UCL Research Department of Genetics, Evolution & Environment

2018 Graduate Research Symposium

Programme & Abstracts

Wednesday 2nd May & Thursday 3rd May

University College London
Darwin Building
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Programme

Presentations: Wednesday 2nd May, 10am – 2:30pm

Location: Anatomy J Z Young LT

10:00	*Welcome Tea/Coffee, Anatomy G04 Gavin de Beer LT*
10:15	*Introduction from a GEE Post Graduate Tutor*

Chair: - Max REUTER – Final year talks
(Evolution and Genetics)

10:20	Macarena **FUENTES-GUAJARDO**	*Identification of genes responsible for the variation in facial and teeth morphology in Latin Americans*
10:35	Sam **FINNEGAN**	*Male mate preferences are not condition-dependent due to low genetic fitness caused by meiotic drive*
10:50	Filip **RUZICKA**	*Sexual antagonism constrains adaptation across the Drosophila melanogaster distribution range*
11:05	Carla **BARDUA**	*Morphological evolution and modularity of the caecilian skull*

11:20 *Tea/Coffee break (20mins) in Anatomy G04 Gavin de Beer LT*

Presentations: Wednesday 2nd May, 10am – 2:30pm

Location: Anatomy J Z Young LT

Chair: Tim Newbold - Final year talks
(Biodiversity)

11:40	Dan **BAYLEY**	*Evaluating the efficacy of small scale MPAs for preserving reef health through the application of 'Structure from Motion' photogrammetry*
11:55	Tatsiana **BARYCHKA**	*Sustainable Bushmeat Harvesting by a Virtual Ecologist*
12:10	Sérgio **MILHEIRAS**	*Assessing the links between biodiversity and ecosystem services in the tropical forests of Amapá, Brazil*
12:25	Nonthiwat **TAESUK**	*Using Ecological Niche Modelling to assess the impact of environmental changes on species distribution of large mammals in Southeast Asia: past, present and future*
12:40		*Lunch (60mins)*

Presentations: Wednesday 2nd May, 10am – 2:30pm

Location: Anatomy J Z Young LT

Chair: Lazaros Foukas – Final year talks
(Ageing)

13:40	Fiona **SPOONER**	*Rapid warming is associated with population decline among terrestrial birds and mammals globally*
13:55	Lea **BROCHARD**	*Novel effectors of metabolic stress signalling in adipocytes*
14:10	Matias **FUENTEALBA VALENZUELA**	*Using the drug-protein interactome to identify anti-ageing compounds for humans*
14:17	Pongsakorn **WANGKUMHANG**	*fastGLOBETROTTER: efficient identification and dating of admixture events inference in large-scale population data cohorts*
14:32		*End of day one*

Presentations: Thursday 3rd May, 10:15am – 2:30pm

Location: Anatomy J Z Young LT

10:15   *Welcome Tea/Coffee in G04 Gavin de Beer LT*

10:30   *Welcome from a GEE Graduate Research Tutor*

Chair: Nick LANE – First year talks
(Evolution, Genetics, and Ageing)

10:35 Robert **BAINES**   *Evaluating the suitability of social amoebae Dictyostelium discoideum as an alternative model in developmental toxicity testing*

10:42 Marco **COLNAGHI**   *Oocytes quality depends on mitochondrial segregation and selective transfer into the Balbiani Body*

10:49 Stuart **HARRISON**   *Nucleotide synthesis in hydrothermal vent conditions*

10:56 Seth **JARVIS**   *Analysis of 3' end sequencing data in FUS mutant mice using QuantSeq*

11:03 Silvana **PINNA**   *Substrate-level phosphorylation of ADP to ATP by acetyl phosphate under abiotic conditions*

11:10 StJohn **TOWNSEND**   *Metabolic memory effects in fission yeast ageing*

11:17   *Tea/Coffee break (20mins) in Anatomy G04 Gavin de Beer LT*

Presentations: Thursday 3rd May, 10:15am – 2:30pm

Location: Anatomy J Z Young LT

Chair: Julia Day – First year talks
(Biodiversity)

11:37	Guilherme **BRAGA FERREIRA**	*Strict protected areas are crucial for the conservation of threatened and larger mammal species in the Brazilian Cerrado*
11:44	Benjamin **Aaron TAYLOR**	*Caste plasticity in Vespid wasps*
11:51	Benjamin **BURGESS**	*Testing a mechanistic general model of global ecosystems: improving prediction by increasing simplicity?*
11:58	Jessica **WILLIAMS**	*Does human land use systematically favour species adapted to warmer and drier climates?*
12:05	Lea **DAMBLY**	*Substituting reality: A virtual approach to assess bias in a citizen science programme*
12:12	Joseph **MILLARD**	*Assessing the computational response of pollinators to environmental change: a computational approach to diversity, distribution, and value*

GEE 2018 Graduate Research Symposium continues with a
Lunch and a poster session in Anatomy G04 Gavin de Beer LT
(Lunch available from 12:00pm – Award presentations 1:30pm)

