UCL Research Department of Genetics, Evolution & Environment

2019 Graduate Research Symposium

Programme & Abstracts

Wednesday 8th May & Thursday 9th May

University College London
Darwin Building
Gower Street
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http://www.ucl.ac.uk/gee/

GEE Graduate Research Tutors:
Julia **DAY**
Lazaros **FOUKAS**

GEE Graduate Research Administrator:
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Programme

Presentations: Wednesday 8th May 10:00 – 3:15pm
Location: Anatomy JZ Young LT

10:00	Welcome Tea/Coffee	**Location: Anatomy Gavin de beer LT**
10:15	Introduction from GEE Departmental Graduate Tutor: Julia DAY	

Session 1: Chair – Duncan GREIG
(Ageing and Evolution)

10:20	Anob M. **CHAKRABARTI**	*Discovery of dynamic RNA secondary structures bound in vivo by Staufen 2 across mammalian brain development*
10:35	Robert **BAINES**	*Evaluating dictyostelium discoideum as a model for the evaluation of teratogenic compounds*
10:50	Carina **KERN**	*Reproductive death accelerates ageing in C. elegans*
11:05	Catalina-Andreea **ROMILA**	*Parallel profiling of mutants for chronological lifespan*
11:20	Natalie **WOOD**	*Investigating the role of neuropeptides in the development of the sea urchin, Strongylocentrotus purpuratus*
11:35	**Tea/Coffee break (25mins) Location: Anatomy Gavin de beer LT**	

Session 2: Guest Speaker

12:00	Alistair **McGREGOR**	*The evolution of developmental regulation in spiders and flies* Host: Paola Oliveri
13:00-14:00	Lunch	

Session 3: Chair - Julia DAY
(Biodiversity, Evolution and Human Genetics)

14:00	Filipa L. **SAMPAIO**	*Convergent evolution in a clade of burrowing snakes (Serpentes: Uropeltidae)*
14:15	Iulia **DAROLTI**	*Extreme heterogeneity in sex chromosome differentiation and dosage compensation in livebearers*
14:30	Catherine **WALKER**	*Quantifying human dietary change over the last 30,000 years*
14:45	Christopher J. **DOBLE**	*Testing the performance of eDNA metabarcoding for surveying highly diverse tropical fish communities: A case study from Lake Tanganyika.*
15:00	Rory **GIBB**	*Understanding and predicting effects of land use change on zoonotic disease risk: a process-based perspective*

Day ends at 3:15pm

Presentations & Posters: Thursday 9th May 10:00am – 3:15pm
Location: Anatomy JZ Young LT

10:00	Welcome Tea/Coffee **(20mins)**	**Location: Anatomy Gavin de Beer LT**
		Session 1: Chair – Julia DAY (Biodiversity and Evolution)
10:20	Gonzalo **ALBALADEJO ROBLES**	*Global scenarios of terrestrial vertebrate diversity*
10:27	Shawn **DOVE**	*Improving biodiversity trend assessment methods*
10:34	Adrienne **ETARD**	*Global land-use change promotes the functional homogenisation of local vertebrate communities*
10:41	Sean **JELLESMARK**	*Measuring the impact of conservation on RSPB reserve species*
10:48	Paschalis **NATSIDIS**	*A new computational method to detect the phenomenon of the hidden break in 28S rRNA reveals its evolutionary distribution*
10:55	Carina **PHILLIPS**	*The legacy of W.C. Osman Hill, a founder of primatology: the historical, museological and biological significance of the Osman Hill primate collection*
11:02	Laura **PIOVANI**	*The evolutionary and cellular origins of the Lophotrochozoan larva*
11:09	Bouwe R. **REIJENGA**	*The impact of biotic interactions on the evolution of biodiversity*
11:16		**Tea/Coffee break (20mins) in the Anatomy Gavin de Beer LT**
		Session 2: Chair - Nazif ALIC (Evolution, Human Genetics and Ageing)
11:36	Mislav **ACMAN**	*Towards a natural classification of bacterial plasmids based on sequence similarity*
11:43	Helen **FRASER**	*Annotating age-related diseases with ageing hallmarks, exemplified here by annotation of neoplastic disorders with cellular senescence & therapeutics terminology*
11:50	Shaimaa **HASSAN**	*Establishing killifish as model for ageing-related diseases*
11:57	Michael **JARDINE**	*The genetics and evolution of sexual antagonism: Testing for sex-specific fitness associated with allelic variation at the fruitless locus*
12:04	Sam **MORRIS**	*Inferring patterns of haplotype sharing from low-coverage samples: ChromoPainter for ancient DNA*
12:11	Christopher J. **OWEN**	*The influence of temperature on genetic and phenotypic variation in DNA viruses*
12:18	Bowen **XU**	*Does inhibition of Ras/ERK signaling promote longevity in Drosophila through inhibition of RNA polymerase III by the repressor Maf1?A*
12:25		**Poster session/Lunch - 12:30 - 2:30 Anatomy Gavin de Beer LT**

Poster Presentations: Thursday 9th May, 12:30 – 2:30pm
Location: Anatomy Gavin de Beer LT

Poster Assessors: Julia **DAY** & John **LABADDIA**

Posters (Alphabetical - Last name order)

Benjamin **BURGESS**	*Stressing communities: determining the prevalence and strength of interactions resulting from multiple stressors*
Marco **COLNAGHI**	*Bacterial genome size determines the conservative benefits of lateral gene transfer*
Ellen **COOMBS**	*Ecological influences on cranial morphology in whales*
Lea I. **DAMBLY**	*Citizen scientists and difficult species - committed volunteers make all the difference*
João Vasco **LEITE**	*Scaling patterns of metacarpus dimensions and body size in non-avian dinosaurs*
Helen **FRASER**	*Annotating age-related diseases with ageing hallmarks, exemplified here by annotation of neoplastic disorders with cellular senescence & therapeutics terminology*
Matias **FUENTEALBA**	*Understanding the hallmarks of aging*
Stuart **HARRISON**	*Non-enzymatic nucleotide synthesis*
Mikael **MAES**	*Mental health and cognitive development responses in London's children shift depending on natural habitat type exposure*
Joseph **MILLARD**	*Text-analysis reveals taxonomic and geographic disparities in animal pollination literature*
Silvana **PINNA**	*Synthesis of ATP via substrate-level phosphorylation of ADP by acetyl phosphate enhanced by various catalysts under abiotic conditions*
Catalina-Andreea **ROMILA**	*Parallel profiling of mutants for chronological lifespan*
Stjohn **TOWNSEND**	*Reproducing irreproducibility: establishing a robust ageing model in yeast*
Benjamin A. **TAYLOR**	*Conflict resolution and caste plasticity in a social wasp*
Jessica J. **WILLIAMS**	*Proximity to realised climatic tolerance limits affects responses to land-use change*

Abstracts

Towards a natural classification of bacterial plasmids based on sequence similarity (1st year talk)

