity in samples of unknown origin. Deep time fossil record is sparse, and studies of this kind can result in huge leaps in our understanding of the evolution of life and can have immediate application in astrobiological investigations, that use ancient Earth analogues. More generally, the results can be used to advertise the research and its global implications for our field of science to the wider community through media, University science events and school outreach programs.

Evaluating trace element variability and putative biosignatures in terrestrial digitate sinters: Implications for Mars exopaleontology

Ema Nersezova[1]

[1]University of Aukland

Since the discovery of hydrothermal silica deposits at Gusev Crater on Mars, with morphologies resembling siliceous digitate sinter deposits of terrestrial hot springs on Earth, these deposits have represented an important potential target in the search for extraterrestrial life. The diagnosis of life, past or present, requires corroboration of morphological and chemical biosignatures in an environment expected to host life, such as a hot spring. Textural biosignatures in all facies of sinters along a temperature gradient (~100-15ºC) are well characterized, but studies on organic and metabolic biosignatures preserved within digitate sinters are sparse.

This research investigates geochemical variability and potential biosignatures within modern and fossil digitate sinters formed in hot springs from the Taupō Volcanic Zone (TVZ), New Zealand; El Tatio, Chile; and Opal Mound, Utah, U.S.A. We analyzed in-situ major and trace elemental variability with wavelength-dispersive X-ray spectroscopy (WDS) and Synchrotron micro-X-ray fluorescence mapping (S-µXRF). These analyses were integrated with in-situ identification of carbonaceous material using Raman spectroscopy. S-µXRF and WDS indicate an enrichment of Al, Ca, Fe, Ga, As, Rb, and Sr around the sheaths of silicified, filamentous cyanobacteria preserved within the digitate sinters from El Tatio and Whangapaoa Spring (TVZ). Raman spectra of these filaments show a complex carbon fingerprint attributed to a mixture of cyanobacterial carotenoid pigments, including scytonemin (a UV protection compound).

Microbial mineralization is generally limited to the sheath, which suggests that this enrichment is due to adsorption onto reactive groups on the sheath surface for use as a nutrient source, or UV protection. The utility of these pigments and trace elements as biosignatures depends on their preservation potential into the 'deep time' geological record. However, as the >3.6Ga martian silica deposits remain amorphous (opal-A) and have not recrystallized to quartz, it is more likely that morphological and chemical biosignatures may still be preserved.

ORAL PRESENTATION

The effects of prebiotically-available organic materials on inorganic silica sinter deposition and its role as a putative biomarker

Khushi Daga[1]

[1]UNSW

The Spirit rover's detection of silica-rich regolith in the Columbia Hills region of Mars quickly garnered attention as it appeared similar to silica sinter found in geothermal springs on Earth. Because sinter is an indicator of complex aqueous chemistry and only been found in microbe-rich environments on Earth, scientists gravitated toward the conclusion that these silica structures could indicate the presence of microorganisms on other planets. Whilst there have been previous attempts to recreate these silica structures in the absence of microbes, resulting in nano-mineral aggregations, there exists little research on how silica deposition can be affected by the presence of prebiotic organic matter i.e., organic molecules that could have existed prior to the advent of biology.

This study seeks to use a colloidal physics perspective to understand the effect of prebiotic materials on silica deposition and identify the abiogenic aspects of the process. A lab-simulated hot pool cyclically evaporates and precipitates silica-rich fluids onto glass slides, in which mixtures of fatty acids and other simple molecules alter the interfacial properties of the fluids. By controlling temperature, surface tension, pH, and concentration, we observe the effect of these physicochemical factors on the 'coffee-ring effect' to identify how changes in interfacial tension and charge between molecules can alter silica precipitation and subsequently, aggregation.

Preliminary results suggest altering pH has significant effect on deposition patterns and can assemble silica with great diversity in shape. The long-term aim is to generate macro-scale structures with morphologies that can be compared to sinter structures. As a result, this study can help reinforce our scientific understanding of the role of abiotic processes in driving silica deposition, which could change our understanding of how sinter structures form. This will clarify the conditions necessary for sinter formation and ascertain its potential to indicate analogue environments for life to exist beyond Earth.