Poster Session & Lunch: Thursday 3rd May, 12pm – 2:30pm

Location: Anatomy G04 Gavin de Beer LT

Name	Poster Title
Ella **BROWNING**	*The efficacy of low cost passive acoustic sensors for monitoring bats*
Iulia **DAROLTI**	*Haploid selection slows evolution of plant sex-biased genes*
Chris **DOBLE**	*The effectiveness of eDNA metabarcoding approaches for surveying Lake Tanganyika's diverse littoral fish communities*
Rory **GIBB**	*Global effects of land use on zoonotic host communities*
Carina **KERN**	*Reproductive death in ageing in the nematode Caenorhabditis elegans*
Thalassa **MCMURDO HAMILTON**	*Risky business: Deciding how to conserve New Zealand's rarest bird*
Adrian **TIMPSON**	*Identifying milk in archaeological pot sherds using compound specific stable isotopes*
Natalie **WOOD**	*Using CRISPR/Cas9 to investigate the role of neuropeptides in the development of the sea urchin Strongylocentrotus purpuratus*

Abstracts

Evaluating the Suitability of Social Amoebae Dictyostelium discoideum as an Alternative Model in Developmental Toxicity Testing (1st 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.

Morphological evolution and modularity of the caecilian skull (3rd year talk)

Carla **BARDUA,** David GOWER, Mark WILKINSON, Emma SHERRATT & Anjali GOSWAMI

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Abstract:

Gymnophiona are the least speciose extant amphibian order, yet exhibit a broad range of skull morphologies. Very few studies have explored morphological evolution or modularity (the division of a structure into subsets of correlated traits) within this clade. We used an intensive landmarking approach to quantify cranial morphological variation across all 33 extant caecilian genera. We defined 16 cranial regions using 53 anatomical landmarks and 343 sliding semi-landmarks, followed by a semi-automated procedure to place 729 surface semi-landmarks across the regions. We then analysed modularity and shape evolution through time using a phylogenetic framework.

We found highest support for a ten-module model, with the skull more integrated posteriorly. Skull morphology has a strong phylogenetic signal (Kmult=0.80, p=1e-4), and allometry accounted for 18% of shape variation (Rsq=0.18, p=1e-4), with the strength of these influences varying across the cranial modules. The quadrate is the most disparate and fastest evolving module, and is free from phylogenetic constraints. Fossoriality, development and reproductive strategy were small but significant influences on morphology (Rsq=0.03-0.06, p<0.025). Our analysis of modularity broadens the phylogenetic breadth of current modularity studies, and suggests the previously identified patterns of modularity found in a diversity of amniotes cannot be extrapolated across Tetrapoda.

Sustainable bushmeat harvesting by a Virtual Ecologist (3rd year talk)

Tatsiana **BARYCHKA**

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Abstract:
Subsistence hunting has resulted in over-harvesting and population declines in many wild animal species across sub-Saharan Africa, and is sure to continue for some time. Here I show how theoretical modelling can be used to address practical resource management problems, by highlighting crucial information needs. To keep my modelling grounded I use duiker *Cephalophus* species - the most widely harvested ungulate in West and Central Africa, as my case study. Although these species are still classified as least concern, their numbers are declining; this decline poses a threat to livelihoods of the most marginalised people in Africa. Despite their commercial importance, we still know very little about duikers. Because of this uncertainty, policy makers have struggled to predict sustainable off-take rates for duikers – and many other heavily exploited species. Much time and money may be saved if we knew when extra survey work would bring the highest returns. Could ecological models, combined with adaptive management, help pinpoint where information is of the most value to future conservation planning? In this talk I show how better-informed harvesting could lead to significant improvements in both bushmeat yields and species survival.

Evaluating the efficacy of small scale MPAs for preserving reef health through the application of 'Structure from Motion' photogrammetry (3rd year talk)

D.T.I. **BAYLEY**, H.J. KOLDEWEY, A.O.M. MOGG & A. PURVIS

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Abstract:

Human activity is having a global negative impact on species and habitats in aquatic ecosystems. In the oceans, marine protected areas (MPAs) are increasingly being used as a management mechanism to conserve individual species or entire systems at risk. Managers have particularly focussed MPA creation on biogenic reef environments, because of their importance as habitat for multiple species, their importance for human services such as food provision, and their fragility to disturbances such as intense fishing[3]. However, due to a range of difficulties in creating and enforcing MPAs, coastal developing countries, which often have large extents of tropical coral reefs and high dependence on their resources, appear to be lagging behind better resourced countries, leaving their reef areas at high risk of degradation.

This study uses reef community data collected at three reserves within the heavily populated Western Visayas region of the central Philippines to assess the state of reef benthic structure inside and outside of small-scale locally managed MPAs. Data were captured through the use of recently developed 'Structure from Motion' photogrammetry techniques, allowing multiple metrics of physical 3D structural complexity and benthic health to be recorded, which can be further matched to the community structure of associated fish species.

Our results demonstrate the benefit of community run MPAs even when applied on a small scale, and show clear negative shifts in both the structure and function of un-managed reef communities through time relating to a range of chronic and acute pressures from the surrounding human population (primarily in the form of dynamite fishing), and from climate events.

Strict protected areas are crucial for the conservation of threatened and larger mammal species in the Brazilian Cerrado (1st year talk)

Guilherme **BRAGA FERREIRA**, Marcell Soares PINHEIRO, Marcelo Rabelo OLIVEIRA, Fernando FERREIRA DE PINHO, Tim NEWBOLD, Chris CARBONE, Marcus ROWCLIFFE & Ben COLLEN.

