

# Te Ao Mārama Conference

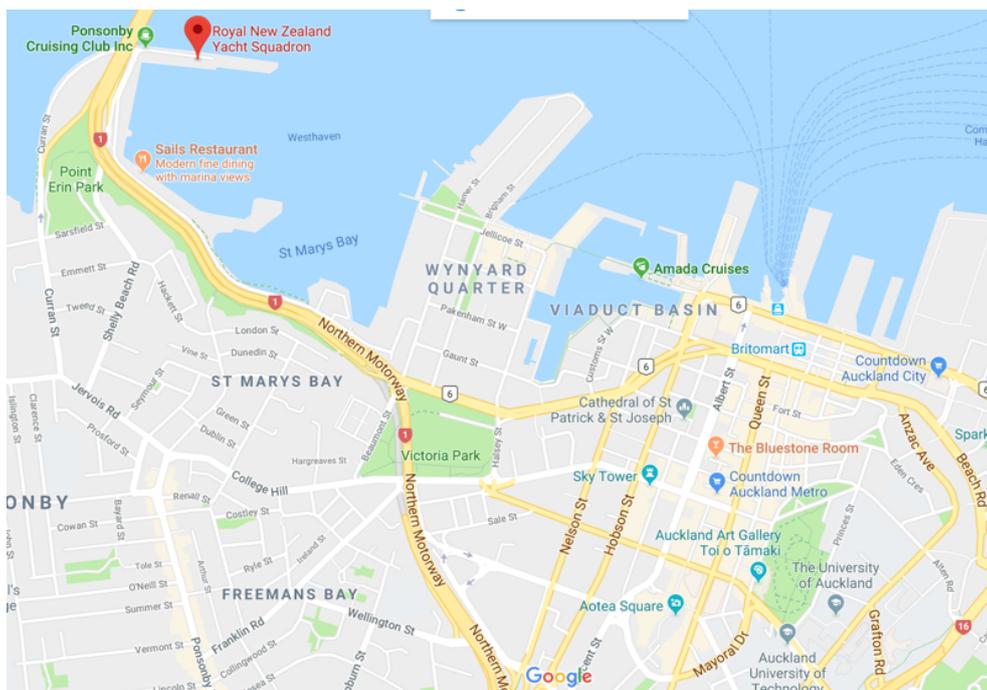
24 – 25 October 2018



**The Royal New Zealand Yacht Squadron, Westhaven Marina**  
Room: RNZYS Ballroom

## Location on Maps:

<https://goo.gl/maps/eLofdbGAc5R2>



## Getting to the venue:

Walking: approx. 30 minutes from Britomart, along waterfront, via Wynyard Quarter.

## Parking information:

All day parking is free of charge for event guests of RNZYS.

Guests are required to park in spaces with white lines and must request a parking ticket issued from the parking machine located at the RNZYS reception and displayed on the car dashboard.

Additional free parking is available at the Western side of the Marina near the Marina Office.

**Conference:**

**Te Ao Mārama Conference 2018**

**Date:**

24 - 25 October - Conference

**Location:**

RNZYS Ballroom, Royal New Zealand Yacht Squadron

**WEDNESDAY, 24 OCTOBER - CONFERENCE, DAY 1**

8:15 AM	9:00 AM	Registration Open	Arrival coffee and tea served
<b>9:00 AM</b>	<b>Conference Day 1 Begins</b>		
9:00 AM	9:30 AM	Welcome Remarks	Michael Steedman, K Campbell
9:30 AM	10:00 AM	Keynote 1: Anthony Aguirre	Chair: R Easter
10:00 AM	10:20 AM	Contributed Talk 1: Matthew Egbert	
10:20 AM	10:40 AM	Contributed Talk 2: Heather Hendrickson	
<b>10:40 AM</b>	<b>11:10 AM</b>	<b>Morning Tea</b>	
11:10 AM	11:40 AM	Keynote 2: Daniella Scalice	Chair: N Rattenbury
11:40 AM	12:00 PM	Contributed Talk 3: Sam Woolley	
<b>12:00 PM</b>	<b>1:10 PM</b>	<b>Lunch</b>	
1:10 PM	1:40 PM	Keynote 3: E Parke	Chair: M Egbert
1:40 PM	2:00 PM	Contributed Talk 4: Alex Poppinga	
2:00 PM	2:20 PM	Contributed Talk 5: Danielle Maddock	
2:20 PM	2:40 PM	Contributed Talk 6: Wayne Patrick	
2:40 PM	3:00 PM	Contributed Talk 7: Peter Wills	
3:00 PM	3:20 PM	Contributed Talk 8: Nobuto Takeuchi	
<b>3:20 PM</b>	<b>3:40 PM</b>	<b>Afternoon Tea</b>	
3:50 PM	4:10 PM	Contributed Talk 9: Michael Rowe	Chair: K Campbell
4:10 PM	4:30 PM	Contributed Talk 10: Angelica Angles	
4:30 PM	5:00 PM	Keynote 4: Martin van Kranendonk	
5:00 PM	5:30 PM	Social Mixer	
<b>5:30 PM</b>	<b>7:00 PM</b>	<b>Poster Session - nibbles &amp; drinks</b>	
<b>7:00 PM</b>	<b>Conference Day 1 Ends</b>		

**THURSDAY, 25 OCTOBER - CONFERENCE, DAY 2**

8:30 AM	9:00 AM	Registration Open	Arrival coffee and tea served
<b>9:00 AM</b>	<b>Conference Day 2 Begins</b>		
9:00 AM	9:05 AM	Welcome Remarks	
9:05 AM	9:35 AM	Keynote 5: Rangi Matamua	Chair: D Hikuroa
9:35 AM	9:55 AM	Contributed Talk 11: Tim Cooper	
9:55 AM	10:15 AM	Contributed Talk 12: JJ Eldridge	
<b>10:15 AM</b>	<b>10:45 AM</b>	<b>Morning Tea</b>	
10:45 AM	11:05 AM	Contributed Talk 13: Dan Hikuroa	Chair: E Parke
11:05 AM	11:25 AM	Contributed Talk 14: Quentin Atkinson	
11:25 AM	11:45 AM	Contributed Talk 15: Kathleen Campbell	
11:45 AM	12:05 PM	Contributed Talk 16: Nicholas Rattenbury	
12:05 PM	12:10 PM	Closing Remarks	
<b>12:10 PM</b>	<b>Conference Day 2 Ends</b>		

## **TAM 2018 Abstracts**

### **Keynote 1: What is the Origin of Order in the Universe?**

**Anthony Aguirre**

Department Of Physics, University of California at Santa Cruz, USA

The observed universe is full of beautiful and interesting structure – from patterns of galaxies to stars, planets, and living creatures. Yet physics, and particularly the “second law of thermodynamics” tell us that systems tend to become disordered over time: “entropy” increases. So where did all the order come from, and why hasn’t everything descended into chaos? I’ll first discuss the meaning of entropy (and the related idea of “information”), why and how entropy grows, and how order can nonetheless be generated. After touching on the relation between entropy and the nature of time, this will take us through everyday and biological systems, then outward to the sun, gravitating systems, and the entire observable universe. I’ll argue that order is ultimately inherited from the Universe as a whole and its evolutionary process, while also being intimately tied up in what it means to be an observer that sees and understands that Universe.

