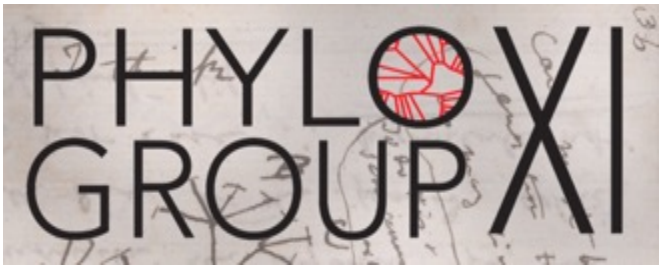

WHEN: Wednesday 28th March 2018

WHERE: Malet Place, Engineering Building UCL - Room 1.03, London, WC1E 6BT

SCHEDULE:

9.30 – 10.25	**Coffee & registration (room 1.04)**	
10.25 – 10.50	**Sandra Álvarez-Carretero** *Queen Mary University of London*	*Bayesian estimation of species divergence times using quantitative characters*
10.50 – 11.15	**Conor Walker** *European Bioinformatics Institute*	*Short template switch events explain mutation clusters in the human genome*
11:15 – 11.40	**Audrey Lin** *University of Oxford*	*Ancient DNA of domesticated animals*
11.40 – 12.05	**Benjamin Singer** *University of Oxford*	*Approaches to Phylogeographic Incompatibility under Recombination*
12.05 – 13.30	**Lunch break**	
13:30 – 13:55	**Massimo Maiolo** *Zurich University of Applied Sciences*	*Inferring Multiple Sequence Alignments with Explicit Model of Indel Evolution*
13.55 – 14.20	**Zachary Ardern** *Technical University of Munich*	*Phylogenetic evidence confirms ribosomal profiling data for overlapping genes in bacteria*
14.20 – 14.45	**Xiyun Jiao** *University College London*	*Mixing Efficiency of Trans-model Markov Chain Monte Carlo Algorithms in Bayesian Phylogenetics*
14.45 – 15.10	**Fabio Pardi** *LIRMM, University Montpellier*	*Rapid alignment-free phylogenetic placement via ancestral k-mers*
15.10 – 15.40	**Coffee (room 1.04)**	
15.40 – 16.05	**Tomas Flouris** *University College London*	*bpp-hpc: high-performance bayesian phylogenetics and phylogeography*
16.05 – 16.30	**Laura Kelly** *Queen Mary University of London*	*Phylogenomics of Fraxinus (ash trees) and analysis of molecular convergence*
16.30 – 16.55	**Nicola De Maio** *University of Oxford*	*BADTRIP: Bayesian Reconstruction of Transmission within Outbreaks using Genomic Variants*
16.55 – 17.20	**Guy Baele** *Rega Institute, KU Leuven*	*Adaptive MCMC for multi-partite data in Bayesian Phylogenetics*

Bayesian estimation of species divergence times using quantitative characters

Sandra Álvarez-Carretero[1], Anjali Goswami[2,3], Ziheng Yang[2] & Mario dos Reis[1]

[1]School of Biological and Chemical Sciences, Queen Mary University of London, E1 4NS, UK

[2]Department of Genetics, Evolution and Environment, University College London, WC1 6BT, UK

[3]Department of Life Sciences, The Natural History Museum, London SW7 5DB, UK

We have implemented a model of quantitative (continuous) character evolution for the estimation of species divergence times. We use the Brownian diffusion model of Felsenstein (1973) allowing for correlations among the characters. We show the results of computer simulations and the tests performed on a real data set of landmark measurements from carnivoran skulls.

Short template switch events explain mutation clusters in the human genome

Ari Loytynoja[1], Conor Walker[2] & Nick Goldman[2]

[1]Institute of Biotechnology, University of Helsinki, Helsinki, Finland

[2]European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, UK

We have detected a genome mutation mechanism that has previously been considered inconsequential. Systematic searches of human genomes indicate that it is widespread, accounting for a proportion of "complex mutations". These short regions with many differences between sequences are caused by individual template switch events rather than by a succession of point mutations. We consider the consequences for population resequencing projects and phylogenetics.