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Abstract:
Most protected areas (PAs) performance evaluations conducted so far have used deforestation metrics, with only a few assessments focusing on local biodiversity. However, because biodiversity loss can happen without major changes in vegetation cover, reliable measures of conservation outcomes based on local biodiversity are crucial to assess PA effectiveness. To this end we conducted camera trap surveys in seven PAs in the Brazilian Cerrado to investigate the effect of stricter forms of habitat protection on large mammals. We estimated species occupancy in strict and multiple-use PAs, while controlling for variables influencing both PA location and mammal populations. Occupancy was significantly higher in strict PAs than in multiple-use PAs for six species (37.5%), whereas none of the species investigated had significantly higher occupancy in multiple-use PAs. Species with greater occupancy in strict PAs were generally threatened and/or large, as they included three of the four globally threatened species recorded and five of the six largest species investigated. Our findings give further support to the call for expanding strict PA coverage in the Cerrado, particularly if we are to safeguard more sensitive species. Furthermore, they could be used as an argument against the ongoing events of PA downgrading, downsizing and degazettement happening in Brazil.

Novel effectors of metabolic stress signalling in adipocytes (3rd year talk)

Lea **BROCHARD**

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Abstract:
Insulin resistance has been shown to be caused by saturated fatty-acids (SFA), especially palmitate, found in abundance in Western diets. Phosphatidylinositol 3-kinase (PI3K), a molecule has been identified as a key modulator of SFA-induced insulin-resistance. To further the current understanding of the molecular mechanisms at play, we performed a transcriptome analysis comparing the gene expression profiles of 3T3-L1 adipocytes treated with palmitate, in the presence or absence of an inhibitor of p110α, one of the catalytic subunits of class IA. It revealed that the expression of a number of genes induced by type I interferon (IFN) is stimulated in response to palmitate, an effect abrogated by PI3K p110α inhibition. This finding was of particular interest as IFN is known, like palmitate, to trigger insulin resistance. We studied the the molecular links between IFN- and palmitate-mediated insulin resistance. in both mice and human preadipocytes and mature adipocytes, which allowed us to confirm the positive metabolic effect of p110α inhibition. The effect of palmitate on components of the IFN pathway was further explored and led to the establishment of a pivotal role of IFN-stimulated genes in the development of SFA-induced metabolic dysfunctions in adipocytes.

The efficacy of low cost passive acoustic sensors for monitoring bats (Poster)

Ella **BROWNING**

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Abstract:
Rapid increases in the application and development of passive acoustic sensors promise effective environmental monitoring in the face of rapid global biodiversity declines, but device cost frequently limits the spatial and temporal scale of surveys. Recently there has been a move towards open-source, more affordable ecological monitoring equipment, including passive acoustic recorders such as the AudioMoth, which may enable higher temporal and spatial coverage for monitoring studies. For such sensors to be reliably utilized to assess ecological changes, the quality of the acoustic data compared to that collected by favoured commercial sensors must be empirically tested. Here the performance of AudioMoths and two commercial devices - Pettersons and SM2s – in surveying bats, species commonly monitored using passive acoustic sensor, was compared.   The detection range of AudioMoths was first determined for both open and cluttered habitats using synthetic bat calls of frequencies from 20 kHz – 80 kHz at 5 m intervals away from and either side of the device. An automated bat call detector and classifier was then used to identify the calls from the recordings and the distance at which the classifier failed to detect the call was defined as the maximum detection range. Simultaneous deployment of three sensors was then carried out in UK woodland to survey bats and determine the probability of detecting different species with each of the sensors. This poster will discuss the results of these tests, demonstrating whether there is a significant difference in ability to record and subsequently identify different bat species between the low-cost AudioMoths and commercial sensors, and highlighting the implications this has for wider biodiversity monitoring. Understanding the impacts of using low-cost devices on data quality and the derived ecological information is vital if there is to be widespread uptake of these devices.

Testing a mechanistic general model of global ecosystems: improving prediction by increasing simplicity? (1st year talk)

Benjamin **BURGESS**

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Abstract:
Ecosystems can be incredibly complex entities, with even simple food chains being dictated by relationships that are not inherently obvious. Consequently, understanding how ecosystems respond to stressors can equally complicated; though given the threat to ecosystems by climate change, pollution and harvesting this insight is required.

The response of a food chain to stressors is being determined through the use of mechanistic equations for determining population abundances at multiple trophic levels. Within the equations the parameters of attack rate, conversion efficiency and mortality are iteratively varied, in pairs, to represent changes to a food chain under stress; in doing so generating large-scale datasets for analysis. Comparisons of expected and actual changes to population abundance at a given trophic level are made. Analysis is also conducted to determine how the response of a food chain to forcing varies with the equations used.

Future work will compare these theoretical analyses to empirical ecosystem observations, determining when the predictions and observations align or contrast. The overall intentions of this project are to investigate a complex mechanistic ecosystem model, the Madingley Model, to determine whether it incorporates any ecological processes that are functionally redundant and therefore may be altered or removed from the model.