### **Contributed talk 1: Self-Preserving Behaviours Preceded and Perhaps Facilitated Early Evolution**

**Egbert M D**

Department of Computer Science, University of Auckland, Auckland, New Zealand

A number of simple physical systems demonstrate remarkably life-like forms of self-preservation. These include motile-oil droplets, diffusing autocatalytic reactions, and other dissipative structures such as ramified charge transportation networks and Benard convection cells. The self-preserving behaviours demonstrated in each these systems all share a simple underlying mechanism that involves a positive feedback system/environment interaction in asymmetric environmental conditions. The mechanisms are common and simple enough to have spontaneously emerged before neo-Darwinian evolution. In this talk, I will explain the underlying mechanism providing concrete examples, why it is reasonable to think of these as self-preserving behaviours, and how these behaviours could have facilitated the earliest stages of life’s evolution.

**Contributed talk 2:** The Evolution of Pathogenic Traits in Bacteria can be Stimulated by Protozoan Predation.

Golzar, F.S,<sup>1</sup> Kok, D.N.,<sup>1</sup> Yulo, P.R.,<sup>1</sup> and **Hendrickson, H.L.**<sup>1</sup>

<sup>1</sup>Institute of Natural and Mathematical Sciences/Massey University, Auckland, New Zealand

While the life-styles of the soil associated microbes are often of little interest to the multicellular, this nonchalance changes to terror when bacteria express pathogenic traits in the wrong places; places like food crops, farm animals or friends.

Why do bacteria become pathogens? In 1988 Dr Karen G. Porter proposed Amoeboid predation serves as a training ground for pathogenicity based on the observation that many nasty pathogens appear to survive and thrive by living within their amoeboid predators<sup>1</sup>. Amoebae are a common, ancient, and nearly ubiquitous selective pressure on bacteria<sup>2</sup> and they are strikingly similar to phagocytic immune cells. The hypothesis that amoebae are an effective training ground for bacterial pathogenicity has not yet been tested directly<sup>3</sup>.

We have co-evolved a plant-associated bacterium, *Pseudomonas fluorescens* SBW25 with a common soil amoebae, *Naegleria gruberi*. I will describe our preliminary results and observations regarding the surprising degree to which these formerly harmless bacteria have rapidly evolved virulence against protozoa and a multicellular nematode.

1. C. H. King et al., "Survival of Coliforms and Bacterial Pathogens Within Protozoa During Chlorination." Applied and Environmental Microbiology, December 1, 1988, 3023–33.
2. M. Clarholm, "Protozoan Grazing of Bacteria in Soil-Impact and Importance." Microbial Ecology 7, no. 4 (December 1981): 343–50, doi:10.1007/BF02341429.
3. S. Sun, P. Noorian, and D. McDougald, "Dual Role of Mechanisms Involved in Resistance to Predation by Protozoa and Virulence to Humans." Frontiers in Microbiology 9 (2018): 1017, doi:10.3389/fmicb.2018.01017.

**Keynote 2:** Astrobiology as Origin Story: Bringing Together Astrobiology Science and Navajo Cultural Knowledge for Native Youth

**Daniella Scalice**

Education and Communications Lead, NASA Astrobiology Program

American Indian/Alaskan Native Working Group Lead, NASA Science Mission Directorate

Many STEM opportunities pull Indigenous people away from their homes, families, communities, and cultures. Many Indigenous students walk between "two worlds," their Indigenous Universe and the Western worldview. How can we work together to go beyond increasing Indigenous access to and participation in STEM to *decolonizing* it?

One way is to bring Western and Indigenous scientific knowledge together in a dual-learning environment where both are held as equals. Many traditional Indigenous knowledge systems hold information that is just being explored by Western sciences. Through a partnership between the NASA Astrobiology Program and the Navajo Nation, Navajo people are able to explore the creation of the Navajo Universe in parallel to the scientific theory of the life cycle of stars. Instead of teaching Indigenous students a colonized perspective of what is fact and what is myth, we can embrace the two ways of knowing and hold each as valid and vital.

Hopefully this talk will spur discussion about how these and other strategies can evolve our common vision for a future where Indigenous youth can fully express themselves as scientists, technologists, engineers, and mathematicians in a decolonized STEM enterprise.

### **Contributed talk 3: Life as an individual versus Life as a collective**

**Woolley SJ**

School of Humanities, University of Auckland, Auckland, New Zealand

There are a variety of opposing camps within the ‘life definitionism’ debate. Fortunately, much of the contention is of a kind that identifies where mutually beneficial discussion can occur, stemming from mutual understanding and agreement about what is to be accounted for – namely, what “life” refers to – in conjunction with genuinely divergent interests or goals. One unfortunate departure, I argue, involves debate surrounding whether “life” is an *individual* or *collective* phenomenon. Two distinct ‘threads’ of definitions have been presented as rivals: the first addresses features that manifest primarily in individual instances, and thus treats *individual organisms* as exemplary of life; the second addresses features that manifest only in populations of individual organisms, and thus treats *collectives* as exemplary of life. I demonstrate that for each kind of definition, the term “life” has a real-world referent that is different but compatible with the other, such that the two kinds of definition are not really rivals but reflections of different research interests. Further, each definition accounts for distinct features we find salient about life, and thus has independent explanatory value. I present a “holistic” definition of life that reflects these facts, containing both an individualist and collectivist component.