Mislav **ACMAN**

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Abstract:
Bacterial plasmids are promiscuous and changeable mobile genetic elements helping the spread of antimicrobial resistance (AMR) and virulence via horizontal gene transfer (HGT). Current classification systems, such as those based on replicon (PlasmidFinder) or conjugation (MOB-suite) machinery, are failing to capture the full scope of the plasmid diversity with more than 70% of publicly available complete plasmid sequences remaining unclassified. Moreover, replicon-based classification scheme is sometimes difficult to interpret and it is relying on detection of a single relatively conserved gene with larger plasmids often falling into multiple groups. This project aims to devise an improved classification scheme based on genomic distances between plasmids and their core genome composition. We examined plasmid distance matrix by using hierarchical clustering and community detection algorithms. This uncovered a distinct population structure with layered and overlapping plasmid groups. We found good accordance between emerging plasmid groups and current plasmid classifiers. Many groups were found to have unique private backbones comprised of multiple genes, while other sporadically shared their core genes with other plasmids thus highlighting the plasticity of plasmid genomes. Extensive HGT between plasmids is certainly a limitation of sequence-based classification approaches and assessing its effect on the formation of plasmid groups remains a challenge. Our future work will consider how this large-scale population structure reflects plasmid evolution and some key phenotypic features like HGT potency, virulence, AMR, heavy metal resistance, transposon carriage, or host range.

Global scenarios of terrestrial vertebrate diversity (1st year talk)

Gonzalo **ALBALADEJO ROBLES**

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Centre for Biodiversity and Environment Research, Department of Genetics, Evolution and Environment,
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Institute of Zoology, Zoological Society of London, Regent's Park, London, United Kingdom

Abstract:
Global impacts of human activities, such as the increase of greenhouse gases on the atmosphere and the over-exploitation of natural ecosystems, have created a situation where wildlife struggles to survive. In this scenario, habitat degradation is one of the main drivers of biodiversity loss at a global scale, and climate change is predicted to become a major driver of ecosystem degradation. However, the combined effect of these two drivers of change has been assessed only for a limited number of species with different results. This suggests that other hidden drivers could be affecting biodiversity.

Predicting how biodiversity will respond to these threats is of paramount importance to the development of future strategies of conservation. The aim of this project is to assess the combined effects of climate and land-use change, as well as other potential drivers, on the distribution of biodiversity under different scenarios.

The project will follow an ecological hierarchical model approach to combine the effects of different drivers, that affect species distribution, acting at different scales. The results of this project will help develop future biodiversity conservation plans.

Evaluating dictyostelium discoideum as a model for the evaluation of teratogenic compounds (Final year talk)

Robert **BAINES**

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Abstract:
The evaluation of the safety of new compounds both for medical and environmental application is a tightly regulated process with worldwide legislation. Guidelines for developmental and reproductive toxicity (DART) testing are a critical aspect of new compound evaluation requiring strict *in vivo* testing. Current EU DART testing guidelines result in DART accounting for the majority of animals used and financial costs of new compound compliance testing. The improvement and critically the development of new alternative models is essential for the improvement in current DART testing processes.

Dictyostelium discoideum's unique developmental cycle has innate advantages over current alternative assays and has the potential to be developed as a new model for DART testing. However, previous attempts to characterize *D. discoideum* as a model have had limited scope. By developing new HTP *D. discoideum* toxicity screening assays we have been able to show that different toxicity endpoints across a broad range of compounds significantly correlates between *D. discoideum* and mammalian model systems. These results are together with the application of next generation functional genomic REMI-Seq screens highlighting the potential for the *D. discoideum* model to be developed into an alternative system for DART testing.

Stressing Communities: Determining the prevalence and strength of interactions resulting from multiple stressors (Poster)

Benjamin **BURGESS**

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Abstract:
Multiple stressors, including climate change, pollution, invasive species or land use change, are impacting almost all ecosystems across the planet. However, understanding how these stressors can combine to alter ecosystems is poorly understood. Often the effects of two stressors acting together can be greater, or less than, the sum of the effects of the stressors acting individually. I have used a newly developed theoretical framework to predict the effects of stressors on simulated communities. These communities encompass food-chains of differing lengths and underlying mechanisms, but allow for processes such as attack rate, conversion efficiency, and mortality to be altered as a consequence of one or more stressors. Overall, this framework has allowed for novel predictions to be made regarding the interactions of multiple stressors, and the effects that they may have upon communities.

Discovery of dynamic RNA secondary structures bound in vivo by Staufen 2 across mammalian brain development (Final year talk)

*A. M. **CHAKRABARTI**[1,2], *F. C. Y. LEE[2,3], S. M. FERNÁNDEZ-MOYA[4], J. EHSES[4], M. A. KIEBLER[4], N. M. LUSCOMBE[1,2,5], J. ULE[2,3]

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Abstract:
Interactions between RNA and associated *trans*-acting factors, notably RNA binding proteins, are important for post-transcriptional regulation. The structure of RNA molecules plays an important role in this interplay. Staufen proteins contain multiple domains that bind to double-stranded RNA, held together primarily with complementary base-pairing and have context-dependent roles in mRNA localisation, stability and translation. To investigate these interactions in a physiological context, we studied RNA structures bound by the neuron-enriched Staufen 2 *in vivo* in primary tissue.

With iterative improvements to hiCLIP (RNA hybrid individual-nucleotide resolution UV cross-linking and immunoprecipitation) we now identify an atlas of RNA duplexes bound by Staufen 2 in rat cerebral cortex at three developmental stages (P0, P7 and 5 weeks). The majority of these structures are in *cis*, with thousands of unique structures in mRNA transcripts. They are predominantly located within the long 3' untranslated regions (UTRs) of neuronally expressed transcripts, and can bring together evolutionarily conserved regions that are more than a kilobase apart in linear sequence length. Their arrangements are often complex suggesting alternative or intercalated structures. Furthermore, we examine quantitatively how usage of these structures changes across brain development. We identify dynamic binding in known neuronal transcripts important for synaptic plasticity.

Altogether, the RNA structures we detect here reflect hitherto underappreciated complex 3' UTR structural configurations. Developmental dynamics and sequence conservation indicate their physiological relevance, and their characterisation will give insight into the post-transcriptional regulation of neuronal transcripts.