Ancient DNA of domesticated animals

Audrey T. Lin[1,2], Laurent Frantz[2,3], Simon Ho[4], Daniel G. Bradley[5], Ivica Medugorac[6], Joris Peters[7], Greger Larson[2]

[1]Department of Zoology, University of Oxford, New Radcliffe House, Woodstock Road, Oxford, OX2 6GG, United Kingdom
[2]Palaeogenomics & BioArchaeology Research Network, University of Oxford, Oxford, OX1 3TG, United Kingdom
[3]School of Biological and Chemical Sciences, Queen Mary University of London, Mile End Road, London E1 4NS, United Kingdom
[4]School of Life and Environmental Sciences, University of Sydney, Sydney, NSW 2006, Australia
[5]Smurfit Institute of Genetics, Trinity College Dublin, Dublin 2, Ireland
[6]Department of Veterinary Sciences, Ludwig-Maximilian University, Veterinaerstr. 13, 80539 Munich, Germany
[7]Institute of Palaeoanatomy, Domestication Research and the History of Veterinary Medicine, Ludwig-Maximilian University, D-80539 Munich, Germany

Canis lupus was the first animal to be domesticated by humans ~15,000 years ago, setting in motion the transition from foraging to farming. The development and expansion of agriculture allowed for further domestication and dispersal of livestock and companion animals.

Because of their short generation time and ubiquity in the archaeological record, domestic animals and their wild progenitors are used as a proxy to test the hypothesis of time-dependent molecular evolution. By comparing the directly-dated high-coverage mitochondrial genomes of archaeological samples, and performing analyses using molecular clock models, changes in the substitution rate across different timescales can be estimated.

Approaches to Phylogeographic Incompatibility under Recombination

Benjamin Singer[1], Luca Ferretti[2] & Jotun Hein[1]

[1]University of Oxford, [2]Pirbright Institute

Phylogeographic methods often ignore recombination. The evolutionary history of recombining genomes is better understood by taking into account multiple phylogenetic trees and comparing phylogeography across them. I will present a family of measures and methods to perform such comparisons, defining phylogeographic incompatibilities and distances in phylogeographic space.

Inferring Multiple Sequence Alignments with Explicit Model of Indel Evolution

Massimo Maiolo[1,2,4], Simone Ulzega[1,4], Xiaolei Zhang[3], Manuel Gil[1,4] & Maria Anisimova[1,4]

[1]Institute of Applied Simulation, School of Life Sciences and Facility Management, Zurich University of Applied Sciences (ZHAW), CH-8820 Waedenswil

[2]Institute of Molecular Life Sciences, University of Zurich, CH-8057 Zuerich, Switzerland

[3]National Heart and Lung Institute, Imperial College London, London SW7 2AZ, UK

[4] Swiss Institute of Bioinformatics (SIB), CH-1015 Lausanne, Switzerland

Since multiple sequence alignment (MSA) inference is inherently hard, state of the art aligners employ a progressive approximation. Lacking an explicit evolutionary indel model, these methods cause biased gap placement and evolutionary rate inferences. We present a frequentist progressive MSA method with the recently proposed Poisson Indel Process (PIP) by means of 3D dynamic programming. Compared to previous efforts (TKF models) the computational complexity is reduced from exponential to polynomial. Further, we improve our algorithm building upon MAFFT's idea of fast fourier transform (FFT) to detect homologous regions. This makes our method suitable for large-scale evolutionary analyses. The resulting alignments display phylogenetically meaningful gap patterns and are of similar length compared to PRANK. The presented developments open a number of novel avenues in the analysis of genomics sequences. In particular, it forms the core for proper joint MSA and phylogeny inference in the frequentist framework (through combinatorial optimization). Further, more realistic model features can be implemented allowing for variation of indel rates along sequences and over time.

Phylogenetic evidence confirms ribosomal profiling data for overlapping genes in bacteria

Zachary Ardern[1], Klaus Neuhaus[1] & Siegfried Scherer[1]

[1]Technical University of Munich

Evidence for significantly overlapping genes in bacteria is controversial. We explore some ways in which phylogenetic evidence can test the strength of such evidence from ribosomal profiling (a form of RNA sequencing) studies. We examine some putatively overlapping genes' phylogenetic distribution and sequence conservation in comparison to negative control sequences.

Mixing Efficiency of Trans-model Markov Chain Monte Carlo Algorithms in Bayesian Phylogenetics

Xiyun Jiao[1], Tomáš Flouris[1] & Ziheng Yang[1]

[1]Department of Genetics, Environment and Evolution, University College London, UK

We investigate the change of cross-model acceptance probability and efficiency of trans-model MCMC used in Bayesian phylogenetics with different proposal distributions, and we aim to improve the mixing properties of these algorithms by deploying more efficient proposals. Both toy and phylogenetic examples are used for illustration.