### **Keynote 3: Finding, explaining, and engineering life**

**Parke EC**

Philosophy, School of Humanities, University of Auckland, Auckland, New Zealand

People have been debating for millennia how to distinguish living from nonliving things. Over 100 definitions of life have been proposed to date, and there is little movement towards consensus within disciplines, let alone across them. This has led some philosophers and scientists to dismiss the whole project of defining life as misguided or hopeless. A sticking point in this debate is that most parties have assumed that the aim is to converge on a single, unanimous definition of life. I suggest a middle ground between converging on a single definition and giving up, which involves accounting for the multifaceted roles that the notion of life plays in scientific practice. Those roles span (at least) three theoretical and empirical agendas which I abbreviate as *finding*, *explaining*, and *engineering life*. I identify three key ways accounts of life vary: (1) treating living/nonliving as a dichotomy versus a matter of degree, (2) defining living individuals versus living collectives, and (3) defining life materially versus functionally. Depending on whether the aim is to find, explain, or engineer life, which sort of account of life is useful or appropriate can vary.

#### **Contributed talk 4: The Role of Proteins in the Origin of the Genetic Code**

**Popinga AN**<sup>1</sup>, Bouckaert R<sup>1</sup>, Carter Jr. CW<sup>2</sup>, Wills PR<sup>3</sup>

<sup>1</sup>Department of Computer Science/University of Auckland, Auckland, New Zealand

<sup>2</sup>Department of Biochemistry and Biophysics/University of North Carolina at Chapel Hill, North Carolina, USA

<sup>3</sup>Department of Physics/ University of Auckland, Auckland, New Zealand

Proteins are often overlooked in research focused on the origin of life and the development of the genetic code. The RNA World Hypothesis supposes that nucleic acids once replicated alone and incorporated proteins later on to boost the process. Other hypotheses propose that nucleic acids and proteins coevolved. We provide evidence for the latter by examining certain proteins with vital roles in the functioning of the genetic code. The aminoacyl-tRNA synthetases (aaRSs) are enzymes which catalyse the attachment of amino acids to tRNA molecules, effectively translating genes into functional proteins which then propagate the replication of the code and in doing so, themselves. There are two classes of aaRSs based on their core structures: Class I and Class II. Each has distinct structure and ways of interacting with tRNA, which differ greatly between the two classes but are universally shared across all domains of life within each class. Life is estimated to have originated ~4 billion years ago, yet these internal structures have been remarkably well-conserved. Using structural alignment and a unique perspective on amino acid substitution in the organisational stages of the genetic code, we investigate the evolutionary signals preserved in the aaRSs and gain insight into early life.

#### **Contributed talk 5: Building Rube Goldberg machines to explore unnecessary complexity in biology**

**Maddock D**, Ganley, AR, Poole AM

School of Biological Sciences, The University of Auckland, Auckland, New Zealand

It is tempting to assume that all molecular complexes have been crafted by natural selection to maximise performance with minimal components. However, molecular evolutionists have proposed that biological systems are actually much more complex than they need to be – analogous to Rube Goldberg machines. This ‘unnecessary’ complexity is thought to arise through chance evolutionary processes, without any adaptive benefit via a process known as Constructive Neutral Evolution (CNE). CNE has been used to describe the complexity of diverse biological phenomena, such as the seemingly gratuitous number of proteins that comprise the mitochondrial ribosome, and the arguably convoluted processes of RNA editing and splicing.

However, there is little clear experimental evidence demonstrating the validity of this proposal. Therefore, the aim of my project is to build an unnecessarily complex multi-protein machine that is deliberately constructed via neutral, non-adaptive interactions. Once constructed, my ‘Rube-Goldbergesque’ protein machine will be subjected to experimental evolution to explore how nature reacts to complexity that is demonstrably unnecessary. This machine will provide an experimental test of whether convoluted molecular systems can arise despite having no direct fitness benefit. This will allow me to assess the role that neutral processes might play in the evolution of biological complexity.

## **Contributed talk 6: Nature sets a surprisingly low bar (when it comes to enzymes)**

**Patrick WM**

School of Biological Sciences, Victoria University, Wellington, New Zealand

When I was a student (last millennium!), I was heavily influenced by enzymologists such as Knowles and Wolfenden, who emphasised the supreme catalytic power of enzymes. The accepted view was that 4 billion years of biochemical evolution had given rise to enzymes that were highly active and impressively specific. In this talk, I will describe our recent work to characterise non-model enzymes from non-model organisms. It turns out that enzymologists have been studying a rather biased subset. Most of the enzymes on Earth are slow and sloppy, just as they have been since the dawn of life.

## **Contributed talk 7: Reinterpreting molecular biology: more semantics than mechanism**

**Wills PR<sup>1</sup>, Carter CW<sup>2</sup>**

<sup>1</sup>Department of Physics, University of Auckland, Auckland, NZ

<sup>2</sup>Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill, , NC, USA

What most clearly distinguishes living cells from other molecular systems is that they process information in a quasi-computational manner. There is no reason to believe that anything happens inside a cell that is inconsistent with the quantum mechanics, which govern events in the material world, but the principles of physical mechanism do not enlighten us concerning the origin and maintenance, but more particularly the causative agency, of abstract patterns like nucleotide sequences. The intracellular milieu is very information rich, but the Shannon (“negentropy”) measure does not capture the features of extended mutual information, unrelated to any possible state of thermal equilibration, that characterise the relationships between nucleic acid and protein sequences. And it is these arbitrary relationships between otherwise unrelated patterns that are responsible for the cell’s existence. What preconditioned the historical establishment of these relationships? We will argue that the transfer of sequence information from one symbolic alphabet (nucleotide triplets) to another (amino acid sidechains) was only possible because this system coevolved with a form of molecular semantics: the description of amino acid sidechains in terms of arrangements of amino acid sidechains in the active sites of aaRS enzymes, enabled by the different chemical properties of amino acid sidechains.

**Contributed talk 8:** The origin of the central dogma through conflicting multilevel evolution.

**Takeuchi N**<sup>1,2</sup>, Kaneko K<sup>2,3</sup>

<sup>1</sup>School of Biological Sciences , University of Auckland, Auckland, New Zealand

<sup>2</sup>Research Center for Complex Systems Biology, University of Tokyo, Tokyo, Japan

<sup>3</sup>Department of Basic Science, University of Tokyo, Tokyo, Japan

Molecular biology embodies three asymmetries between genomes and enzymes. Information flows from genomes to enzymes, but not from enzymes to genomes: informatic asymmetry (the central dogma of molecular biology). Genomes serve as templates, whereas enzymes serve as catalysts: functional asymmetry. Genomes are less abundant than enzymes per cell: numerical asymmetry. How did these asymmetries originate? Although existing theories can explain subsets of them, no theory has been able to explain all at one stroke. Here we provide such a theory by showing that all these asymmetries can spontaneously arise from conflicting multilevel evolution. Our model assumes a population of protocells, each containing a population of self-replicating catalytic molecules. The molecules are assumed to face a trade-off between providing catalysis and serving as templates, a dilemma that causes conflict between molecular-level evolution and cellular-level evolution. We find that this conflicting multilevel evolution creates positive feedback with the asymmetric flow of information between the molecules. This destabilising mechanism causes symmetry breaking whereby the molecules differentiate into genomes and enzymes. Our work proposes an evolutionary mechanism for the origin of the fundamental molecular asymmetries underlying life, making the central dogma no longer a dogma.