Bacterial genome size determines the conservative benefits of lateral gene transfer (Poster)

Marco **COLNAGHI**

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Abstract:
Lateral Gene Transfer (LGT) makes bacterial genomes extremely dynamical objects. Previous theoretical studies suggest that LGT is maintained during evolution because it can prevent the irreversible fixation of deleterious mutations in a population, a phenomenon known as Muller's ratchet. Using a simple mathematical model, I am able to show that LGT can slow the fixation of mutations at a single locus. However, when multiple loci are considered, the efficiency of LGT declines with genome size. The effect of genome size has been overlooked in previous theoretical models: here we show that it is crucial in determining ratchet dynamics. The rate of fixation of deleterious mutations drastically increases with genome size, while the conservative benefits of LGT decrease. In presence of high mutation rates or small population size, this generates a strong constraint on bacterial genome size. Species with smaller population size are more vulnerable to Muller's ratchet and have correspondingly smaller genomes. Increases in recombination length are able to relax this constraint and allow a further genome size expansion. This mechanism can shed some light on the transition from LGT to sexual reproduction, which followed the massive expansion in genome size during the early stages of eukaryotic evolution.

Ecological influences on cranial morphology in whales (Poster)

Ellen **COOMBS**[1,2], Morgan CHURCHILL[3], Jonathan GEISLER[4], Brian BEATTY[4], Travis PARK[2] & Anjali GOSWAMI[1,2]

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Abstract:
The order Cetacea is composed of two extant suborders, Odontoceti (toothed whales) and Mysticeti (baleen whales), which diverged ~39 Ma ago. Of ~90 extant cetaceans, >70 are odontocetes. Oligocene odontocetes rapidly evolved refined, high frequency echolocation, shifted cranial bones further posteriorly and developed cranial asymmetry, while mysticetes evolved huge masses and filter feeding. However, to date there has been little quantitative study of shape evolution spanning the full-breadth of cetacean diversity.

62 cetacean crania (25 extant, 37 fossil) were landmarked and analysed in the 'geomorph' package in R. Landmarks were subjected to generalised Procrustes analysis, followed by a Principal Components Analysis. Centroid size was used to measure allometric effects, and ecological correlates of cranial shape were assessed with non-parametric MANOVAs.

Most cranial variation (PC1 = 35.2%) reflects telescoping and a shift in the nares position. There is high variation in the length of the rostrum (PC2 = 25.6%) with dolicocephalic (e.g., *Pontoporia blainvillei*), and brachycephalic (e.g., *Kogia sima*) crania representing the extremes. Habitat does not significantly correlate with skull shape in this sample of extant species ($r^2 = 0.31$, $p = 0.14$), but diet does ($r^2 = 0.57$, $p = 0.001$).

This correlation allows for ecological reconstructions of extinct taxa.

Citizen scientists and difficult species - committed volunteers make all the difference (Poster)

Lea I. **DAMBLY**[1,2], Kate E. JONES[2], Katherine BOUGHEY[3] & Nick J. B. ISAAC[1]

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Abstract:
Many long-term monitoring programmes now rely on citizen scientists for their data collection, which has led to a discussion about the challenges associated with data collected by volunteers. We make use of two decades of citizen science data collected as part of the National Bat Monitoring Programme (NBMP) on the relative abundance and activity of bats through multiple survey methods. For some species, NBMP population trends derived from roost counts differ substantially when compared to other survey methods. We assessed the potential biases in the roost counts and then explored their impact on observed population trends through a simulation study. The dynamics of two virtual bat populations were modelled, as well as several data collection scenarios with different levels of biased site selection and long-term observer commitment. Finally, population trends were modelled, and the differences between true and observed trends were evaluated. We found that the NBMP roost counts are likely systematically biased due to a lack of volunteer commitment influenced by the low side fidelity of some species. This suggests that long-term participation of citizen scientists is critical to produce reliable population trends of hard to monitor species. We conclude that monitoring schemes that involve citizen scientists need to be aware of this potential for bias and assess their methods of volunteer engagement and retention.

Extreme heterogeneity in sex chromosome differentiation and dosage compensation in livebearers (Final year talk)

Iulia **DAROLTI**

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Abstract:
With the loss of recombination between the X and the Y chromosome, sex chromosomes begin to differentiate and transition to a heteromorphic state. Moreover, as the Y chromosome degenerates, males are left with only one functional copy of X-linked loci. In consequence, different species have developed different mechanisms to compensate for this imbalance in gene dose. While there is a remarkable variation in the degree of sex chromosome divergence across clades, far less is known about the variation in sex chromosome differentiation within clades. Here, I combine whole genome and transcriptome sequencing data to characterise the structure and conservation of sex chromosome systems across Poeciliidae, the livebearing clade that includes guppies. I uncover a sex chromosome system which, despite being shared across closely related species, shows an extreme heterogeneity in the extent of sex chromosome recombination and Y chromosome decay. Remarkably, I additionally show evidence for the first instance of complete sex chromosome dosage compensation in fish. These results have important implications to sex chromosome evolution and regulation.

Testing the performance of eDNA metabarcoding for surveying highly diverse tropical fish communities: A case study from Lake Tanganyika. (Final year talk)

Christopher J. **DOBLE**, David J. MURRELL & Julia J. DAY

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Abstract:
While recent studies have demonstrated the effectiveness of environmental DNA (eDNA) metabarcoding methods for surveying temperate aquatic fish communities, important questions remain surrounding the ability of these approaches to detect species across different habitats and scales. We address this by applying an eDNA metabarcoding approach to survey the highly diverse littoral fish communities of Lake Tanganyika, East Africa. This system provides two unique challenges. Firstly, rocky sites contain a high local species richness, including species challenging to survey using traditional methods. Secondly, a large number of species, such as cichlid fishes, comprise evolutionary radiations resulting from rapid diversification and are difficult to identify using barcoding approaches.

To test the potential of eDNA metabarcoding in such a complex ecosystem we developed an extensive reference database (355 species) for the lake's fish species across three mitochondrial gene regions. Four separate primer pairs including a novel cichlid-specific primer are used to investigate the diversity of these fish communities across a 25km section of coastline. Resolutions obtained for the cichlid fishes varied greatly across the four primer sets with the greatest resolution, often down to species level, obtained with the cichlid-specific primer. Furthermore, the universal fish primers enabled the identification of a number of non-cichlid fishes that are challenging to survey with traditional methods. The accuracy and scale of eDNA detections are further assessed through comparisons made with visual survey data.

Improving biodiversity trend assessment methods (1st year talk)

Shawn **DOVE**

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Abstract:
Global biodiversity is declining. But why, where and how fast? The Living Planet Index aims to quantify the changing state of global biodiversity from changes in population time series data. Unfortunately, there are little to no data available on most species, nor do we have the resources to obtain them. Various statistical methods have been applied to try to overcome this problem, such as weighting and interpolation. But much improvement is still needed.

How many species do we need to survey to provide a robust indication of the state of global biodiversity? Are there better methods of constructing the index? Can confidence intervals be reduced? Is it feasible to use predictive methods to increase our available data, and to what extent?

My goal is to find answers to these questions by developing new statistical methods and exploring the application of machine learning and other novel techniques to the Living Planet Index. The outcome will be a more efficient, more robust and more representative version of the index, which can then be used as a model to improve other global and national biodiversity indices.