Oocytes quality depends on mitochondrial segregation and selective transfer into the Balbiani Body (1st year talk)

Marco **COLNAGHI**

PhD Supervisors: Prof Nick LANE, Prof Andrew POMIANKOWSKI

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Abstract:

Mitochondria provide the energy and metabolic precursors needed for normal cell function. The frequent turnover and replication of mitochondrial DNA makes it uniquely vulnerable to the accumulation of mutations. This problem is compounded by the high copy number of mitochondria in cells, which results in individual mutations having negligible effect on cell fitness. So mutants are not easily eliminated by selection and can be amplified to high numbers through stochastic processes, with the resulting high mutation loads being responsible for a range of severe diseases. But the process of inheritance of mitochondrial genomes is still far from understood. The simple hypothesis that mitochondrial mutants segregate randomly during female germline development is undermined by experimental studies showing complex collective dynamics, with evidence that developmental processes lead to a reduction in mutation load.

I will present a new model for the inheritance of mitochondrial genomes that considers three hypotheses on the underlying germline dynamics: a) a bottleneck in mitochondrial numbers during development, b) elimination of dysfunctional organelles during cytoplasmic transfer to the Balbiani body, and c) purifying selection on oocytes as they mature before ovulation. We infer the distribution of mitochondrial mutations in oocytes, and compare the outcome of the model with data on mutation levels and the incidence of mitochondrial diseases in humans. Our results beautifully explain the dynamics of female germline development, notably Balbiani body formation, the loss of 80% oogonia as apoptotic nurse cells, the proliferation of mitochondria in maturing oocytes, and the observed patterns of mitochondrial disease. We show that the female germline is fashioned by the requirement to minimise the new mitochondrial mutations while maximising mitochondrial numbers in the mature oocyte.

Substituting reality: A virtual approach to assess bias in a citizen science programme (1st year talk)

Lea **DAMBLY**[1,2,3], Kate JONES[2], Katherine BOUGHEY[3], Charlotte HAWKINS[3] & Nick ISAAC[1]

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Abstract:
The National Bat Monitoring Programme (NBMP) has engaged thousands of citizen scientists across the UK in the past twenty years. The volunteers employ multiple survey methods to collect data on the relative abundance and activity of bats. The data is used to produce population trends for eleven resident bat species, which aid the Government and conservation organisations to monitor the state of the environment, inform policy and improve bat conservation.

For some bat species, population trends derived from roost counts differ substantially when compared with other survey methods. This is likely a reflection of bias in the roost count surveys, caused by non-random site selection, observer behaviour and/or species-specific behaviour. It needs to be assessed whether bat population trends are detected correctly in the presence of bias.

I apply the 'virtual ecologist' method, where simulated data and observer models are used to mimic ecological processes, data collection and analysis. The 'true' trend of the virtual population can then be compared to the trend derived from the data collected by the virtual observers. Here, I discuss the simulation approach, preliminary results and future plans.

Haploid selection slows evolution of plant sex-biased genes (Poster)

Iulia **DAROLTI,** Alison E. WRIGHT, Pascal PUCHOLT, Sofia BERLIN & Judith E. MANK

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Abstract:

Conflicting selection pressures in males and females over optimal expression acting on shared genetic content can give rise to sex-biased gene expression. As such, sex-biased genes are increasingly being used to study signatures of sex-specific selection within the genome. While, there is a wealth of studies on the evolutionary dynamics of sex-biased genes in animal systems, little is known about the molecular evolution of sex-biased genes in plants in general, and in dioecious angiosperms in particular. Here we use male and female transcriptome data from both reproductive and vegetative tissues of the basket willow, *Salix viminalis*, a woody angiosperm with wind-dispersed pollen and a young sex-chromosome system, to investigate for the first time the sequence evolution of sex-biased genes in a dioecious plant species. In striking contrast to findings from animal systems, where high levels of sperm competition have been found to produce higher rates of protein evolution in male-biased genes, we observe slower rates of evolution of sex-biased genes compared to unbiased genes. These findings are consistent with purifying selection, resulting from stronger haploid selection in plants compared to animals, acting forcefully to remove recessive deleterious variation.

The effectiveness of eDNA metabarcoding approaches for surveying Lake Tanganyika's diverse littoral fish communities (Poster)

Chris **DOBLE**

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Abstract:
Despite recent studies highlighting the effectiveness of eDNA metabarcoding methods for surveying aquatic fish communities, important questions remain surrounding the ability of these approaches to detect species across different habitats and scales. Most notable is the lack of studies within diverse tropical ecosystems containing much of the world's freshwater diversity. This study starts to address this issue, applying an eDNA metabarcoding approach to survey Lake Tanganyika's diverse littoral fish communities. eDNA samples collected across two field seasons were extracted, amplified using four primer sets and sequenced to produce a novel metabarcoding dataset. Taxonomic identifications made with a unique reference database are used to investigate the effectiveness of these primer sets for detecting fish species within the lake, particularly those within complicated groups such as the cichlid fishes. Through comparisons with survey data from traditional methods, the relative effectiveness of these approaches for surveying the lake's littoral fish communities is also assessed.