**Contributed talk 9:** Characterization of extra-terrestrial amorphous materials in potentially habitable environments

**Rowe MC**<sup>1</sup>, Jenna Li, Brewer, B<sup>2</sup>

<sup>1</sup>School of Environment, University of Auckland, Auckland, New Zealand

<sup>2</sup>Department of Statistics, University of Auckland, Auckland, New Zealand

The study of the origin of life on Earth and in extra-terrestrial environments builds upon the foundation of habitability determined from geologic investigations. Recent investigations combine mineralogy (crystalline) with chemistry to provide an enhanced glimpse into depositional environments. Amorphous (non-, or partially-crystalline) materials provide another significant avenue of geomaterials research which has practical applications to habitable environments. This investigation utilizes a new statistical approach (AMORPH) to processing X-ray diffraction (XRD) data to characterizing amorphous materials. Combining terrestrial “known” examples of amorphous materials with diffraction patterns from the Mars Scientific Laboratory CheMin instrument provides a mechanism to identifying amorphous materials such as amorphous silica (e.g. sinter), clays, and/or volcanic and impact glass.

Results demonstrate the X-ray characteristics of the amorphous material changes as a function of bulk mineralogy but that purely amorphous materials are statistically distinguishable. Analysis of the Martian surface samples demonstrates significant and distinct variations in the X-ray characteristics of Martian amorphous materials, demonstrating a range of amorphous products and processes. Ongoing and future investigations focus on identifying different populations of amorphous materials and associated depositional environments, particularly for materials indicative of water-rock interaction including deposition of silica (opal) and the formation of clays.

## Contributed talk 10: Ooids, putative signatures of past life

Angélica Anglés<sup>1</sup>, Yiliang Li<sup>2</sup>

<sup>1,2</sup>Department of Earth Sciences, The University of Hong Kong, Hong Kong

The study of ancient carbonate sediments in terrestrial analogues is essential for understanding the putative life-involved carbon cycle on Mars. Because of their optically recognizable structures, calcium carbonate ooids raise interests in Martian life exploration for their potential biogenesis. We identified ooids in one of the numerous layers of the Xiaoliangshan anticline, which is part of a hyper-arid dry saline lake in the northwest of the Qaidam Basin. The structure and surface feature of those ooids indicate that they precipitated in the low-energy lake waters without post-depositional transportation. They exhibit well-preserved radial-fibrous rays in the cortexes, showing their preservation of the primary features of aragonite microcrystallines. The  $\delta^{13}\text{C}$  composition of the oolitic carbonate reveals an abiogenic carbon source, however, we detected the presence of scytonemin, a biomarker of cyanobacteria, by Raman spectroscopic measurements of the organic extraction from those ooids. Scytonemin is shown to be highly resistant to the sedimentary evolution of the Qaidam Basin by showing its preservation over 550,000 years, dated by uranium-disequilibrium method on the fresh ooid grains. The detection of scytonemin is of considerable importance as it indicates the easily recognizable oolitic structure may carry signatures of past life, being directly relevant to the search for extant or extinct Martian life by *in situ* observation of carbonate depositions and the following measurements of organic extraction by vibrational spectroscopies.

**Keynote 4:** “It’s elemental, my dear Watson”: Contextual clues from Deep Time Earth to the search for our origins and for life in the Solar System

**Van Kranendonk MJ**

Australian Centre for Astrobiology, School of Biological, Earth, and Environmental Sciences, University of New South Wales Sydney, Kensington, NSW 2052 Australia

“Are We Alone”? and “How Did Life Originate?” are the Big Questions that relate to understanding our place in the Universe. The Australian Centre for Astrobiology, in collaboration with research colleagues from the University of Auckland and around the world, is actively engaged in pursuing these questions through investigations of the Deep Time record of life on Earth and using this to inform our understanding of the setting for the Origin of Life and our pursuit in the search for life elsewhere in the Solar System.

The remote Pilbara region of northwestern Australia contains the best-preserved, oldest record of life on our planet, stretching back to 3.5 billion years old. This signature of life is manifest as the fossilised remnants of microbial communities and as chemical traces of past metabolic activity. Critically, the results of a broad research program show that life was already diverse at this time and employed a variety of metabolisms to gain energy using a range of elements (S, Zn, Ni, H<sup>+</sup>) and even, possibly, sunlight. This supports suggestions that life originated and evolved rapidly on early Earth. One of the habitats occupied by this ancient life was a terrestrial hot spring field, characterised by alternating pH and silica/carbonate effluents. A recreation of this setting shows that it contains all of the elements required to support a diverse microbial community. More importantly, however, this ancient setting contains all of the critical elements and geochemical and physical parameters for complex prebiotic chemistry leading to RNA and DNA and thus an Origin of Life **On Land**.

This new model for the Origin of Life has far-reaching implications for Astrobiology and the search for life in the Solar System; specifically a rocky planet with liquid water and exposed land. Such a setting would presumably exclude the possibility of life developing on the water-ice covered moons of Jupiter and Saturn, but promote the chances of life having developed on our nearest neighbor, Mars.

In this talk, I will show how the discovery of life’s traces and concentrations of prebiotically important elements in a 3.5 billion-year-old hot spring setting is transforming the way we think about our origins and our thinking about how and where to search for life on Mars.

**Keynote 5:** Te Whānau Mārama – The Family of Light

**Rangi Matamua**

Faculty of Māori and Indigenous Studies, University of Waikato, Hamilton, New Zealand

Māori have always believed that everything in the universe one once contained within the embrace of Ranginui the sky and Papatūānuku the earth. These two beings were torn apart in a violent motion that created space, time and ultimately life. Following the separation, Tāne suspended the various celestial object against the chest of his father Ranginui, and there they remain today. This presentation will look at a Māori understanding of origins and evolution, with a particular focus on Matariki as a means to better connect with Māori astronomy and the wider field of Māori science.

