

Wednesday Jan 4<sup>th</sup>

Time	
9.30 – 10.30	Plenary - Drapers Austin Burt Prospects for genetic biocontrol

10.30 – 11.00 Tea/coffee (Maths and Fogg)

Time	Session I Drapers	Session II Fogg	Session III Maths
11.00 – 11.15	Ruzicka, Filip Wright or Fisher? A genomic test of alternative theories of dominance	Pilling, Olivia* Selective whole-genome amplification reveals population genetics of <i>Leishmania braziliensis</i> from primary patient samples	Mario dos Reis A mutation-selection model of protein evolution under persistent positive selection
11.15 – 11.30	Reynolds, Josh* Utilising rare variant sharing to identify non-recurrent rare mutations in <i>Anopheles gambiae</i> mosquitoes	Willis, Katie Autosomal editors for efficient genetic biocontrol	Korfmann, Kevin* Simultaneous Inference of Past Demography and Selection from the Ancestral Recombination Graph under the Beta Coalescent
11.30 – 11.45	Charmouh, Anders* Inferring the distributions of fitness effects and proportions of strongly deleterious mutations	Breistein, Bjørghild* Geographic variation in gene flow from a genetically distinct migratory ecotype drives population genetic structure of coastal Atlantic cod ( <i>Gadus morhua</i> L.)	Achaz, Guillaume The Baldwin effect reloaded (BE 2.0)
11.45 – 12.00	Aninta, Sabhrina* Using site frequency spectrum to detect purifying selection on endemic island ungulates	Schley, Rowan J. Do reticulate relationships between tropical trees drive diversification?	Braichenko, Svitlana Inferring different modes of natural selection using PoMos in RevBayes
12.00 – 12.15	Ho, Tammy* Does genetic diversity predict fitness in wild arthropod populations?	Cerca, José Re-re-re-re-re-re-re-re-re defining parallel and convergent evolution	Hitchcock, Thomas Reproductive value and selection in age-structured populations
12.15 – 12.30	Rayner, Jack Endless forms most beautiful, some not: a novel adaptive phenotype illustrates the large mutational target of a trait under negative selection	McMullan, Mark Introduction to a crop wild relative to investigate plant & pathogen co-evolution	Wong, Yan Storing and analysing ARGs using tskit

12.30 – 14.00 Lunch (Maths and Fogg)

13.00 – 14.00 Meet the editors (Fogg)

Time	Session I Drapers	Session II Fogg	Session III Maths
14.00 – 14.15	Johnston, Susan Sexual dimorphism in recombination rates & landscapes in wild house sparrows.	Yen, Eugenie (Charley)* Quantifying genome-wide DNA methylation to assess the adaptive capacity of endangered sea turtles in a warming world	Cunningham, Phoebe* The role of microbial symbioses in the evolution of specialised lifestyles in tropical ants

14.15 – 14.30	Obbard, Darren Mutation, recombination, and transposition rates in <i>Drosophila melanogaster</i> and <i>D. simulans</i>	Hui, Tin-Yu Drift and temporal dynamics of allele frequency with aestivation. How do we interpret temporal estimates?	Emma Curran Exploring the effects of whole genome duplication on structural variation using pangenomics
14.30 – 14.45	Selvaraju, Divya* A P-element invasion in experimental populations sheds light on the silencing of a newly invading transposon	Priebe, Marian* Gene duplication facilitates phenotypic innovation in ant castes	Green, Rowan* Ecologically mediated mutation rate plasticity provides new insights on microbial evolution
14.45 – 15.00	Chebib, Jobran Mutation rate estimates in mice using mutation accumulation experiments	Wright, Charlotte* The hidden Merian Element of Lepidoptera disguised by a conserved karyotype	Panossian, Balig* A dynamic epibiont community associated with the bone eating worm <i>Osedax</i>
15.00 – 15.15	Topaloudis, Alexandros* Recombination in the barn owl	Baird, Robert* Evolution of a sex-linked supergene determines unusual reproductive strategies in fungus gnats	De Sanctis, Bianca* Genetic structure, host specificity and speciation of small ermine moths ( <i>Yponomeuta</i> )
15.15- 15.30	López-Cortegano, Eugenio The rate and spectrum of de novo structural mutations in <i>Mus musculus</i>	Elmer, Kathryn Evolution, ecology, and genetics of live-bearing and egg-laying reproduction	Hildebrand, Falk The human gut microbiome explored at single nucleotide resolution.