Rapid alignment-free phylogenetic placement via ancestral k-mers

Benjamin Linard[1] & Fabio Pardi[1]

[1]LIRMM, University Montpellier, CNRS, Montpellier, France

The most informative way to classify sequences in metagenomics is phylogenetic placement, which entails aligning the query sequence to a reference alignment and seeking its maximum likelihood position in the reference tree. We describe a novel, fast alignment-free approach for phylogenetic placement, based on the precomputation of a table of k-mers present with non-negligible probability in any relative of the reference sequences. The placement is performed by inspecting the stored phylogenetic origins of the k-mers in the query, and their probabilities. The table can be reused for the analysis of several different metagenomes. Experiments show that our software is faster and nearly as accurate as maximum likelihood approaches.

bpp-hpc: high-performance bayesian phylogenetics and phylogeography

Tomáš Flouris[1], Xiyun Jiao[1], Bruce Rannala[2], Ziheng Yang[1]

[1]Department of Genetics, Environment and Evolution, University College London, UK

[2]Department of Evolution and Ecology, UC Davis, USA

We present bpp-hpc – a Bayesian MCMC program for analyzing DNA sequence alignments under the multispecies coalescent model. Compared to traditional phylogenetic analysis, which assumes the same tree underlies all gene loci, the MSC accounts for the coalescent process in both modern and ancestral species and the resultant gene tree-species tree conflicts. Apart from new MCMC proposals, we also discuss the computational challenges of extending BPP to work with distantly-related species by implementing the GTR substitution model and relaxed clock models with species tree branch rates.

Phylogenomics of *Fraxinus* (ash trees) and analysis of molecular convergence

Laura J Kelly[1], Steve Lee[2], Rob Sykes[2], Jennifer Koch[3], David Carey[3], John E Carlson[4], Stephen J Rossiter[1], William Crowther[1,5] & Richard JA Buggs[1,6]

[1]School of Biological and Chemical Sciences, Queen Mary University of London, Mile End Road, London E1 4NS, UK

[2]Forest Research, Northern Research Station, Roslin, Midlothian, EH25 9SY, UK

[3]U.S.D.A. Forest Service, Northern Research Station, Delaware, OH 43015, USA

[4]Department of Ecosystem Science and Management, Pennsylvania State University, University Park, PA 16802, USA

[5]Current address: School of Life Sciences, Gibbet Hill Campus, The University of Warwick, Coventry, CV4 7AL

[6]Jodrell Laboratory, RBG Kew, Richmond, TW9 3DS, UK

Fraxinus species (ash trees) face severe threats from an invasive beetle (emerald ash borer) in North America and an invasive fungal pathogen (causing ash dieback) in Europe. Using phylogenomic approaches and analysis of molecular convergence we are aiming to identify genes that are associated with low susceptibility to these threats.

BADTRIP: Bayesian Reconstruction of Transmission within Outbreaks using Genomic Variants

Nicola De Maio[1], Colin J Worby[2], Daniel J Wilson[1] & Nicole Stoesser[1]

[1]University of Oxford,[2]Princeton University

Within-host pathogen genomic variants can reveal linked cases within outbreaks, and direction and time of transmission, but also presents challenges. We propose a new Bayesian approach explicitly modeling within-host pathogen population evolution, transmission bottlenecks, and sequencing error, and using genomic and epidemiological data to infer transmission within outbreaks.

Adaptive MCMC for multi-partite data in Bayesian Phylogenetics

Guy Baele[1], Philippe Lemey[1], Andrew Rambaut[2,3] & Marc A. Suchard[4,5,6]

[1]Department of Microbiology and Immunology, Rega Institute, KU Leuven, Leuven, Belgium

[2]Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, UK

[3]Centre for Immunology, Infection and Evolution, University of Edinburgh, Ashworth Laboratories, King's Buildings, Edinburgh EH9 3JT, UK

[4]Department of Human Genetics, David Geffen School of Medicine, University of California, Los Angeles, CA 90095, USA

[5]Department of Biostatistics, School of Public Health, University of California, Los Angeles, CA 90095, USA

[6]Department of Biomathematics, David Geffen School of Medicine, University of California, Los Angeles, CA 90095, USA

Novel sequencing technology continues to deliver increasingly large molecular sequence data sets that are often heavily partitioned in order to accurately model the underlying evolutionary processes. We propose an MCMC approach using an adaptive multivariate transition kernel to estimate in parallel a large number of parameters, by exploiting multi-core processing.

Phylogroup XI

Wednesday, 28 March 2018 from 09:00 to 18:00 (CDT)
University College London - Room 1.03, Engineering Building - Malet Place - WC1E 6BT London - United Kingdom