**Contributed talk 11:** Mutations interact globally to promote repeatability and constrain evolvability of experimentally evolved bacteria

Wünsche A<sup>1</sup>, Dinh D<sup>1</sup>, **Cooper TF**<sup>1,2</sup>

<sup>1</sup>Department of Biology and Biochemistry, University of Houston, Houston, USA

<sup>2</sup>Institute of Natural and Mathematical Sciences, Massey University, Auckland, New Zealand

The mutations that underlie adaptation interact with one another so that their combined effect is often different to an expectation based on their individual effects. Theoretical models predict that these deviations, known as epistasis, can have a major impact on evolutionary outcomes, effecting the rate and repeatability of evolution. To examine these predictions directly, we have constructed a set of bacterial strains that comprise the complete set of steps in the early part of an evolutionary trajectory. We found that mutation interactions, while unpredictable at an individual mutation level, nevertheless follow global patterns that predict a regular decelerating pattern of fitness increase. These interactions depend on the fitness effect of individual mutations, not on their specific physiological activity, a pattern that promotes evolutionary repeatability by making the effect of late mutations less dependent on the specific identity of earlier mutations. By introducing the same mutations into a set of natural isolate bacterial strains, we extend our finding of global mutation interactions to divergent strains and find that they act in a way to promote the spread of mutations between strains.

**Contributed talk 12:** Exploring the Cosmic Evolution of Habitability with Galaxy Merger Trees

Stanway E.R.<sup>1,2</sup>, **Eldridge J.J.**<sup>3</sup>

<sup>1</sup>Department, University of Warwick, Gibbet Hill Road, Coventry CV4 7AL, UK

<sup>2</sup>Centre for Exoplanets and Habitability, University of Warwick, Gibbet Hill Road, Coventry CV4 7AL, UK

<sup>3</sup>Department of Physics, University of Auckland, Private Bag 92019, Auckland, New Zealand.

We will discuss recent results on work to understand the habitability of the Universe through cosmic time. By using models of galaxy evolution through the history of the Universe with the latest stellar population synthesis models we explore stellar-mass fraction of galaxies irradiated by energetic astrophysical transients and thus the fraction which is potentially habitable by life like our own. We find that 18 per cent of the stellar mass in the Universe is likely to have been irradiated within the last 260 Myr. We do not see a strong dependence of irradiated stellar-mass fraction on stellar mass or richness of the galaxy environment. We also consider a Local Group analogue, and find that there are galaxies at all masses which have retained a high habitable fraction (>40 per cent) over the last 6 Gyr, but also that there are galaxies at all masses where the merger history and associated star formation have rendered galaxies effectively uninhabitable. We will outline our plans to extend this work in future by considering other sources of irradiation within galaxies.

**Contributed talk 13:** Whaia te pae tata – Seek the distant horizon

**Hikuroa DCH**

Te Wānanga o Waipapa, University of Auckland, Auckland, Aotearoa New Zealand

In a Māori worldview we exist in a kinship-based-relationship with Te Taiao – the Earth, Universe and everything within it. What is described as ‘the universe’ in scientific theory is conceptualised in mātauranga Māori as ‘process’, constructed around a whakapapa or kinship framework. Whakapapa is the central principle that orders the universe, demonstrates an interconnectivity between everything, and is a cognitive genealogical framework connecting creation of the universe to everything that exists within it via descent from primal parents. This whakapapa ontology lies at the very core of Māori thinking, knowledge, identity and practice.

What role could such thinking, knowing and being play in seeking to explore our fundamental questions - what is the origin of life? Is our own universe part of a much larger multiverse? What types of planets circle other stars in our galaxy?

In this presentstion I will explore the evidential basis of mātauranga and propose processes that we may choose to use in Te Ao Mārama – Centre for Fundamental Inquiry.

**Contributed talk 14:** Evolution beyond biology

Quentin Atkinson

School of Psychology, University of Auckland, Auckland, New Zealand

Since Darwin, it has been recognised that the process of evolution is not unique to biology. Like species, cultures and the languages they speak also evolve. The last decade has seen an explosion of computational modelling and experimental work seeking to understand how cultural systems evolve. In this talk I will briefly review work on the evolution of culture and speculate about what the field can tell us more generally about evolution beyond biology.

**Contributed talk 15:** Building robust conceptual models in the search for life beyond Earth – terrestrial and extraterrestrial hydrothermal systems

**Campbell KA**<sup>1</sup>, Guido DM<sup>2</sup>, Van Kranendonk, MV<sup>3</sup>, Ruff, SW<sup>4</sup>, Farmer, JD<sup>4</sup>, Westall, F<sup>5</sup>, Djokic, T<sup>3</sup>

<sup>1</sup>School of Environment & Te Ao Mārama—Centre for Fundamental Inquiry, The University of Auckland, Auckland, New Zealand

<sup>2</sup>CONICET & Universidad Nacional de La Plata, La Plata, Argentina

<sup>3</sup>Australian Centre for Astrobiology, School of Biological, Earth, and Environmental Sciences, University of New South Wales, Sydney, Australia

<sup>4</sup>School of Earth & Space Exploration, Arizona State University, Tempe, Arizona, U.S.A.

<sup>5</sup>Centre de Biophysique Moléculaire, Centre National de la Recherche Scientifique (CNRS), Orléans, France

‘Follow the water’ – hot or cold – has been a key component in exploration of the martian surface for habitable environments and potential signs of ET life for more than 20 years, as liquid water is essential for life as we know it. This ‘mantra’ guides current and planned orbiter and robotic missions to Mars, including sample return proposals. It also has been applied to the outer Solar System, where Enceladus and Europa send jets of water ice into space, potentially driven by hydrothermal circulation arising from the floors of liquid-water oceans beneath the moons’ fractured ice shells. Some suggest life may be lurking in oceanic hydrothermal vents on these Icy Worlds. In the case of Mars, where water once flowed across the surface >3 billion years ago, several types of ancient, water-laid sedimentary deposits have been identified as favourable targets in the search for (fossil) life beyond Earth. Clement conditions for life to have originated/survived on Mars’ surface were fleeting, and the obvious ‘biosignatures’ that are replete on Earth are lacking there. Research on both terrestrial and martian hydrothermal systems over the past 20 years has led to development and refinement of robust conceptual models, underpinned by nested scales of observation in the field and laboratory, which have advanced our understanding of where and how life may most likely have been preserved. Thus, such studies substantially help narrow search windows in the quest to find a second outpost of life in the Solar System.