15.30 – 16.00 Tea/coffee (Maths and Fogg)

Time	Session I Drapers	Session II Fogg	Session III Maths
16.00 – 16.15	Basuony, Ali* Mito-nuclear discordance explains the ambiguous phylogenetic relationship of the red fox ( <i>Vulpes vulpes</i> ) and Rüppell's fox ( <i>V. rueppellii</i> )	Wurm, Yannick Evolution of a young social supergene in fire ants	Lesaffre, Thomas Sex allocation trade-offs can explain the evolution of male and female heterogamety
16.15 – 16.30	Ignatieva, Anastasia Threading new data into reconstructed genealogies	Wu, Taoping* Local adaptation to hosts and parasitoids shape <i>Hamiltonella defensa</i> genotypes across aphid species	Hegde, Tejashwini* Plastic response in population-specific gene networks to a common stressor: larval crowding in <i>Drosophila simulans</i>
16.30 – 16.45	Chen, Yu-Chi* Phylogenomics uncovers ancient mitogenes in vertebrate genomes	Witwicka, Alicja* Dose-, tissue- and pesticide-specific effects of insecticides on gene expression in bumblebees	Gamblin, Jasmine* Bottlenecks can constrain and channel evolutionary paths
16.45 – 17.00	Forest, Thomas* Birds demography inference based on genomic data	Hernandez, Gabriel* Multiple optima - evidence of balancing selection in the genome of the fire ant	Prigent, Iris* How ecological inheritance shapes polymorphism
17.00 – 17.15	Pavan, Flavia* Rapid evolution of the regulatory network formed by miRNAs and their target genes in <i>Arabidopsis halleri</i> and <i>A. lyrata</i> .	Cogni, Rodrigo Wolbachia reduces virus infection in a natural population of <i>Drosophila</i>	Chehida Yacine, Ben Genes controlling mimicry in two morphs of a South American moth ( <i>Chetone histrio</i> )
17.15 – 17.30	Florencia Camus		

	Contribution of mitonuclear genomes to local adaptation		
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17.30 – 19.30 Poster session (Drapers Lounge)

Thursday Jan 5<sup>th</sup>

Time	
9.30 – 10.30	Plenary - Drapers Aida Andres Interrogating genomes to understand local adaptation in humans and endangered primates.
10.30 – 10.45	Kenneth Mather Prize Mitchell, Sam Investigating the drivers of diversity maintenance after a colonisation bottleneck

10.45 – 11.15 Tea/coffee (Maths and Fogg)

Time	Session I Drapers	Session II Fogg	Session III Maths
11.15 – 11.30	Mackintosh, Carl* The establishment of locally adaptive inversions in structured populations	Jaron, Kamil Quantifying the consequences of haploid selection inferred on springtail sex chromosomes	Yanqian, Ding* Species divergence driven by ecology and mating system in taxonomically complex British Euphrasia
11.30 – 11.45	Arnason, Einar Sweepstakes reproductive success via pervasive and recurrent selective sweeps	Flintham, Ewan The scope for sexual antagonistic polymorphism in polygenic traits	Pfennig, Aaron* Hybrid fitness effects modify fixation probabilities of introgressed alleles
11.45 – 12.00	Wang, Yiguan Selective sweeps in <i>Drosophila serrata</i>	Gardner, Andy The rarer-sex effect	Roux, Camille Speciation dynamics in plants versus animals
12.00 – 12.15	Götsch, Hannah* An Infinite Sites Model for Polygenic Adaptation: Sweeps or Allele-Frequency Shifts?	Mrnjavac, Andrea* Slower-X: Reduced efficiency of selection in the early stages of X	Baird, Stuart J.E. Genome polarisation for detecting barriers to geneflow
12.15 – 12.30	Soni, Vivak How much power do we have to detect recurrent selective sweeps?	Khatri, Bhavin Weakly deleterious natural genetic variation greatly amplifies probability of resistance in multiplexed gene drive systems	John Welch What can we learn about the history of divergence from the fitness of hybrids?

12.30 – 14.00 Lunch (Maths and Fogg)

13.00 – 14.00 Business meeting (Fogg)

13.30 – 14.00 Seminar by Nanopore technology (Maths)

Time	Session I Drapers	Session II Fogg	Session III Maths
14.00 – 14.15	Bates, Sadé * Meiotic drive and sperm competition	Arathoon, Louise* Assessing inbreeding in the genus <i>Antirrhinum</i> using ROH analysis	Pacheco, Carolina* Demography and evolutionary history of grey wolf populations around the Bering Strait
14.15 – 14.30	Forster, Annie* What selective forces drive the coevolution of sickle-associated haplotypes in the malaria parasite <i>P. falciparum</i> ?	Hewett, Anna* Chromosome-specific inbreeding depression in red deer	Jia, Xiaowen* Investigating the population history of present-day Georgia using diachronic archaeogenomic data
14.30 – 14.45	Grace, Cooper Alastair Hybridisation in parasites of the <i>Leishmania Viannia</i> subgenus	Lavanchy, Eléonore* Quantifying Inbreeding DepressionD	Barrera Redondo, Josué Uncovering gene-family founder events during major evolutionary transitions in

