

Thursday 4 th January				
Time	LT1	LT2	LT3	LT4
8.30 – 8.50	Registration (Chemistry)			
8.50 – 9.00	Welcome & information			
9.00 – 9.50	Plenary 1 Mike Brockhurst Taking a dip in the mobile gene pool			
9.50 – 10.30	Coffee (Chemistry)			
10.30 – 10.50	Daniel Falush Admixture of <i>Helicobacter pylori</i> driven by deleterious mutation load	John Turner The flexible lek: a bundle of evolutionary puzzles	Jennifer James (S) Investigating the life history and demographic traits that are Predictive of Ne	Helena Batalha (S) Genetic diversity and divergence in the endangered Cape Verde warbler
10.50 – 11.10	Tim Downing Bacterial genomes from the UK and Ireland highlight transposable elements as drivers of antibiotic resistance	Eniko Szep (S) Does migration help or hinder local adaptation?	Reuben Nowell Comparative genomics of desiccating and non-desiccating bdelloid rotifer species	Toni Gossmann Severe loss of genetic diversity in the alpine marmot genome as a long-term consequence of cold temperature adaptation in a warming climate

11.10 – 11.30	Ana Zhu Strain variation in gut microbiota	Claire Armstrong (S) Genomic associations with bill length and disease reveal drift and selection across island bird populations	Casper Lumby (S) Inference of viral transmission events	Eliika Faust (S) Cleaner fish escape salmon farms and hybridise with local wrasse populations
11.30 – 11.50	Henry Barton (S) The strength of GC biased gene conversion is conserved across two passerine species	Thomas Mathers Evolutionary genomics of host range expansion in the green peach aphid	Bjarki Eldon Modelling gene genealogies in highly fecund populations	Pirita Paajanen <i>Arabidopsis arenosa</i> and its cousins, autotetraploid <i>arenosa</i> and allotetraploid <i>suecica</i>
11.50 – 12.10	Jane Charlesworth Do bacterial pathogens have smaller genomes than their non-pathogenic relatives?	Jitka Polechová Is the sky the limit? On the expansion threshold of a species' range	Peter Keightley Can you say which is the derived or ancestral allele at a polymorphic site?	Andrew Helmstetter Population genetics of wild and domesticated hazelnut (<i>Corylus avellana</i>) in Turkey
12.10 – 14.00	Lunch (Life Sciences Building)			
14.00 – 14.20	Tom Booker (S) Estimating the parameters of selective sweeps from patterns of diversity around functional elements in wild house mice	Maria Cuenca Cambronero (S) Evolution of thermal tolerance in multifarious environments over five decades of global change	Andrew Pomiankowski Sexual conflict explains the extraordinary diversity of mechanisms regulating mitochondrial inheritance	Hanja Pisa (S) The Pitfalls of Adaptation: the Better Niche

14.20 – 14.40	Leo Speidel (S) A method for estimating genome-wide genealogies for thousands of samples	Sheng-Kai Hsu (S) Sexually antagonistic gene expression evolution in <i>Drosophila simulans</i> populations adapting to a novel thermal environment	Homa Papoli Yazdi (S) A genetic map of ostrich Z chromosome allows for the inference of inversions in avian sex chromosome evolution	Levi Yant A genus-wide view of gene flow and selection in outcrossing <i>Arabidopsis</i> species
14.40 – 15.00	Josiah Seaman (S) Genome assembly and alignment using maps-style visualisation	Sian Bray A possible role in adaptation to low calcium serpentine soils by Two Pore Channel 1	Steven Van Belleghem Patterns of Z chromosome divergence among <i>Heliconius</i> species highlight the importance of accounting for demography	Joel Peck What is adaptation and should it be measured?
15.00 – 15.20	Kevin Dawson Using population genetic methods to infer the demographic parameters of an in vivo population of human stem cells from a combination of NGS data and single cell genomes	Joe Colgan Signatures of selection in a wild pollinator revealed through population genomics	Deborah Charlesworth Associations of SNPs with the sex-determining locus of the young guppy sex chromosome	Bruno Nevado Adaptive evolution during evolutionary radiation in plants
15.20 – 15.50	Coffee (Chemistry)			
15.50 – 16.10	Mechthild Lütge (S) Speciation events in functional co-occurrence networks across pan-genomes	Matthew Ackerman Quantitative genetics in structured populations	Jörg Bachmann (S) Genetic basis and timing of the transition to selfing in <i>Capsella orientalis</i>	Melanie Brien (S) Comparing the genetic basis of structural colour in <i>Heliconius</i> butterflies