**Contributed talk 16:** Discovering Alien Worlds

**Rattenbury NJ**, Donachie, M

Department of Physics, The University of Auckland, Auckland, New Zealand

The discovery of thousands of extra-solar planets over the last few decades has brought into sharp relief the questions surrounding the emergence of life elsewhere in the Universe. I will review briefly the extra-solar planet discoveries to date and the principal methods for planet discovery. I will outline some of the tensions in the field which drive future research and how New Zealand has contributed to the field and our ambitions for the future.

**Poster 1: Probing the deep evolutionary origin of DNA using synthetic biology**

**Samantha. D. M. Arras**, Nellie Sibaeva & Anthony M. Poole

Te Ao Mārama/Centre for Fundamental Inquiry & School of Biological Sciences, University of Auckland, Auckland, New Zealand

The transition from the RNA to the DNA world is thought to have been a major event in the history of life, but little is known about the exact details of how and when this might have occurred. Today, the building blocks of DNA are synthesised exclusively through the process of ribonucleotide reduction, but the complexity of this reaction suggests it did not evolve until well after protein synthesis was established. It is possible that deoxyribonucleotides may have first been synthesised through an alternative, chemically simpler route: the reverse of the deoxyriboaldolase (DERA) step in deoxyribonucleotide salvage. Recent studies have shown *in vitro* that this pathway can drive the synthesis of deoxyribonucleotides from glucose and acetaldehyde. Our aims for this project are to: 1. reverse this simpler pathway in the model organism *Escherichia coli* to see if DNA building blocks can be made *via* this route, and, 2. explore what makes the modern, 'chemically-sophisticated' pathway ubiquitous. Here, we will present progress on the creation of an *Escherichia coli* cell that synthesises deoxyribonucleotides through this retrosynthesis pathway. If successful, the implication of this work is that life is capable of generating DNA *via* an existing, chemically simpler, ancient pathway present in all domains of life.

**Poster 2: Development of biodegradable nanoparticles using mycobacteriophage endolysins to infect *Mycobacterium smegmatis* mc<sup>2</sup>155 exogenously**

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The *Mycobacterium* genus includes over 190 species with pathogens such as *M. bovis* posing an increasing threat to the New Zealand dairy industry. Whilst bacteriophages - the natural parasites of bacteria - are a promising line of defense against such pathogens, bacteria rapidly evolve resistance to these viruses to prevent infection or destroy DNA. A strategy that is gaining traction, is to harness the late acting lytic enzymes from bacteriophages, thereby avoiding common resistance strategies. We are exploring this approach by developing mycobacteriophage lysins and attaching them to biodegradable nanobeads as a potential prophylactic barrier against infection. To begin, we have analysed and selected a set of eight endolysins from over 1,600 entries on the publicly available mycobacteriophage database (PhagesDB.org). The genes for the lysin proteins have been codon-corrected and cloned into an overexpression plasmid that generates polyhydroxyalkanoate (PHA) nanobeads in *Escherichia coli* cells. This presentation discusses nanobead production and the preliminary results testing their effectiveness against *Mycobacterium smegmatis* mc<sup>2</sup>155 using a combination of fluorescent microscopy and growth assays. If successful, this research can serve as a proof of concept for a potentially time-effective, cost-efficient and simple-to-implement solution for an array of infectious *Mycobacterial* species in New Zealand and beyond.

**Poster 3: Spatial Analysis of Hydrothermal Deposits and Siliceous Spicular Sinter at Tikitere Geothermal Field, Taupō Volcanic Zone, New Zealand**

**Dobson M. J**<sup>1</sup>, Campbell K. A<sup>1</sup>, Rowe M<sup>1</sup>, Drake B<sup>1</sup>, Hamilton A<sup>1</sup>, Ruff S<sup>2</sup>, Van Kranendonk M<sup>3</sup>

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Mapping of varied hydrothermal facies by drone at Hell's Gate/Tikitere, Taupo Volcanic Zone, Rotorua, New Zealand, enabled a spatial reconstruction of their distribution, including that of distinctive spicular siliceous hot spring deposits (sinter) developing in spring outflow channels. Geochemical analysis of microbial digitate sinters was undertaken as they have similar morphology and geochemistry compared to opaline silica deposits found at Columbia Hills, Mars (1,2). At Columbia Hills, the silica – formed >3 billion years ago – has been interpreted as hydrothermal in origin, possibly deposited as alkali chloride-spring derived sinter (1,2). The martian features have been compared to siliceous microstromatolites forming in the shallow outflow channels of alkali-chloride thermal springs in El Tatio, Chile (3). Several hot springs around Rotorua, New Zealand, have broadly similar features, and form in the same position on the discharge aprons suggesting a rather ubiquitous occurrence of these morphologically distinctive textures.

Analysis of hot springs temperature, pH and water chemistry provides insight controls on the formation of these deposits. In-depth field mapping of variations in morphology and densities of spicular to digitate sinter deposits defines spatial context. As these deposits form from evaporation shallow discharge channels, higher densities are seen forming in areas of increased slope angles.

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#### Poster 4:

Bryan Drake

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Humankind has been denigrated as a late arrival on an insignificant planet orbiting a nondescript star. However, in *Homo sapiens* the Universe has become self-aware. While we may speculate at intelligent life in other parts of the Universe, we are the only known instance in which this has occurred. We are not the reason for the existence of the Universe....but we are special within it. Life is a complex thermodynamic system that accelerates disorder in the universe by generating localized complex chemical interactions, predominantly carbon based molecules within an aqueous medium. On Earth, this process has produced modern Humankind, but there is no reason to assume this process is incapable of further novelty, nor to assume that it cannot occur elsewhere in the Universe.

However, all forms of life are subject to the basic laws of physics and thermodynamics, giving reason to believe our current physical form is the most convenient to equip us to be the dominant global predator, and rational life in other star systems should be similar. Further evolution of *Homo sapiens* will be similarly constrained, and will produce little variation in phenotype, but considerable development in socialization and community.