Male mate preferences are not condition-dependent due to low genetic fitness caused by meiotic drive (3rd year talk)

Sam **FINNEGAN**

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Abstract:

Despite a historical narrative of indiscriminate males attempting to mate with choosy females, male mate choice is now recognised as a widespread phenomenon in sexual selection. There is increasing evidence that female preference is a condition-dependent trait, with high quality females expressing the strongest preferences. It is not known, however, how condition affects the expression of male mate preferences. In the Malaysian stalk-eyed fly, *Teleopsis dalmanni*, males prefer to mate with large, high fecundity females. Some males of this species also exhibit X-linked meiotic drive, a sex-ratio distorter. This distorter is located in a low-frequency inversion covering most of the X chromosome and is associated with reduced fitness. We took advantage of this variation in genetic fitness to assess whether males of low genetic condition (SR) expressed weaker mating preferences to those of high genetic condition (ST) in a simple binary choice trial. We found that both SR and ST males preferred large females, but the strength of preference did not vary according to genetic condition. SR males, however, were unable to mate as frequently as ST males. These findings suggest that male mate preference is not a condition-dependent trait in this species, but that the presence of meiotic drive limits male mating capacity.

Using the drug-protein interactome to identify anti-ageing compounds for humans (1st year talk)

Matías **FUENTEALBA VALENZUELA**[1,2], Handan Melike **DÖNERTAŞ**[2], Janet **THORNTON**[2] & Linda **PARTRIDGE**[1,3]

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Abstract:

Advancing age is the dominant risk factor for most of the major killer diseases in developed countries. Hence, ameliorating the effects of ageing, in theory, may prevent multiple diseases simultaneously. Existing drugs have proved to be effective in extending the lifespan and healthspan in animal models, and there is therefore scope for drug repurposing, with a few drugs already under study for ageing in humans. There is thus a need for new bioinformatic methods to identify and prioritise potential anti-ageing compounds for humans. Using drug-protein interaction information we ranked 1,147 drugs by their likelihood of targeting ageing-related gene products. Among the 19 statistically significant drugs after multiple testing correction, 6 have already been shown to have pro-longevity properties in animal models. We evaluated the beneficial or detrimental effect on ageing of the top-ranked compounds based on literature mining and by performing an interaction-based similarity analysis. Our results propose cAMP, selenium, tanespimycin as novel anti-ageing candidates.

Identification of genes responsible for the variation in facial and teeth morphology in latin americans (3rd year talk)

Macarena **FUENTES-GUAJARDO**

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Abstract:
Facial and dental features are of considerable importance in biomedicine and forensics. Facial appearance has a strong genetic component and could have evolved to facilitate individual recognition. Teeth are the hardest and well-preserved parts of the body and they have been used to establish biological relatedness among past and current human populations and to identify victims. Although genes have been identified for various facial and dental phenotypes, the genetic basis of normal variation for both traits is still poorly understood.

A GWAS using ~700,000 genome-wide markers from ~6,000 Latin American individuals (CANDELA cohort) was performed. Ordinal and quantitative facial traits were assessed in individual photographs. Another GWAS was conducted using the same markers from a subgroup of ~500 dental casts from the same cohort. Dental casts were obtained from each volunteer and eighty-six dental traits were categorized using the ASUDAS scale.
SNPs situated in four gene regions showed associations with three ordinal and quantitative traits related to nose morphology. Quantitative analyses, in addition, detected an association of SNPs in EDAR with chin protrusion. Consistently, Edar mouse mutants was characterized to observe alterations of mandible length. Furthermore, six SNPs showed association with four dental traits, including EDAR.

Global effects of land use on zoonotic host communities (Poster)

Rory **GIBB,** David W. REDDING, Kai Chin, Tim BLACKBURN, Tim NEWBOLD & Kate E. JONES

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Abstract:
Land use change is increasingly recognized as a key driver of zoonotic disease, but the underlying ecological processes are complex and often poorly understood. Ecological community changes associated with land use may impact disease risk by changing reservoir host populations, their contacts with people and associated pathogen transmission dynamics, but critically it is unknown whether anthropogenic habitat modification drives consistent and predictable changes in the local diversity and species composition of zoonotic host taxa. We analyze a global dataset of over 7000 ecological assemblages to show that the richness and abundance of potential host species is consistently higher in human-modified than nearby undisturbed habitats. However, this effect varies markedly among mammal orders, with mammalian communities in modified land uses increasingly dominated by rodent, bat and ungulate zoonotic host species. As a result, while future global land use trends may drive overall increases in epidemiological contact between people and zoonotic host communities, our findings suggest that their impacts on different host taxa, and by extension different diseases, are likely to be highly variable.

Nucleotide synthesis in hydrothermal vent conditions (1st year talk)

Stuart **HARRISON**

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Abstract:

Current hypotheses for the origins of life suggest it may have begun in iron-sulphur rich, alkaline hydrothermal vents that are thought to have been widespread on the early earth. These vents provide a long-lived, far-from-equilibrium environment that would favour the consistent production of reduced carbon and provide abundant inorganic catalysts. Also, their structure enables mechanisms for concentrating organic molecules. In addition there is evidence that key biochemical pathways such as the Krebs cycle may have been preceded by mechanistically similar non-enzymatic versions, the existence of which permits the evolution of more complex enzymes or ribozymes without needing to select for every intermediate. An entire pathway can evolve without needing all enzymes to exist simultaneously.

Nucleotides are essential at the origins of life given their importance as a hereditary molecule, energy source and catalyst. The synthesis of nucleotides has been achieved non-enzymatically before but they use toxic starting materials, harsh environmental conditions which are not reminiscent of the vents and proceed in a way which is highly dissimilar to biology. As such, my work is focused on whether it is possible to synthesise nucleotides in conditions broadly similar to alkaline hydrothermal vent conditions whilst also being reminiscent of the extant biosynthesis pathway providing a more rational explanation for the origins of nucleotide synthesis.