Global land-use change promotes the functional homogenisation of local vertebrate communities (1st year talk)

Adrienne **ETARD**

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Abstract:
Land-use change is one of the most important drivers of biodiversity loss. Land-use change globally impacts vertebrate ecological communities by reducing local species richness. Nevertheless, not all species respond similarly to land-use. Species ability to cope with anthropogenic pressures is dependent on their functional traits: empirical evidence has shown that long-lived, slow breeding specialists respond more negatively to land-use change than shorter-lived, generalist animals. By preferentially removing certain functional types, land-use change is reshaping the functional composition of ecological communities. Understanding how land-use change impacts the functional diversity of ecological systems is key to assess the potential consequences on ecosystem functioning. Here, I used a meta-analytic approach to investigate how land-use change impacts the functional diversity of terrestrial vertebrate communities at global scales. Land-use change globally promotes the functional homogenisation of ecological assemblages by favouring species that are both less functionally distinct and less functionally rare. Where functional indices correlate with species richness, reduction of functional diversity in human-disturbed habitats exceeds expected decreases based on species loss alone. As such, land-use change is likely to globally impact local ecosystem processes, and, consequently, services rendered by terrestrial vertebrates.

Annotating age-related diseases with ageing hallmarks, exemplified here by annotation of neoplastic disorders with cellular senescence & therapeutics terminology (1st year talk + Poster)

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Abstract:
Europeans have been living longer at a rate of ~6 hours per day until recently. This increase in life expectancy with a reduction in birth rates has led to an increase in prevalence of Age-Related Diseases, such as Neoplastic Disorders. Neoplastic Disorders have been considered the "emperor of all maladies", and among these, cancers have only 54.3% average 5-year survival rates. Although cellular senescence has traditionally been considered protective against the development of Neoplastic Disorders, the activities of senescent cells are now frequently being associated with pro-tumorigenic consequences. Using actuarial approaches, we defined 39 age-related Neoplastic Disorders which explode into disorder subcategories. We developed dictionaries of 980 Neoplastic Disorders and neoplasm-related sequela. These were identified in 3.7million unique PubMed articles. Using extensive manual literature review, cellular senescence terms and targeting therapeutics were expanded into dictionaries of related terms including Senescence Associated Secretory Phenotype and Senolytics, respectively. Using literature mining approaches, we examined the literature associations between cellular senescence terms and the 980 Neoplastic Disorders. The results will be accessible in an online database, primarily for the use of biomedical researchers. This could, for example, be used to assist decisions regarding further research into prognostic indicators in cancers (e.g. senescence markers).

Understanding the hallmarks of aging (Poster)

Matias **FUENTEALBA**[1], Janet THORNTON[1,2] & Linda PARTRIDGE[1,3]

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[3] Max Planck Institute for Biology of Ageing, Cologne, Germany

Abstract:
People worldwide are living longer than ever before. In fact, it has been estimated that a third of the world's population will be over 60 years old by 2050. However, because people are living longer but not healthier, this "Silver Tsunami" is expected to hit the nations with a huge impact on their economy, healthcare, politics and society. Fortunately, studies in animal models have shown that preventative interventions into the aging process (as opposed to treating one disease at a time) may lead to individuals surviving longer and with less age-related diseases. In this regard, it is expected that a further understanding of the aging process will lead to therapeutics to delay aging and ameliorate multiple diseases simultaneously. In this study, we aimed to dissect the interconnections between the hallmarks of aging and their relative contribution to age-related diseases and anti-aging drugs.

Understanding and predicting effects of land use change on zoonotic disease risk: a process-based perspective (Final year talk)

Rory GIBB[1], David W. REDDING[1], Kai Qing CHIN[1], Tim BLACKBURN[1], Lauren ENRIGHT[1,2,3], Chioma C. DAN-NWAFOR[4], Elsie ILORI[4], Yashe Rimamdeyati USMAN[4], Oladele H. SALIU[4,5], Amedu O. MICHAEL[4], Iniobong AKANIMO[4], Oladipupo B. IPADEOLA[4,6], Christl A. DONNELLY[3,7], Chikwe IHEKWEAZU[4], Ibrahim ABUBAKAR[8], Tim NEWBOLD[1] & Kate E. JONES[1,2].

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Abstract:
Global environmental changes such as agricultural expansion, climate change and urbanisation are projected to profoundly impact both public health and biodiversity this century. Much attention has been paid to predicting effects of climate change on the global burden of zoonotic (animal-borne) and vector-borne infectious diseases. However, the effects of land use change are much less well-understood at regional and global scales, despite increasing local evidence of the importance of land use as a mediator of reservoir host populations, pathogen transmission dynamics, and human-wildlife epidemiological contact. Characterising the land use-mediated synergies and trade-offs between zoonotic disease burden and other key ecosystem outcomes such as food security is a critical but under-researched dimension of environmental health. In this talk I will discuss these issues with reference to my PhD research, including a global analysis of the impacts of land use on the zoonotic potential of ecological communities, where we show that, across more than 5700 sites worldwide, human-dominated landscapes favour increasing species richness and abundance of hosts of zoonotic pathogens and parasites. I will also discuss results from a case study of the present-day and predicted future contributions of agricultural land use, climate and socioeconomic factors to the incidence of Lassa fever, a rodent-borne disease that is a growing public health concern in West Africa.

Non-enzymatic nucleotide synthesis (Poster)

Stuart **HARRISON**

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Abstract:
The origins of life is a highly divided field with multiple overlapping and conflicting hypotheses. A newly emerging concept is that of non-enzymatic metabolism; low-activity interconversions of metabolites mimicking extant metabolic processes may have provided early cells with essential material and a platform onto which enzymes can emerge. Evidence for abiotic versions of the acetyl-CoA pathway, the Krebs cycle, glycolysis and the pentose phosphate pathway have been found.

Nucleotides not only provide genetically encoding information, but also are key catalysts in diverse chemical processes within organisms and are undeniably essential to the origins of life. Chemically, they can be synthesised from a diverse range of starting materials, but whilst these syntheses are impressive feats, they are disparate from biochemical pathways.

Non-enzymatic pathways neatly resolve some key problems in the origins of life. They narrow the gap between chemistry and metabolism and have been shown to be capable of producing a range of essential metabolites. It is not unreasonable to suggest that nucleotides could also have non-enzymatic origins. This PhD is focused on exploring and evaluating chemical synthesis of nucleotides in a manner reminiscent of the *de novo* biosynthetic pathway.

Establishing killifish as model for ageing-related diseases (1st year talk)

Shaimaa **HASSAN**, Giovanni STEFANI & Jurg BAHLER

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Abstract:
Killifish has tremendous potential as a new ageing model. This annual killifish survives the dry season in diapause, a state of suspended embryonic development. Diapause features delayed or absent ageing, and likely shares genetic mechanisms with longevity. Recent data reveal that similar genes are regulated during diapause and ageing. We want to provide much-needed groundwork for the molecular understanding of diapause in killifish and its connections to aging. Analogous dormant states in lower eukaryotes, like dauer worms and quiescent yeast, have enlightened us about conserved ageing-related processes.