#### Poster 5: Illuminating the twilight zone with phylogenetic analysis of protein structures.

**Matthew S. Fullmer**<sup>1</sup>, Ashar J. Malik<sup>2</sup>, Jane R. Allison<sup>1</sup>, Anthony M. Poole<sup>1</sup>

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Over large evolutionary distances sequences can accumulate so many changes that evolutionary analysis becomes challenging. In some instances this sequence change is so great that homologous sequences are no longer recognizably related. In this “twilight zone” the three-dimensional structures of proteins may nevertheless retain clear similarities. This grants the opportunity to plumb greater evolutionary depths and ask broader questions about relationships by comparing structure instead of sequence. Prior work has demonstrated that the evolutionary relationships within a protein superfamily can be recovered from structural analyses<sup>1</sup>. While credible phylogenies can be inferred for well-characterized protein groups using structural comparisons there has been no method to assess the robustness of the data to the topology. We present a novel method of generating a parametric support set of protein topologies using molecular dynamics simulations. This method allows assessment for the reliability of all branches of the inferred best topology. We also present our progress in using structural phylogenetics for uncovering the evolutionary history of protein superfamilies. These developments offer the potential to further develop and refine the organization of protein repositories such as CATH and SCOP, which group proteins hierarchically into, e.g. superfamilies, but do not assess the evolutionary relationships between superfamily members.

1. Lundin, D., Poole, A. M., Sjöberg, B.-M. & Högbom, M. Use of structural phylogenetic networks for classification of the ferritin-like superfamily. *J. Biol. Chem.* 287, 20565–20575 (2012).

**Poster 6:** Characterisation of iron rich, acidic hot springs, North Island, New Zealand

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Expanding the field of terrestrial hot spring research requires a closer look at non-typical spring systems. For this study, three acidic, highly variable spring sites, with associated iron rich deposits have been chosen, located in different parts of the central North Island of New Zealand. The intention is to investigate the character, location and distribution of the iron, as well as characterize some of the variability found in non alkali chloride hot springs. Fluid and solid samples were collected from Orange Springs, Tikitere and White Island. Facies maps contextualised the samples, which were analyzed for mineralogy and elemental makeup using petrography, ICP-MS and SEM. Preliminary results show iron acting as an amorphous coating or 'cement' alongside silicification, as well as being incorporated mineralogically as iron sulfides. Future work will involve in-situ analysis to target concentrations of iron within samples. With terrestrial springs being hot contenders for the site of life formation on earth, and iron being a biologically ubiquitous element, this study sits neatly beside studies focussing on questions of early life formation. We hope to expand the library of hot spring knowledge used to interpret fossil hydrothermal systems, be it on earth, mars or elsewhere.

**Poster 7:** Protozoan Predation Can Influence Bacterial Cell Shape Evolution

**Kok D,** Hendrickson H

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Cell shape is a fundamental characteristic of single-celled organisms. Analysis revealed all bacteria evolved from a rod-shaped ancestor and has adopted spherical cell shape over 14 times since, losing a single gene, *mreB* in each case. *Pseudomonas fluorescens* SBW25 is a rod-like bacterium, capable of surviving the loss of *mreB*. We observe these cells are not only spherical, but have a 6-fold increase in cell volume. Suggesting an alternative narrative for the adaptation conferred by deletion of *mreB*: large cell size.

An instance in which large size may confer an advantage is under protozoan predation. We tested *Naegleria gruberi* and a *Dictyostelium* sp. for predation preferences between three different cell morphologies of otherwise isogenic mutants of *P. fluorescens* SBW25. Our results suggest *Dictyostelium* sp. has an 5-fold preference, while *N. gruberi* has an 8-fold preference for WT cells over their larger *mreBΔ* derivatives.

Conditions in the laboratory cannot replicate the predation parameters encountered in nature. An agent-based model was developed, to take a wide range of conditions into account. A minimum predator population of 10 (to 100 bacterial cells) and a 4-fold preference of WT over *mreBΔ* cells favours the increase of *mreBΔ* cells. This work allows us to speculate about ecological parameters in which *mreBΔ* cells might have a transient fitness advantage against predators which could lead to the evolution of coccoid cell shape in bacteria.

**Poster 8: Synergies in Space: A Pilot Programme Bringing Astrobiology Science to Oxford Area School, Christchurch NZ**

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<sup>5</sup> The University of Hong Kong, Department of Earth Sciences, Hong Kong

<sup>6</sup> Hutt City Libraries, Lower Hutt

Synergies in Space is a week-long pilot programme for students to learn and practice effective collaboration, management, and leadership in the context of Astrobiology-focused scientific exploration and discovery. The programme was introduced to the student body of Oxford Area Schools in September 2018, and we focused on curriculum metrics for Years 7-10. Team activities were introduced as astrobiology science mission operations on Mars, where one day similar decisions and operational procedures could have life and death consequences. Students used the scientific method and effective teamwork to complete required tasks, rotating through several operational roles. An interdisciplinary team of educators and scientists collaborated with Oxford Area School teachers to maximize engagement and supervise. Students were given mission objectives and were asked to self-organise, assess and direct their own teams, and keep observation logs, and present results at the completion of each of three mission opportunities. We produced a materials kit for the programme, so that it can be deployed to other schools around New Zealand. Initial feedback was extremely positive, and teacher and student survey input will be evaluated quantitatively in order to characterise educational metrics and understand the efficacy of the project.

**Poster 9: Siliceous sinter deposits at the Te Kopia geothermal field, Taupo Volcanic Zone, New Zealand, and their relevance to astrobiology**

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Te Kopia is a high-temperature geothermal field 25km north of Taupo. It sits along the northeast-trending Paeroa Fault in the TVZ, which is thought to be controlling the migration of deep hydrothermal fluids in the area. Current activity at Te Kopia is dominated by acid sulphate fluids/vapours that develop due to boiling of deep chloride fluids, producing features such as fumaroles, mud pots and dissolution craters at the surface. However, scattered remnants of fossil silica sinter (dated to 1,800-5,148 yrs BP) at Te Kopia indicate that alkali chloride fluids were discharging here as recently as 1,800 years ago, and the change in surface manifestations are consistent with a lowering of the water table. Biologically influenced sinter facies record dynamic sub-environments (eg. fast-flowing outflow channels, shallow to deep pooling) and an entire geothermal gradient, from proximal vent (>75°C) to distal apron (<40°C). Some of the earliest evidence of life on Earth occurs in Precambrian cherts that originated as terrestrial hot spring deposits, and prebiotic chemists are increasingly favouring these settings as crucibles for early life. Exposure of sinter deposits at Te Kopia to hydrothermal alteration and an active tectono-volcanic setting provide an opportunity to explore the effects of post-depositional alteration and diagenesis on primary sinter fabrics in the transition from modern sinter to the geologic record.