Analysis of 3' end sequencing data in FUS mutant mice using QuantSeq (1st year talk)

Seth **JARVIS**

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Abstract:
3' end processing of RNA is directed and controlled by multiple RNA-binding proteins allowing mRNAs of various lengths and functions. This is particularly important as changes in the 3' untranslated region (3'UTR) sequence content and length have consequences for cellular localisation and mRNA stability.
Mutations in the RNA-binding protein Fused in Sarcoma (FUS) have been linked to two neurological diseases Amyotrophic Lateral Sclerosis and Frontotemporal Dementia. The role of FUS mutations in directing 3' end processing is, as is whether this influences the localisation of these transcripts within neurons.

We are developing a bioinformatic pipeline to analyse RNA-sequencing data produced from 3' end RNA sequencing (QuantSeq, Lexogen). To this end we have prepared both total RNA and QuantSeq libraries from mice carrying mutations in FUS and FUS knockout mice.

Our results highlight systematic differences and key challenges in estimating and comparing both gene expression and differential 3' end processing from total RNA and 3' end enriched RNA sequencing libraries. We also shed light on a new method for analysing the change in contributions from multiple polyadenylation sites across conditions by fitting a Dirichlet multinomial model. Our method increases the power of detection compared to previous methods.

Reproductive death in ageing in the nematode Caenorhabditis elegans
(Poster)

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Abstract:

Ageing (senescence) is the major cause of death in the world today, yet its mechanisms remain unsolved. To overcome this, simple short-lived animal models have been employed, e.g. the roundworm C. elegans. One theory about ageing is that genes selected for early life fitness traits promote pathology in later life (antagonistic pleiotropy), potentially via harmful gene action late in life (hyperfunction). Recent work in the Gems lab has focused on understanding how hyperfunction promotes pathology, partly by senescent pathology characterization. New findings suggest that worms undergo environmentally-modulated reproductive death. This is an unusual form of senescence where rapid self-destruction is a byproduct of a burst of reproductive effort (as in Pacific salmon). The occurrence of reproductive death in C. elegans is both important to understanding senescence in this organism, and for relating findings to senescence in higher animals. I am exploring this possibility by looking at how environmental factors affect reproduction and senescent pathogenesis and also by exploring alternative life histories in C. elegans.

Risky business: Deciding how to conserve New Zealand's rarest bird (Poster)

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Abstract:

Making decisions for endangered species is not easy, often because managers are proposing novel techniques or more intensive management such as captive management and translocations, creating multiple unknowns. Furthermore, when a population is very small, risk is heightened as decisions need to be made with little information data and the consequence of making a poor choice can mean populations, or species, are lost.

Structured Decision Making (SDM) is a powerful tool for conservationists in this environment. It provides a systematic and transparent examination of complex decision problems and allows choices between possible alternatives to be clearly informed by scientific evidence plus the values and risk attitudes of stakeholders. We are applying SDM tools to the management planning for New Zealand's rarest indigenous bird, New Zealand fairy tern, *Sternula nereis davisae* (hereon, NZFT). This is a presentation of the results of the first workshop with the stakeholders, which was held in March 2018.

Six fundamental objectives and associated performance indicators were defined by the group, which included biological, social and economic objectives. Participants worked in groups to identify alternative management strategies, which included actions for predator control, captive management of NZFT and breeding habitat management. This represents the first part of the SDM process for this rare bird and forms the basis for the next steps. Ultimately, it will provide information to the NZFT Recovery Group on which alternative management strategy will perform best for all the identified objectives.

Assessing the links between biodiversity and ecosystem services in the tropical forests of Amapá, Brazil (3rd year talk)

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Abstract:
Preserving the benefits that ecosystems provide to society is increasingly recognised by policy makers as essential, as exemplified in UN's Aichi Biodiversity Targets. This research explores the interactions between biodiversity, ecosystem services (ES), and forest use, within a tropical forest-rich socio-ecological system in eastern Amazon. I will present results from a study assessing spatial patterns and the effect of landscape heterogeneity on ES provision at regional scale. I will also discuss results from a study assessing local perceptions on the links between biodiversity and ES, including which factors influence them, and if those perceptions have in turn an influence on attitudes towards conservation. Finally, I will mention ongoing work analysing the impact of forest use change on biodiversity and the provision of different ecosystem services in a tropical landscape. Ultimately this research aims to support land use management that promotes multifunctional landscapes and a sustainable balance between biodiversity conservation and ES provision in tropical forests.