			animals, plants and fungi using GenEra
14.45 – 15.00	Jacobs, Arne The genomics of parasitism loss in European lampreys	Hiu, Tin-Yu Drift and temporal dynamics of allele frequency with aestivation. How do we interpret temporal Ne estimates?	Tengstedt, Aja* No doubting the Houting: Genomic insights into the evolutionary and demographic history of whitefish ( <i>Coregonus</i> spp.) populations in Denmark
15.00 – 15.15	Bradshaw, Sasha* Meiotic drive adaptive testes enlargement during early development in the stalk-eyed fly	Sudbrack, Vitor* Limited dispersal speeds up genetic adaptation via non-additive mutations	Blumer, Moritz* Large polymorphic chromosome inversions in the Lake Malawi cichlid radiation
15.15- 15.30	Stevens, Lewis Hyper-divergent haplotypes punctuate the genome of the model parasitic nematode <i>Heligmosomoides bakeri</i>	Ipsita, Agarwal Relating the evolutionary fitness costs of loss-of-function mutations to their pathogenic consequences in humans	Thomas Thorpe, Jessica A. Isopoda phylogenetics

15.30 – 16.00 Tea/coffee (Maths and Fogg)

Time	Session I Drapers	Session II Fogg	Session III Maths
16.00 – 16.15	Schlötterer, Christian Two different adaptive speciation mechanisms operate during adaptation to a novel hot environment	Corval, Hugo* Local adaptation through time and space: the case of the European barn owl	Hood, Emily* Investigating the Functional Effects of Genes Involved in Male Genital Divergence between <i>Drosophila</i> Species
16.15 – 16.30	Harrison Ostridge* Local genetic adaptation in chimpanzees	du Plessis, Sarah* Unexpected genomic variation in eastern British Eurasian otters ( <i>Lutra lutra</i> ) revealed by whole genome sequencing	Schneemann, Hilde* Fitness landscapes and the role of ploidy in heterosis.
16.30 – 16.45	Moutinho, Ana Filipa What can intra-molecular variation tell us about patterns of adaptation at the species level?	Gathercole, Louise* Population structure, distribution and hybridisation of British oak trees	Duarri-Redondo, Sara* Unraveling dynamics of long-term polygenic adaptation in <i>D. simulans</i>
16.45 – 17.00	Rees, Jasmin* Identifying the Nature of Adaptation to Micronutrients in Modern Humans	Vlček, Jakub* Conservation genetics of Galápagos mockingbirds: from immune genes to genomes	Kotari, Ioanna* The patterns of codon usage between chordates and arthropods are different but co-evolving with mutational biases
17.00 – 17.15	Reynes, Lauric How directional selection and genetic drift drive contemporary evolution of the kelp <i>Laminaria digitata</i> : a spatio-temporal genomic study	Cumer, Tristan Genomic basis of insularity and ecological divergence in barn owls ( <i>Tyto alba</i> ) of the Canary Islands	Leitch, Andrew Genome downsizing after polyploidy: mechanisms, rates and selection pressures
17.15 – 17.30	Whiting, James Repeated genomic adaptation to climate and its drivers across >300 million years of plant evolution	Polechová Jitka Coevolution of species' niche and range in spatially and temporally variable environments	Keightley, Peter Quantitative genetic variation from new mutations in mice

18.30 – 23.00 Banquet (ArceloMittal Orbit)

Time	
9.30 – 10.30	Plenary – Drapers Juliette de Meaux Strength of stabilizing selection on the amino-acid sequence is associated with the amount of non-additive variance in gene expression

10.30 – 11.00 Tea/coffee (Maths and Fogg)

Time	Session I Drapers	Session II Fogg	Session III Maths
11.00 – 11.15	Blaxter, Mark The Darwin Tree of Life project: reference genomes for all of biodiversity	Monnin, David Parallel Evolution in the Integration of a Co-obligate Aphid Symbiosis	Fumagalli, Matteo The genomic footprint of social stratification in admixing American populations
11.15 – 11.30	Carr, Martin Re-evaluating Loricata Choanoflagellate Phylogenetics	Henry, Lee Symbiont-driven niche expansions shape the diversification of insects'	Cenac, Zarus Modern human expansion from (southern?) Africa: Origin, non-African ancestry, and linearity
11.30 – 11.45	Borges, Rui Traditional phylogenetic models are insensitive to variations in the effective population size	Molinier, Cécile Asexuality is not faithfully transmitted by contagion in <i>Daphnia pulex</i>	Leigh, Stewart How Effective is Sexual Selection in Purging Deleterious Mutations in Experimentally Evolved <i>Drosophila</i> ?
11.45 – 12.00	Laumer, Christopher Nanopore transcriptome skimming: a promising strategy for meiofaunal biodiversity assessment	Lipinska, Agnieszka Scarlet tide – the first report of sex chromosomes in red algae	Scott, Michael F Equilibrium allele frequency in terms of invasion and fixation conditions

Time	
12.00 – 13.00	Plenary - Drapers Oscar Gaggiotti Deep learning in population genetics

13.00 – 14.00 Lunch (Maths and Fogg)