**Poster 10:** Role of petrogenetic processes in promoting pre-biotic syntheses and creating LUCA-friendly environments: implications for abundance of extraterrestrial life

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It has been proposed<sup>1,2</sup> that the last universal common ancestor (LUCA) arose not from some primordial soup, but in warm alkaline springs where it utilised hydrogen as the electron donor for anaerobic respiration. Modern analogues of such springs discharge solutions laden with hydrogen generated by water-rock interactions involving serpentinisation of olivine ((Mg,Fe)SiO<sub>4</sub>) in subjacent ultramafic rock. Coeval Fischer-Tropsch reactions can provide simple prebiotic compounds.

By analogy with petrogenetic relations on Earth, the widespread presence of basalt in the solar system and on rocky extrasolar planets implies a potential abundance of ultramafic rock capable of undergoing serpentinisation via reaction with aqueous solutions to yield *inter alia* hydrogen and alkanes. Evidence for this type of subsurface fluid-rock interaction having taken place on Mars is available from nakhlite alteration assemblages.

These considerations suggest physicochemical conditions under which LUCA developed on Earth may be duplicated elsewhere in the solar system and on many extrasolar planets. If LUCA indeed arose in settings such as those suggested by Lane *et al.* and Sousa *et al.*, life may be more plentiful in the Universe than hitherto predicted.

1. Lane, N. *et al.* 2010: How did LUCA make a living? Chemiosmosis in the origin of life. *BioEssays* 32.
2. Sousa, P.L. *et al.* 2013: Early bioenergetic evolution. *Phil Trans R Soc B* 368.

**Poster 11:** Towards creation of a U-DNA genome using synthetic biology tools.

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The precursors of DNA are produced from RNA precursors through ribonucleotide reduction, suggesting that DNA evolved after RNA. However, deoxythymidine (dT) is produced by further processing of deoxyuridine (dU), which suggests that the evolution of modern DNA might have been via a uracil-containing intermediate form of DNA. We have previously argued that the transition from U-DNA to T-DNA was driven by futile cycling during the repair of U generated by cytosine deamination (C→U) events<sup>1</sup>. A transition to T is an indirect fix to this problem; it enables identification of U:G pairs arising from cytosine deamination, but a repair mechanism is still required to correct C→U mutations. Thus T does not deal with the issue of cytosine deamination itself. To test our model, we are using synthetic biology and experimental evolution tools to generate and refine an *E. coli* lineage containing a U-DNA genome, and will report on progress towards this goal. We will also present results on detection of U-DNA using nanopore sequencing. Finally, we will outline our plans to use our resulting line to test a range of proposed drivers of the U→T transition.

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**Poster 12:** Molecular characterization of digitate siliceous microstromatolites in terrestrial hot springs: analogues for biosignature candidates at Columbia Hills, Mars

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In 2007, the Mars rover 'Spirit' came across what was later confirmed as opaline silica and suggested to be hot spring deposits at Columbia Hills, Mars<sup>[2,3]</sup>. Similar textures of siliceous hot spring deposits with digitate textures are also found in terrestrial hot springs<sup>[3]</sup>, with silicified microorganisms contributing to their morphologies. In hot springs, mineralized laminae of microbes and silica build up over time to produce microstromatolites, akin to structures prevalent in early Earth paleoenvironments<sup>[4]</sup>. Rapid microbial silicification in hot springs is an excellent mechanism for preserving past biological activities<sup>[5]</sup>. Here we identified modern biosignatures in digitate sinter, derived from different geothermal areas in Rotorua and Taupo, New Zealand, with varied pH and temperatures. Scanning electron microscopy was used to determine the contribution of cells to microstromatolite formation. DNA was extracted from spicular sinter samples, and prokaryotic and eukaryotic rRNA genes were amplified for sequencing. Results show that water chemistry, temperature, and pH are strong predictors of species associated with spicules. Moreover, spicules that grow in medium temperature, alkali-chloride hot springs tend to have higher prokaryotic species diversity, while, acid-sulphate-chloride hot springs tend to have higher eukaryotic diversity. Acid-sulphate springs, on the other hands, have the lowest species diversity.

1. Carr, M. H., & Head III, J. W. (2010). Geologic history of Mars. *Earth and Planetary Science Letters*, 294(3-4), 185-203.
2. Ruff, S. W., Farmer, J. D., Calvin, W. M., Herkenhoff, K. E., Johnson, J. R., Morris, R. V., ... & Squyres, S. W. (2011). Characteristics, distribution, origin, and significance of opaline silica observed by the Spirit rover in Gusev crater, Mars. *Journal of Geophysical Research: Planets*, 116(E7).
3. Ruff, S. W., & Farmer, J. D. (2016). Silica deposits on Mars with features resembling hot spring biosignatures at El Tatio in Chile. *Nature communications*, 7, 13554.
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**Poster 13: Categorical Perception With a Simple Sensorimotor-State-Based Robot Controller**

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The sensorimotor approach to perception claims that perceptual experience is governed by an agent's mastery of sensorimotor contingencies (SMCs). To explore robotic behaviour in these terms, we have developed a minimal robot controller which operates expressly at the level of the robot's sensorimotor state, the Static Sensorimotor Medium (SSM), as a simplification of an earlier controller, the Iterant Deformible Sensorimotor Medium (IDSM). We apply this controller to a simple continuous categorical perception task, explored in a previous study to operationalise the concept of SMCs in dynamical systems terms. The key feature of this task is that instantaneous sensory information alone is insufficient to distinguish the categories, and hence the robot must execute a sensorimotor strategy over time in order to identify its target. Early experiments with this controller show that it is capable of solving this task without any state variables or information beyond its two instantaneous sensor *and* instantaneous motor values, suggesting that it is displaying an emergent ability to exploit regions of its sensorimotor-space to capture history-dependent information. Analysing the controller's solutions to the task demonstrates that modelling with such a controller offers new and intuitive modes for visualising and reasoning about SMC theory and sensorimotor behaviour.

**Poster 14: Regular-Carry of a predator defensive tool promoted hominin bipedalism and enabled the bipedal foot and the big brain**

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The bipedal carrying of objects is instinctive behaviour in humans, as are striking with an object and throwing an object. Of all extant primates only humans regularly carry a non-food object bipedally. This paper makes the case that behavioural shifts are the starting point for physiological change and avers that for hominins the frequent bipedal forelimb-carrying of a predator-defensive tool was that behaviour. It offers comparison with other primates' infrequent-carrying of objects and tool use, and the persistence of quadrupedalism in those other groups. It considers how culture can propel evolution. It explores the implications of bipedalism for the development of both the abductable hallux and the big-brained altricial baby and demonstrates how other forelimb pre-emption hominin bipedalism theories are dependent on regular-carry.