Assessing the global response of pollinators to environmental change: a computational approach to diversity, distribution, and value (1st year talk)

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Abstract:
Abstract: 87.5% of wild and crop plant species are thought to be pollinated to some extent by animals, with an estimated global value of $230-410 billion dollars. Across North America and Europe, numerous studies have documented declines in pollinating animals. A number of anthropogenic drivers—primarily land-use modification and climate change—have been associated with these losses. However, the extent to which pollinators may decline in the future, and how this might influence communities of species, is largely unknown. This project will collate current knowledge on pollinator decline, distribution, and functional traits, before building statistical models to predict the response of pollinating animals to future environmental change. The project will also explore developments in the novel field of conservation culturomics, using web-scraping and text mining to develop metrics for pollinator awareness, and in turn progress on Aichi Biodiversity Target 1. The outputs of this PhD project will contribute towards efforts to model future biodiversity scenarios, as well as the current debate on indicators for biodiversity awareness.
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Substrate-level phosphorylation of ADP to ATP by acetyl phosphate under abiotic conditions (1st year talk)

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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, as it is quite a complex molecule. 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. Following a study demonstrating the synthesis of AcP via the phosphorolysis of thioacetate under abiotic conditions, this project considers the next step linking AcP to ATP: can AcP promote ATP formation by phosphorylating adenosine diphosphate (ADP) under abiotic conditions? The study focuses in particular on yield under alkaline hydrothermal conditions, as such vents are a possible site for the origin of life, but being warm (40-90 ^{o}C), alkaline (pH 9-11) and saline may rather favour simple hydrolysis. Preliminary findings suggest preferential production of small amounts of ATP over other phosphate products, indicating that it is indeed possible for ATP to be formed abiotically and encouraging future research on AcP as primordial analogue of ATP.

Sexual antagonism constrains adaptation across the Drosophila melanogaster distribution range (3rd year talk)

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Abstract:

The evolution of sexual dimorphism is mediated by a shared genome. This constraint is reflected at the genetic level by sexually antagonistic genes – that is, genes whose expression is beneficial in one sex but detrimental in the other. Quantitative genetic studies have documented the phenotypic effects of sexual antagonism, but no study has described genome-wide antagonistic genes. The location, function and evolutionary dynamics of such genes therefore remains unexplored. To address this, I exploit a novel genome-wide dataset of candidate sexually antagonistic SNPs from a laboratory-adapted population of *D. melanogaster*. By comparing this dataset with population genomic data from the species' distribution range, I show that sexually antagonistic SNPs are highly evolutionarily persistent. Antagonistic sites bear the hallmarks of balancing selection: elevated heterozygosity and regional polymorphism, with reduced population differentiation. Remarkably, these genomic signatures can be detected in populations separated by ~20,000 years from the source population. Taken together, these results show that sexual antagonism is a major constraint to phenotypic adaptation and a key selective mechanism for the maintenance of genetic variation.

Rapid warming is associated with population decline among terrestrial birds and mammals globally (3rd year talk)

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Abstract:
Animal populations have undergone substantial declines in recent decades. These declines have occurred alongside rapid, human-driven environmental change, including climate warming. An association between population declines and environmental change is well established, yet there has been relatively little analysis of the importance of the rates of climate warming and conversion to anthropogenic land use in causing population declines. Here we present a global assessment of the impact of rapid climate warming and anthropogenic land conversion on 987 populations of 481 species of terrestrial birds and mammals since 1950. We collated spatially referenced population trends of at least 5 years' duration from the Living Planet database and used mixed effects models to assess the association of these trends with observed rates of climate warming, rates of conversion to anthropogenic land use, body mass and protected area coverage. We found that declines in population abundance for both birds and mammals are greater in areas where mean temperature has increased more rapidly. Our results identify a link between rapid warming and population declines, thus supporting the notion that rapid climate warming is a global threat to biodiversity.

Using Ecological Niche Modelling to assess the impact of environmental changes on species distribution of large mammals in Southeast Asia: past, present and future (3rd year talk)

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Abstract:

Ecological Niche Modelling (ENM) is an increasingly common technique used to investigate spatial and temporal patterns of faunal distribution in relation to environmental conditions. It can provide useful information for various applications, including predicting potential impacts of climate change on species distribution and assisting conservation planning. The modelling method has been implemented based on the hypotheses of niche conservatism, which suggest that species require similar ecological niches over time and across space. However, these evolutionary hypotheses are based on small number of empirical studies which are limited due to lack of species records and environmental data. Today, the technological advancements in GIS and the increasing availability of species records allows for more robust testing. Here, we will use four modelling algorithms to project geographical distribution of 17 large mammal species in Southeast Asia and China across three time intervals; Last Glacial Maximum, present day, and predicted potential distribution under future climate change scenarios. The area under receiver operating characteristic curve (AUC) will be used to assess model performance and accuracy. Results from this study will be important for the development of modelling techniques, as well as feeding into the development of effective conservation strategies in Southeast Asia; a region which is undergoing extremely high levels of biodiversity loss.

Caste plasticity in Vespid wasps (1st year talk)

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Abstract:
Social insect castes represent an extremely derived form of division of reproductive labour. The presence of highly specialised castes that are irreversibly determined during development greatly reduces the capacity for conflict between dominant and subordinate individuals over reproduction. This conflict reduction has in turn facilitated the repeated evolution of highly derived 'superorganismal' traits in social insect taxa. Studying the evolution of castes, and specifically the mechanisms by which caste plasticity has been lost over evolutionary time, is thus a key component to understanding the major evolutionary transition to eusociality.

My research will combine behavioural, morphological and molecular data to dissect the process of caste switching in the European paper wasp *Polistes dominula*, in order to reveal the mechanisms of caste plasticity. Additionally, I will be investigating the molecular mechanisms by which caste is controlled across multiple levels of eusociality displayed by wasp species in the Vespid clade.