16.10 – 16.30	Katharina Böndel Mutation accumulation in <i>Chlamydomonas</i>	Bonnie Fraser Genomic basis of convergent evolution in the Trinidadian guppy	Samuel Perini (S) The contribution of size and ecotype variation to sexual isolation in <i>Littorina saxatilis</i>	Hans Recknagel (S) Support for a reversal oviparity in <i>Zootoca vivipara</i> from genome-wide SNPs phylogenomics
16.30 – 16.50		James Buckley RAD-genotyping at multiple spatial scales in <i>Arabidopsis</i> <i>lyrata</i> reveals signatures of pathogen-mediated selection	Victor Soria-Carrasco Demographic patterns and processes in <i>Timema</i> stick insects	Kathryn Elmer Synteny and co-localization of ecologically relevant quantitative trait loci across salmonid species
17.00 – 18.00	Fisher Memorial Lecture Joe Felsenstein Is there a more fundamental theorem of natural selection?			
18.00 – 20.00	Posters & drinks reception (Life Sciences Building)			

Friday 5 th January				
Time	LT1	LT2	LT3	LT4
8.50 – 9.00	Welcome & information			
9.00 – 9.50	Plenary 2 Tracey Chapman Sexual conflict: mechanisms and emerging themes			
9.50 – 10.10	Kenneth Mather Prize Jessica King The evolution of phenotypic plasticity when environments fluctuate in time and space			
10.10 – 10.50	Coffee (Chemistry)			
10.50 – 11.10	Nick Priest Alcohol medicates against STIs: evidence that non-immunological costs are justified	Simon Segar Speciation in figs and their pollinating wasps along the slopes of a New Guinean mountain	Waldir Berbel-Filho (S) Is epigenetic variation related to genetic background in a selfing species?	Daniel Crouch The genetics of the human face

11.10 – 11.30	Joanna Hagen (S) The genetic and developmental basis of male genitalia evolution between <i>Drosophila</i> species	Emma Curran (S) Population genomics of parallel clines in iridescent structural colour in <i>Heliconius</i> butterflies	Kang-Wook Kim Spatio-temporal heterogeneity of transcriptome evolution in <i>Drosophila melanogaster</i>	Reto Burri Interpreting differential landscapes in the light of long-term linked selection
11.30 – 11.50	Filip Ruzicka (S) Sexual antagonism maintains genetic variation across the <i>Drosophila melanogaster</i> distribution range	Tom Hill Adaptation of baculoviruses and nudiviruses in <i>Drosophila</i> and other arthropods	Darren Parker Convergent gene expression changes across independent transitions to asexuality: insights from stick insects	Nick Barton Establishment in a new habitat by polygenic adaptation
11.50 – 12.10	Stuart Wigby Quantitative proteomics reveals seminal fluid plasticity in <i>Drosophila melanogaster</i>	Josie Paris Brown trout and toxic metals: adaptation to the legacy of Britain's mining history	Samuel Lewis The evolution of DNA methylation across non-insect arthropods	Susan Johnston Are individual recombination rates under selection in contemporary populations?
12.10 – 13.50	Lunch & Business Meeting (Life Sciences Building)			
13.50 – 14.40	Plenary 3 Katie Peichel Genetics of adaptation in sticklebacks: the roles of pleiotropy and linkage			
14.40 – 15.10	Coffee (Chemistry)			