Surname	First Name	Qty	Ticket Type	Payment Status
Álvarez-Carretero	Sandra	1	Registration	Free Order Order 40021321851-724642545
Anisimova	Maria	1	Registration	Free Order Order 40021321851-706523758
Ardern	Zachary	1	Registration	Free Order Order 40021321851-715718078
Baele	Guy	1	Registration	Free Order Order 40021321851-719250505
bai	fan	1	Registration	Free Order Order 40021321851-709264307
Bhatia	Sangeeta	1	Registration	Free Order Order 40021321851-730145556
Borges	Rui	1	Registration	Free Order Order 40021321851-719261690
Carruthers	Tom	1	Registration	Free Order Order 40021321851-717357246
Charlesworth	Jane	1	Registration	Free Order Order 40021321851-747794670
De Maio	Nicola	1	Registration	Free Order Order 40021321851-706403155
Donoghue	Philip	1	Registration	Free Order Order 40021321851-706825107
dos Reis	Mario	1	Registration	Free Order Order 40021321851-706142125
du Plessis	Louis	1	Registration	Free Order Order 40021321851-721701502
Eccleston	Ruth Charlotte	1	Registration	Free Order Order 40021321851-747935592
Escalera Zamudio	Marina	1	Registration	Free Order Order 40021321851-706401982
Ferretti	Luca	1	Registration	Free Order Order 40021321851-724084776
Gatti	Lorenzo	1	Registration	Free Order Order 40021321851-706400413
Gil	Manuel	1	Registration	Free Order Order 40021321851-746278227
Goldman	Nick	1	Registration	Free Order Order 40021321851-708204301
Goldstein	Richard	1	Registration	Free Order Order 40021321851-706351672
Gutierrez	Bernardo	1	Registration	Free Order Order 40021321851-732051700
Jackson	Raphaella	1	Registration	Free Order Order 40021321851-744556462
Jatoi	Hoorain	1	Registration	Free Order Order 40021321851-717632004
Jiao	Xiyun	1	Registration	Free Order Order 40021321851-720290661
Kelly	Laura	1	Registration	Free Order Order 40021321851-733050169
Knapp	Andrew	1	Registration	Free Order Order 40021321851-744546321

Phylogroup XI

	Surname	First Name	Qty	Ticket Type	Payment Status
☐	Kosiol	Carolin	1	Registration	Free Order Order 40021321851-719276187
☐	Lin	Audrey	1	Registration	Free Order Order 40021321851-723834500
☐	Maiolo	Massimo	1	Registration	Free Order Order 40021321851-706521283
☐	Massingham	Tim	1	Registration	Free Order Order 40021321851-743875843
☐	Metheringham	Carey	1	Registration	Free Order Order 40021321851-733709972
☐	Monit	Christopher	1	Registration	Free Order Order 40021321851-747933882
☐	Muffato	Matthieu	1	Registration	Free Order Order 40021321851-728171489
☐	Muñoz-Rodríguez	Pablo	1	Registration	Free Order Order 40021321851-717335502
☐	Nascimento	Fabricia	1	Registration	Free Order Order 40021321851-706394637
☐	Odushola	Omolara	1	Registration	Free Order Order 40021321851-710543474
☐	Odushola	Deborah	1	Registration	Free Order Order 40021321851-710543474
☐	Owen	George	1	Registration	Free Order Order 40021321851-714199730
☐	Pang	Juanita	1	Registration	Free Order Order 40021321851-714232705
☐	Paps	Jordi	1	Registration	Free Order Order 40021321851-706168723
☐	Pardi	Fabio	1	Registration	Free Order Order 40021321851-728121773
☐	Patricio	Mateus	1	Registration	Free Order Order 40021321851-728164078
☐	Perron	Umberto	1	Registration	Free Order Order 40021321851-708393145
☐	Plumb	Will	1	Registration	Free Order Order 40021321851-733088952
☐	Pokorny	Lisa	1	Registration	Free Order Order 40021321851-707927108
☐	Potter	Joshua	1	Registration	Free Order Order 40021321851-744677492
☐	Puri	Hasmeet	1	Registration	Free Order Order 40021321851-734294165
☐	Roy	Sunando	1	Registration	Free Order Order 40021321851-706356944
☐	Ruis	Chris	1	Registration	Free Order Order 40021321851-706367688
☐	Singer	Benjamin	1	Registration	Free Order Order 40021321851-724097985
☐	Tarday	Dee	1	Registration	Free Order Order 40021321851-749741405
☐	Thomas	Mark	1	Registration	Free Order Order 40021321851-746204934
☐	Thompson	Andris	1	Registration	Free Order Order 40021321851-724619926
☐	Venkatesh	Divya	1	Registration	Free Order Order 40021321851-706773116
☐	Walker	Conor	1	Registration	Free Order Order 40021321851-708211899

	Surname	First Name	Qty	Ticket Type	Payment Status
☐	Winstone	Helena	1	Registration	Free Order Order 40021321851-714200198
☐	Witney	Adam	1	Registration	Free Order Order 40021321851-706450877
☐	Zhang	Xiaolei	1	Registration	Free Order Order 40021321851-736912882
☐	Zile	Karina	1	Registration	Free Order Order 40021321851-707583348