Identifying milk in archaeological pot sherds using compound specific stable isotopes (Poster)

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Abstract:
Prehistoric pottery preserves traces of the long chain animal fatty acids they once contained, which can be separated using gas chromatography. The ^{13}C isotopic ratios of these compounds differ between dairy fats, ruminant adipose fats and non-ruminant adipose fats.

Working with the University of Bristol Chemistry Department I have built the largest SQL database of modern reference fats, comprising 1610 samples across 243 species, integrating code which automatically identifies compound data from raw mass-spectrometry machine files, to obtain reliable reference distributions of the isotopic values of different fat types.

I then compare these distributions with the pot sherd isotopic values using mixing models, incorporating prior information of archaeological faunal remains also found at the site, to infer what proportion of each fat was present in the original pot. Puzzlingly, whilst genetic evidence suggests Lactase Persistence (the ability to digest the milk sugar lactose as an adult) evolved under extremely strong selection in Europeans and became common around 3 kyr BP, analyses of prehistoric isotopic data indicate a widespread use of milk concomitant with the spread of farming across Europe 8.5 to 6 kyr BP.

Metabolic Memory Effects in Fission Yeast Ageing (1st year talk)

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Abstract:
Ageing presents one of the greatest biomedical and socioeconomic challenges of the 21st century. Unicellular eukaryotes are among the most successful ageing models owing to their simplicity, genetic tractability and the strong conservation of determinants of lifespan. Dietary restriction, which often involves changes in the carbon source or carbon source concentration, is a classic example of a perturbation which can extend lifespan across the tree of life. This holds true for chronological lifespan (CLS), defined as the survival time of non-dividing cells. However, it is notable in this ageing model that the carbon source is long consumed by the time cells begin ageing, meaning that the effects on lifespan must be mediated by some kind of "memory". Furthermore, it is not known what the cells "remember" from the preceding growth phase nor how this "memory" is retained. Using a novel high-throughput CLS assay, I have found that many environmental perturbations which increase CLS are in fact mediated through cell-intrinsic factors (i.e. memories), and that the dynamics of these memory effects are surprisingly diverse. Further work will focus on identifying the nature of these cell-intrinsic factors, providing fresh insights into how metabolic status during growth can subsequently affect ageing.

fastGLOBETROTTER: efficient identification and dating of admixture events inference in large-scale population data cohorts (3rd year talk)

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Abstract:

Intermixing, or "admixture", among populations, e.g. due to past migrations, has had a major influence in shaping genetic diversity. The software *GLOBETROTTER* (Hellenthal et al 2014) shows increased precision over other available techniques for characterising admixture events due to modelling haplotype information, i.e. associations among tightly linked Single Nucleotide Polymorphisms (SNPs). However, *GLOBETROTTER* also has increased computational demands, and hence can only cope with limited data sizes. We present a new statistical method, *fastGLOBETROTTER,* which can effectively infer dates and features of admixture while scaling to larger data resources, an important problem due to the increasing availability of large, genetically homogeneous cohorts sampled from relatively narrow geographic areas.

In particular, *fastGLOBETROTTER* models the decay in linkage disequilibrium among pairs of haplotype segments while prioritising pairs that are likely to be the most informative for admixture. Through applications to a large variety of simulations, we illustrate how this approach can reduce computational time by a factor of ~10 relative to *GLOBETROTTER*, while also improving accuracy in many settings.   Finally, we report findings from applying *fast*GLOBETROTTER to large-scale data cohorts, including a Greek population sample consisting of 742 individuals.

Does human land use systematically favour species adapted to warmer and drier climates? (1st year talk)

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Abstract:

Rapid human population growth has resulted in increasing exploitation of the environment and conversion of land for human use. These changes in land use can alter land cover, which mediates local climatic conditions and in turn may influence community composition. In human-altered landscapes, sites are generally hotter and drier than in natural habitats. By using the PREDICTS project (Projecting Responses of Ecological Diversity In Changing Terrestrial Systems) database, we analysed, for the first time globally, whether human land uses and land-use intensification systematically favour species with certain climatic niches. We found that communities within human-dominated land uses were, on average, composed of species affiliated with warmer and drier climates relative to communities within primary vegetation. In addition, community-average thermal niche breadths were found to be wider in human-altered land uses. The size of these effects differed between geographic zones as well as between endothermic and ectothermic communities. These results enhance our understanding of how biodiversity responds to land-use change, which will help us to predict species' responses to future land-use changes and to design suitable management and conservation strategies.

Using CRISPR/Cas9 to investigate the role of neuropeptides in the development of the sea urchin Strongylocentrotus purpuratus (Poster)

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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. Preliminary data in the purple sea urchin, *S. purpuratus* has suggested a developmental role of neuropeptides. Thirty-eight neuropeptide genes have so far been identified in the sea urchin genome and at least sixteen are expressed in the early phase of embryogenesis. Further some of these are spatially localised. A *pedal peptide-like* neuropeptide (*PPLN1*) shows oral-aboral asymmetric expression, suggesting a role in early axis specification.

Deducing their innovative function(s) will help to elucidate the evolutionary history of these molecules. To identify the putative function of these molecules we are undertaking knockdown/ out experiments using morpholino antisense oligos and the CRISPR/Cas9 system.