Moreover, we will use the diapause state to perform lineage analysis of hematopoietic stem cells and investigate how the hematopoietic niche is maintained and protected from ageing and exhaustion during long-term diapause unlike what happen during the adult life. Furthermore, we will investigate the ability of the diapause state to prevent or decrease the possibility of ageing related hematological diseases in susceptible mutants. There is great interest in understanding the hematopoietic niche, both for advancing basic science and in treating hematologic disease.

This study's overarching objective is to establish the fastest-ageing vertebrate model amenable to laboratory usage, the African turquoise killifish, for the study of ageing related diseases. On the other hand, a diapause model system is considered a unique model to study how the ageing clock is paused and how the same organism can maintain and regulate homeostasis that will provide new strategies to prevent this collapse during aging.

The genetics and evolution of sexual antagonism: Testing for sex-specific fitness associated with allelic variation at the fruitless locus (1st year talk)

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Abstract:
The sexes have been shaped by selection to achieve different evolutionary 'goals' resulting in differences in behaviour, physiology and genetic regulation. Since most genetic material is shared between the sexes, there is likely to be conflict since genetic variation selected for in one sex maybe be detrimental to the other. This genetic disagreement between the sexes is termed sexual antagonism (SA).

There has been much difficulty in identifying precisely the genes involved in SA. We have recently produced a list of candidate sexually antagonistic loci for the first time which we aim to study in detail to confirm their SA nature and their role in evolution

We have chosen to focus on the candidate gene fruitless in *Drosophila melanogaster* due to its important role sexual development and stable polymorphism. Several lines of *D. melanogaster* have been created by introgressing a known allele of fruitless (L or S) into an otherwise identical genetic background. We have performed fitness assays on both sexes from these lines to look for patterns concurrent with a role in SA.

Both sexes performed best in lines introgressed with the S allele than flies with the L allele. Therefore this is no support for SA at this locus. Future work will focus on other potentially important traits, larger scale population experiments and other candidate loci.

Measuring the impact of conservation on RSPB reserve species (1st year talk)

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Abstract:
The state of biodiversity is declining. Global and national indices measuring the state of nature have emerged in recent years, meaning the loss of biodiversity is more apparent than ever before. Substantial resources are annually invested in monitoring populations, initiating and managing conservation projects. However, impact evaluation is rarely incorporated in the design of conservation programs. This means that most conservation interventions are never quantitively evaluated, leading to a lack of understanding of what works, what doesn't and why that is in the world of conservation science.

This study aims at combining and utilizing monitoring data to assess the impact of conservation on a selected set of bird species in RSPB reserves. The aim is to illustrate how conservation impact can be quantified using counterfactual scenarios, thus leading to more robust impact assessments in the eternal hunt for causality. Two different methods are used – One assessing the impact of specific categories of conservation interventions using a classical parsimonious model and another using statistical matching on observational bird data to infer the effect of conservation on trends in species' populations.

Reproductive death accelerates ageing in C. elegans (Final year talk)

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Abstract:
In post-reproductive *C. elegans* hermaphrodites, intestinal biomass is converted into yolk leading to intestinal atrophy and yolk steatosis. We report that post-reproductive *C. elegans* hermaphrodites vent yolk that is consumed by larvae. Thus, post-reproductive mothers can contribute to fitness by converting their biomass into milk, implying that intestinal atrophy is a direct reproductive cost of lactation. Here *C. elegans* resembles species that exhibit semelparous reproductive death, such as Pacific salmon. Lactation was seen in other hermaphroditic *Caenorhabditis* species but not in females, and the latter did not exhibit intestinal atrophy or steatosis, and were longer lived. Moreover, germline ablation strongly increased lifespan in *Caenorhabditis* hermaphrodites but not females; similarly, blocking sexual maturation e.g. by castration can greatly increase lifespan in other organisms that undergo reproductive death. Insulin/IGF-1 signaling, which accelerates *C. elegans* ageing, also promoted lactation. We conclude that *C. elegans* exhibit reproductive death, suppression of which increases lifespan.

Scaling patterns of metacarpus dimensions and body size in non-avian dinosaurs (Poster)

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Abstract:
Hypotheses on locomotor biomechanics of terrestrial tetrapods are widely based on the scaling relationships between the limbs and body size. Less attention has been given to the hand (or manus), even though being one of the body parts in direct contact with the environment and potentially under more diverse selection pressures.

Non-avian dinosaurs provide an excellent opportunity to study manus scaling, due to their wide range of body sizes, ecologies and behaviours. In addition, all early non-avian dinosaurs were bipedal, which allowed diverse manus morphologies to evolve. However, multiple independent reversions to quadrupedality also imposed some shared mechanical constraints.

Here, we present the first study to compile an extensive dataset of metacarpus measurements across all major non-avian dinosaur lineages and use these to assess scaling patterns of the manus against overall body size. Data were analysed using phytools in R and Past.

Across non-avian dinosaurs the metacarpus scales with positive allometry (close to isometry), with no significant differences between metacarpals, major clades, hand function, or locomotive stance. Multivariate analyses show some degree of clustering between clades, as well as identifying some extreme cases, such as tyrannosaurids. Each major clade occupies distinct areas of morphospace, with overlap between some groups.

Mental health and cognitive development responses in London's children shift depending on natural habitat type exposure (Poster)

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Abstract:
Large scale epidemiological studies have established associations between nature, mental health and cognitive development, but the underlying drivers remain unknown. These have relied almost exclusively on classifying nature as green by using vegetation indices (e.g. NDVI), but few epidemiological studies have assessed how this relationship could vary across different vegetation types. Here, we analysed natural spaces (i.e. both green and blue spaces combined and separately) and vegetation types of different height for associations with mental health and cognitive development. Types of natural spaces were assessed using high resolution satellite data (8 x 8 m), OS MasterMap and LiDAR data (2 x 2 m) in buffers of 250 m around each child's home and school (~ 6,616 children) from the age of 10 to 13 at 39 schools across London, United Kingdom. Mental health was assessed through the Strength and Difficulties and KIDSCREEN questionnaire, while cognitive performance was assessed through the Executive Function composed of three computerised cognitive tests (2014-2015). We show that high levels of green space with low height (< 1 m) are associated with improved mental health and cognitive performance during childhood. The association was adjusted for age, ethnicity, gender, school type and individual and area-level socio-economic status. No association was found between blue space and mental health and cognitive development as 64% of children had no blue space within a buffer of 250 m. Our results show that green space with low height during childhood is associated with better mental health and cognitive performance, supporting evidence that natural spaces should be part of urban planning decisions and childhood life.