15.10 – 15.30	Markus Möst The landscape of selection across major colour pattern loci in mimetic <i>Heliconius</i> butterflies	Clarissa Carvalho (S) Spatial epigenetic variation in <i>Timema cristinae</i> stick insects	James Horton (S) Evolutionary trade-offs and innovation in evolving gene regulatory networks	Falk Hildebrand SNP calling in metagenomic datasets
15.30 – 15.50	Hannes Becher (S) Targeted resequencing of hundreds of loci to detect genetic differentiation across a chromosomal hybrid zone in the grasshopper <i>Podisma pedestris</i>	Carlos Martinez Ruiz (S) Has social conflict led to selection for a social supergene and initiated the degeneration of a social chromosome?	Christian Schlötterer Evolution of gene expression in <i>Drosophila</i>	Petri Kemppainen Chromosome partitioning analyses and inference of genetic architecture (natural populations)
15.50 – 16.10	Sara Goodacre Arachnoglobina: Long-distance dispersal- gene flow and the potential for localised adaptation in linyphiid spiders	Lewis Spurgin Genome-wide association studies in natural populations: managing expectations and avoiding error	Agnieszka Lipinska Generation-biased gene expression in brown algae	Jerome Kelleher Inferring ARGs for million chromosomes
16.10 – 17.00	BBC Natural History Unit Q&A			
17.00 – 18.30	Posters & drinks reception (Life Sciences Building)			
19.00 – 01.00	Conference dinner & Ceilidh (MShed)			

Saturday 6 th January				
Time	LT1	LT2	LT3	LT4
8.50 – 9.00	Welcome & information			
9.00 – 9.50	<p>Plenary 4 Daven Presgraves The evolution, genetics, and consequences of species differences in meiotic recombination</p>			
9.50 – 10.30	Coffee (Chemistry)			
10.30 – 10.50	<p>Laurence Hurst Why recombine? Evidence against the hypothesis that gene conversion corrects mutations</p>	<p>Anja Marie Westram Understanding the genomic basis of parallel evolution using hybrid zone analysis</p>	<p>John Brookfield Expected dynamics of preference alleles in the context of cytoplasmic incompatibility</p>	<p>Matthew Hartfield Signatures of selective sweeps with arbitrary dominance and self-fertilisation</p>
10.50 – 11.10	<p>Simon Aeschbacher Distinguishing between primary and secondary gene flow based on pairwise sequence differences</p>	<p>Rui Faria Detection of chromosomal rearrangements in <i>Littorina saxatilis</i>: insights from a hybrid zone</p>	<p>Emma Berdan The population genomics of cuticular hydrocarbons in an inversion system</p>	<p>Konrad Lohse Modelling the genomic landscape of divergence and gene flow</p>

11.10 – 11.30	Mario dos Reis Population genetics of codon substitution	Hernan Morales Genomics of parallel ecotype local adaptation in <i>Littorina saxatilis</i>	Rodrigo Pracana The evolution of the social chromosome supergene across fire ant populations	Zhangyi He A numerical solution of Wright-Fisher SDE with application to transition probability density approximation"
11.30 – 11.50	Kai Zeng New methods for inferring the distribution of fitness effects for INDELs and SNPs	Sean Stankowski Patterns of genome-wide variation across temporal, spatial and ecological axes of the bush monkeyflower radiation	Diala Abu Awad Effects of partial selfing on the equilibrium genetic variance, mutation load and inbreeding depression under stabilising selection	Stuart Baird Compression population genomics
11.50 – 12.10	Adam Eyre-Walker Does evolution proceed by large or small steps at the molecular level	Mark McMullan The population genetics of the ash dieback invasion of Europe highlights huge adaptive potential of the causal fungus <i>Hymenoscyphus fraxineus</i>	Bram Kuijper Sexual conflict over phenotypic plasticity	Wolfram Moebius Range expansions in heterogeneous environments: population front perturbations and effect on genetic diversity
12.10 – 12.30	Brian Charlesworth Genetic load and heterosis in subdivided populations	Jamie Stevens Contrasting patterns of population structure, gene flow and connectivity in octocorals: implications for MPA designation	Elizabeth Duxbury The causes of genetic variation in susceptibility to infectious disease in natural populations	Anne Kupczok Homogeneous rates of molecular evolution in bacteriophage genomes over the decades
12.30 – 14.00	Lunch (Life Sciences Building)			