The evolution of developmental regulation in spiders and flies (Guest Speaker)

Alistair P **McGREGOR**[1]
Professor of Evolutionary Developmental Biology

Host: Paola OLIVERI[2]

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Abstract:
Research in my lab focuses on questions that are key to understanding animal evolution: How does the genetic regulation of development evolve and what is the genetic and developmental bases for morphological variation within and between species. To address these questions we study the genomics and genetics of the development of the spider *Parasteatoda tepidariorum* and morphological evolution among flies of the *Drosophila melanogaster* species subgroup. In this talk I will present our recent work on the regulation of segmentation in Parasteatoda and on investigating the genetic basis for differences in male genital morphology between *D. mauritiana* and *D. simulans*.

Text-analysis reveals taxonomic and geographic disparities in animal pollination literature (Poster)

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Abstract:
Ecological meta-analyses have significantly increased our understanding of global biodiversity decline. However, for some ecological groups incomplete and biased datasets have hindered our ability to construct robust, predictive models. One such group consists of the animal pollinators. 88% of wild and crop plant species are thought to be pollinated by animals, with an estimated annual value of $230-410 billion dollars. Here I reviewed the key anthropogenic drivers of pollinator distribution and diversity, before applying text-analysis (entity recognition) to quantify the taxonomic and geographical distribution of the animal pollinator literature, both temporally and spatially. I show that the distribution of pollinator literature is concentrated in the honeybees (Apis) and bumblebees (Bombus), and geographically in North America and Europe. Temporally, I show that the publication of pollinator literature increased rapidly in the 1980s and 1990s. Although these results indicate strong biases in pollinator literature, they appear less significant than prior studies have implied: pollinator literature is not entirely restricted to Apis and Bombus, and a large number of studies outside North America and Europe do exist.

Inferring patterns of haplotype sharing from low-coverage samples: ChromoPainter for ancient DNA (1st year talk)

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Abstract:
As the field of ancient DNA moves from studying continent-wide geographic scales to more localised regions, newer methods are required which are able to infer fine-scale population histories. Nearly all current studies rely on methods which assume linkage equilibrium between markers (e.g. PCA, ADMIXTURE and F-Statistics); despite their utility, such methods do not exploit patterns of linkage between markers, which have proven to be particularly informative when trying to elucidate fine-scale population structure (e.g. within a country). Specifically, inference of subtle population structure, past admixture events and estimation of ancestry proportions have benefited notably from the use of haplotype-based methods, such as ChromoPainter. However, ChromoPainter is currently not optimised for use an ancient DNA.

Here, we present updates to the ChromoPainter algorithm that incorporate coverage information when inferring haplotype sharing. The modified version incorporates genotype likelihoods in in order appropriately weight regions of variable coverage in the final painting profile. In an application to data from >100 ancient individuals, we demonstrate how these updates improve ancestry inference relative to the current ChromoPainter algorithm that ignores coverage information. We illustrate how reliability of inference relates to coverage, and the power gains that are achievable by use of haplotype information.

A new computational method to detect the phenomenon of the hidden break in 28S rRNA reveals its evolutionary distribution (1st year talk)

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Abstract:
The eukaryotic ribosome is formed of a number of proteins and four structural ribosomal RNAs - 5S, 5.8S, 18S and 28S. The last three of these are transcribed as a single molecule separated by Internal Transcribed Sequences, which are spliced out. In some species, the 28S rRNA undergoes an extra split during post-transcriptional processing, foming 28Sα and 28Sβ. This phenomenon is known as the 'hidden break' and has to date always been investigated via electrophoresis. In species with the hidden break, 28Sα and 28Sβ migrate as a single band along with the equally-sized 18S rRNA. Our new computational approach for identifying the hidden break is based on the expectation that RNA-Seq reads mapping to the region of the spliced region will be extremely rare (derived only from molecules that have not yet been processed). Analysing 51 species from 27 metazoan phyla revealed that the hidden break is a rarely lost protostome-specific feature, and can be regarded as an evolving ITS3. It was found in 16 out of 18 examined protostome phyla, and in none of the deuterostome and non-bilaterian phyla. A further investigation of hidden break occurences across all eukaryotes (currently in progress) will provide a better resolution of its evolutionary origins and reveal events of convergent evolution and non-homologous breaks.

The influence of temperature on genetic and phenotypic variation in DNA viruses (1st year talk)

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Abstract:
Climate change has been identified as a key driver of infectious disease emergence, which are increasing in incidence. Changes in environmental temperature impact host-pathogen interactions in complex ways, particularly in poikilothermic systems, and it is challenging to predict the effect long-term sustained changes will have on the evolutionary dynamics of pathogens. I present an experimental evolutionary system designed to elucidate the genetic and phenotypic effects of thermal adaptation in a large-DNA virus. Ranaviruses are important pathogens of amphibians, fish and reptiles, and we have recently been shown that rising temperatures are linked to increases in disease outbreaks and severity. The experimental system will assess the effects on the rate and nature of genetic changes in ranaviruses adapted to a low and high temperature over 300 generations, and whether changes result in adaptive or plastic phenotypic effects. These assessments will be carried out both in vitro and in vivo though the use fitness assays in culture and in live animal models. Insights gained from these efforts will then be used to assess whether conclusions can be drawn about the adaptive nature of the standing genetic variation amongst natural populations of DNA viruses from different climates.

The legacy of W.C. Osman Hill, a founder of primatology: The historical, museological and biological significance of the Osman Hill primate collection (1st year talk)

Carina **PHILLIPS**[1]

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Abstract:
William Charles Osman Hill (1901-1975) has been described as one of the founders of comparative primatology. An anatomist and former Prosector at the Zoological Society London (ZSL), Hill published prolifically on various species, including an eight-volume monograph on the anatomy and taxonomy of primates. Throughout his career he collected many primate specimens preserving them in fluid, or as embalmed or dried tissue. Surviving parts of his collection are today housed at the Royal College of Surgeons of England and the Natural History Museum, London.

This interdisciplinary research project will assess the significance of Hill's surviving collections within history, biology and museology. It will explore the historical importance of Hill's research within primatology, how the specimens relate to this, and what they tell us about dissection and preservation techniques in the 20th Century. It will evaluate the biological significance of the collections, assessing the type of data that can be collected from the specimens and how this can be used in future research. Finally, it will discuss the implications of managing fluid and dry preserved organic museum collections and making them available for research, proposing a future approach for the use, care and management of Hill's specimens.

Synthesis of ATP via substrate-level phosphorylation of ADP by acetyl phosphate enhanced by various catalysts under abiotic conditions (Poster)

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Abstract:
In living cells, adenosine triphosphate (ATP) functions as a universal energy currency, driving metabolism through phosphorylation and condensation reactions. At the origin of life, however, ATP was most likely preceded by a primordial analogue carrying out similar functions. In many ancient bacteria and archaea, ATP can be formed via substrate-level phosphorylation from acetyl CoA via the obligate intermediate acetyl phosphate (AcP), which could arguably have served as a precursor to ATP. It has been demonstrated that AcP can quickly be synthesised in water from thioacetate under ambient conditions and it is stable for several hours depending on temperature, pH and cation content.

In this study, we show that AcP is proficient at phosphorylating a variety of biologically meaningful molecules, notably adenosine diphosphate (ADP) forming ATP, under alkaline hydrothermal conditions, as such vents are a possible site for the origin of life but being warm (30-90ºC), alkaline (pH 9-11) and saline may rather favour simple hydrolysis. The findings suggest preferential production of small amounts of ATP over other phosphate products, with Fe^{3+} and Fe^{2+} substantially increasing the yield, more than other metal cofactor. These findings are encouraging and suggest that future research on AcP as a primordial analogue of ATP is warranted.

The evolutionary and cellular origins of the Lophotrochozoan larva (1st year talk)

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Abstract:
Most animal phyla go through a swimming larval stage before metamorphosing into adults. These larvae from distantly related phyla often have similar features such as bands of cilia for swimming, apical tufts for sensing and a small larval brain even though their precise structures, may vary in different animals. The Lophotrochozoa is a group of animal phyla including annelids, molluscs and flatworms that makes one of the three main branches of bilaterally symmetrical animals together with deuterostomes and ecdysozoans. Lophotrochozoan larvae share many features beyond those described, such as a stereotypical pattern of cleavages of the early embryonic blastomeres called spiral cleavage, a fixed set of cell fates that mean certain blastomeres consistently give rise to cilia, or apical sense organs or eyes and a particular identifiable cell, called 4d, that generally breaks the initial radial symmetry of the embryo and introduces left-right and dorsal ventral axis. This conservation of early development among animals that are so different in their adult form as annelids, molluscs and flatworms is striking and more so when we consider that in the various lophotrochozoan phyla the development results in an apparently homologous 'trochophore' larva characterized by rings of ciliated cells, an apical organ with sensory cilia, pigmented eyes and protonephridial cells, all of which derive from homologous early blastomeres in different phyla. Discovering whether these shared developmental features seen in these similar larvae also share a similar molecular genetic blueprint may help us to assess the homology of larval cell types and ultimately understand the origin of larval forms in general. In particular our study will compare differentiating cell types in the trochophore larvae of three lophotrochozoans: two molluscs -*Crassostrea gigas* and *Biomphalaria glabrata* - and one polyclad flatworm *Maritigrella crozieri*. Our aim is to characterize different cell types through their expression patterns using single cell sequencing, to assign these expression patterns to actual cells in the trochophore with immunohistochemistry and in situ hybridization and finally to compare similar cell types, their expression and precursors in molluscs and flatworms to potentially assess their homology.

The impact of biotic interactions on the evolution of biodiversity (1st year talk)

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Abstract:
Biodiversity is distributed unevenly across the surface of the Earth and the Tree of Life. Ecological interactions between species are widely regarded as instrumental in regulating diversity and thus driving these patterns. However, our understanding of how ecological interactions shape species diversification over macro-evolutionary timescales remains limited. To address this, I will first simulate the diversification of species across a landscape under different ecological and stochastic scenarios to identify the expected present day signatures of past species interactions. I will particularly focus on how competition, through either local exclusion and/or character displacement – niche evolution driven by competition – may lead to similar or contrasting patterns in the phylogenetic, geographic and phenotypic structure of communities. Second, I will apply these models to empirical datasets to test the importance of species interactions in explaining differences in diversity across clades and geographic space. Together, this project will advance our knowledge and understanding of how biodiversity is generated and maintained.

Parallel profiling of mutants for chronological lifespan (Final year talk + Poster)

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Abstract:
Ageing is a complex biological process associated with a myriad of diseases. A better understanding of cellular lifespan would shed more light onto the underlying spectrum complexity of ageing.
In this work, we are investigating the cellular ageing of the fission yeast, using our own upgraded version of the genome-wide Barcode sequencing (Bar-seq) method. To fully take advantage of this method, we fully characterized the fission yeast deletion collection.

We are implementing high-throughput Bar-seq screens to profile the fitness of the non-essential deletion mutants within the deletion library. The mutant fitness profiling is performed with respect to the non-dividing cells' chronological lifespans (CLS). This CLS approach is explored for the purpose of finding novel genes implicated in both, fission yeast lifespan extension, as well as shortness. In this undertaking, we explore the importance of cellular regrowth for finding such candidates from within the 3,420 mutants present in the deletion library. Data from this work will be presented.

Convergent evolution in a clade of burrowing snakes (Serpentes: Uropeltidae) (Final year talk)

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Abstract:
Fossorial (burrowing) squamate reptiles have a relatively conserved body plan, with elongated bodies, reduced or absent limbs, and strongly reinforced skulls for head-first burrowing. Different snout shapes - rounded, keel- or shovel-snouted – are likely associated with distinct microhabitat use, diet and/or burrowing styles. Shieldtails (Serpentes: Uropeltidae) are a family of small fossorial snakes, endemic to Sri Lanka and peninsular India. There are eight genera and 55 species currently recognised. This is a poorly understood group, partly due to their secretive habits and confusing taxonomic history. Although shieldtails seem to exhibit high levels of morphological diversity and have some highly distinct phenotypic features, their morphology has not yet been studied using a quantitative approach. The analysis and quantification of morphological diversity will allow for a better understanding of the evolutionary history of the group and their ecological traits. Using traditional morphometrics in the context of a new molecular phylogeny, phylomorphospace occupation of head and body shape among shieldtails was analysed and the major axes of morphological variation in this clade were identified. Convergence in head shape between some Indian *Uropeltis* and Sri Lankan *Rhinophis* was identified, so that head shape variation is not only partitioned phylogenetically, and that behavioural and/or ecological factors likely also influence morphology in the group.

Conflict resolution and caste plasticity in a social wasp (Poster)

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Abstract:
Social insect colonies count among the most cooperative societies in nature, yet the extreme reproductive division of labour that characterises such colonies can also give rise to significant fitness conflicts between reproductive ‘queens’ and non-reproductive ‘workers’. Studying the mechanisms by which social insects maintain high levels of within-group cohesion in the face of differences in fitness interests is thus a key component of understanding the major evolutionary transition from solitary life to extreme cooperation. With this aim, we have dissected the process of ‘caste switching’ in the European paper wasp *Polistes dominula* using behavioural, physiological and genomic data generated by queen removal experiments. We show that conflict over the identity of a new reproductively dominant individual is resolved remarkably quickly, seemingly due to the presence of an age-based succession convention. We also identify genes differentially expressed before, during and after the phenotypic transition from subordinate to dominant, and use these to infer the cascade of molecular mechanisms that shape the shift of investment from indirect to direct fitness. This study provides novel insights into the proximate basis of the major evolutionary transition to extreme cooperation.

Reproducing Irreproducibility: Establishing a Robust Ageing Model in Yeast (Poster)

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Abstract:
Ageing research presents unique challenges in biomedical research. It has been observed that lifespan is an extremely sensitive phenotype, and that subtle changes in experimental protocol can lead to dramatic changes in lifespan. These effects can be highly inconsistent, and it is frequent in ageing research for results to be irreproducible between different laboratories. Due to the long and laborious nature of ageing research, there has been minimal effort amongst researchers to systematically understand (and subsequently control for) sources of inter-experiment variation.

Due to their simplicity, genetic tractability and amenability to high-throughput methodologies, yeast are an excellent model for systematic studies. In order to facilitate systematic ageing studies in yeast, we have established a novel high-throughput chronological lifespan assay which can be largely automated using robotics. Using this platform, we have systematically assessed a large number of potential sources of inter-experiment variation in chronological lifespan. We find that lifespan is highly sensitive to an alarming number of these variables, and that these variables can determine whether an anti-ageing intervention is effective or not. It is noteworthy that these variables are often not reported in the scientific literature. We also find examples of "memory", where subtle differences in experimental protocol many generations before the yeast start ageing can still lead to differences in lifespan. Collectively, we anticipate that this study will be a valuable resource to the ageing community and facilitate a reduction in sources of inter-experiment variation between researchers.

Quantifying human dietary change over the last 30,000 years (Final year talk)

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Abstract:
Modern diets are enriched for certain nutrients, for which we have strong taste avidities (e.g. sodium, sucrose, glutamate, certain fatty acids, etc). These nutrients are unlikely to have been as abundant in pre-agricultural diets, and have been implicated in a range of diseases of modernity, including obesity, type II diabetes, some cancers and coronary heart disease. This study compares nutrients in a Palaeolithic diet reconstructed from archaeological data, and modern hunter-gatherer diets as a proxy for ancestral diets, with modern diets. By quantifying the differences in inferred nutrient profiles between the ancient and modern diets, I examine how they have changed, what selection pressures these changes might have invoked, and why we have evolved taste avidities for some nutrients that in a modern setting are considered unhealthy. To achieve this, I have identified nutrients enriched in modern diets and systematically quantified dietary changes at the individual nutrient level. I am now examining how nutrients are correlated in ancestral foods and testing if avidities for nutrients enriched in modern diets would lead to healthy nutrient profiles in an ancestral setting. By understanding how dietary shifts and selective pressures have shaped us, we can better understand our vulnerabilities to diseases of modernity.

Proximity to realised climatic tolerance limits affects responses to land-use change (Poster)

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Abstract:
The importance of species' physiological limits on responses to global climate change has been highlighted, but it is rarely included in studies exploring the effect of localised climatic changes mediated by land-use change. Conversion of land for human use often results in landscapes that are hotter and drier than natural habitats and are linked to community-level shifts towards species tolerant of hotter temperatures and lower precipitation levels. However, within a species' range, populations differ in their proximity to climatic tolerance limits. Consequently, due to the detrimental effects of being pushed close to or beyond physiological limits, populations may differ in their responses to local climatic changes. We analysed, for the first time globally, whether the proximity of terrestrial vertebrate populations to their realised thermal and precipitation tolerance limits affects their responses to land-use change. We found that human-altered habitats filtered out both populations near their upper maximum temperature limit and populations near their lower minimum temperature limit, suggesting that extremes of hot and cold are both important drivers of population losses in these habitats. Unexpectedly, even though human-altered landscapes are often drier, populations closer to their minimum precipitation level tolerance limit had higher probabilities of occurring in human-dominated land uses that those closer to their upper limits. These results highlight the influence physiological tolerances have on the ability of vertebrates to occupy human-altered land uses, enhancing our ability to detect populations that may be under greater risk from land-use change and to predict responses to future environmental change.

Investigating the role of neuropeptides in the development of the sea urchin, Strongylocentrotus purpuratus (Final year talk)

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Abstract:
My project focuses on the role neuropeptides have in the development of the sea urchin, *Strongylocentrotus purpuratus,* with the possibility to uncover new important function(s) for this exciting class of signalling molecules.

Neuropeptides are ancient neuronal signalling molecules that bind to receptor proteins on target cells. Thirty-eight neuropeptide precursor (NP) genes have so far been identified in the *S. purpuratus* genome. Here we present the spatio-temporal data of NP genes during the development of *S. purpuratus* up to larval stage. QPCR and transcriptome data have revealed that almost all of these NP genes are expressed in the late larval stage, when cells differentiate, and localization of nine NP genes expression has revealed distinct sub-populations of peptidergic neurons and has showed that the sea urchin larval nervous system is far more complex than previously thought. Interestingly, sixteen NP genes are also expressed (at levels greater than 300 transcripts per embryo) in the pre-gastrula phase of embryogenesis, suggesting that these NP genes may have a developmental role as well. The spatial expression reveals restricted expression pattern of the *Sp-pedal peptide-like neuropeptide 1* (*Sp-PPLN1*), which is expressed in the aboral ectoderm from blastula stage onwards, and *Sp-Neuropeptide precursor 20* (*Sp-Np20*), which is excluded from the mesoderm and micromeres at blastula stage, while all the others show ubiquitous expression.

To identify the putative function of these molecules we are undertaking knock-down/out experiments using morpholino antisense oligonucleotides (MASO) and the CRISPR/Cas9 system, respectively. Data from the knock-down/out experiments suggest that *Sp- Thyrotropin-releasing hormone (Sp-Trh)* NP gene has a role in the development of the larval skeleton.

Taken together, these data suggest that the NP genes have a conserved neurosecretory role as well as a developmental role.

Does inhibition of Ras/ERK signaling promote longevity in Drosophila through inhibition of RNA polymerase III by the repressor Maf1? (1st year talk)

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Abstract:
The Ras/ERK signaling pathway is highly evolutionarily conserved across eukaryotes. Specific inhibition of Ras/ERK signaling can extend the lifespan of *Drosophila*. RNA polymerase three (Pol III), which has recently been ascribed a new function of lifespan limitation in *Drosophila* gut, acts downstream of Ras/ERK signaling to control protein synthesis and cell growth. The signal from Ras/ERK is relayed to Pol III via its repressor, Maf1. This project aims to understand if the Ras/ERK signaling act upstream of Pol III within the gut to regulate lifespan. This will be addressed by examining the effects of gut-specific reduction in Pol III in combination with treatment with specific small molecule inhibitor for Ras/ERK signaling. We will look at lifespan and molecular phenotypes. Meanwhile, *maf1* null mutation and HA-tagged lines will be generated by Crispr/Cas9 technique to identify if Maf1 repressor mediates the effects of Ras/ERK signaling on Pol III. Beyond these, future work will be extended to explore the possibility of proteostasis improvement and reduced harmful protein-accumulation by protein synthesis reduction under gut Pol III inhibition, which might contribute to the lifespan extension.