2025 Mathematical and Statistical Aspects of Molecular Biology Annual Meeting Seminars – Monday and Tuesday, 8th and 9th September

Monday, 8th September – Day 1

9:00 – 10:00	Arrival / Coffee
10:00 – 10:10	Welcome talk

Day 1, Session 1 – Population Genomics
Chair: Ziheng Yang

10:10 – 10:40	Matteo Fumagalli *Detecting balancing selection using deep learning*
10:40 – 11:10	Ioanna Kotari *Merging evolutionary timescales to quantify adaptation*
11:10 – 11:40	Francisco Perez-Reche *ESPClust: A Method for Unsupervised Identification of Effect Modifiers in Omics Studies*
11:40 – 12:10	Hadi Khan *Lost Founders, Found Haplotypes: Reconstructing Parental Genomes from Offspring Sequencing Data*
12:10 – 13:30	Lunch break & Poster session

Day 1, Session 2 – Reticulate Evolution
Chair: Thomas Flouris

13:30 – 14:00	Diogo da Silva Ribeiro *Inferring gene flow from phylogenies with too many genomes*
14:00 – 14:30	Yuttapong Thawornwattana *TBA*
14:30 – 14:35	Menno de Jong *Concatenation in the anomaly zone*
14:35 – 14:40	Jiayi Ji *The Impact of Sequencing and Genotyping Errors on Bayesian Analysis of Genomic Data under the Multispecies Coalescent Model*
14:40 – 14:45	Wenjie Zhu *Polymorphism-Aware Phylogenetic Models (PoMo) for Species Delimitation*
14:45 – 15:15	Coffee break
15:15 – 15:25	AIBIO-UK

Day 1, Session 3 – Machine Learning Applications
Chair: Matteo Fumagalli

15:30 – 16:00   Bastien Boussau
Characterization of selective pressures acting on protein sites with Deep Learning

16:00 – 16:30   Luc Blassel
TBA

16:30 – 17:00   Pirita Paajanen
TBA

17:00 – 17:05   Giorgio Bianchini
AliFilter: a Machine Learning Approach to Alignment Filtering

17:05 – 17:10   Antonio Pacheco
Deep learning: Balancing, linkage and effects of selection (DEEPBLUES)

17:10 – 17:15   Philipp Schiffer
Hierarchical Patterns of Soil Biodiversity in Extreme Environments: Insights Across Biological Scales

18:00 – 20:00   MASAMB dinner / networking event

Tuesday, 9th September – Day 2

9:00 – 10:00   Arrival / Coffee

Day 2, Session 1 – Comparative & Evolutionary Genomics
Chair: Bastien Boussau

10:10 – 10:40   Claudia Weber
Unsupervised learning as a tool to retrieve genomes from undersampled taxa: Fast and slow evolution in myxozoans

10:40 – 11:10   Lia Obinu
Building a scalable bioinformatics strategy for sequencing historical fungal collections

11:10 – 11:40   Jeff Streicher
Quantifying structural variants in chromosomes using landmark-based disparity

11:40 – 11:45   Artemis Kotoula
TBA

11:45 – 11:50   Olivier Anoufa
Investigating contamination events in SARS-CoV-2 genome data

11:50 – 11:55   Magdalena Strauss
Advancing the classification of variants of uncertain significance: analysis frameworks for precision genome editing at the single cell level

| 11:55 – 12:00 | Miles Rowbottom |
| | *VI-guided NSGA-II: a novel Evolutionary Multi-Objective Optimisation Algorithm for Feature Selection for Single-cell Classification* |

12:00 – 13:00   Lunch break & Poster session

Day 2, Session 2 – Phylogenomics
Chair: Nick Goldman

| 13:00 – 13:30 | Rui Borges |
| | *Phylogenetic inference with not-so-rare mutations and wee tiny organisms* |

| 13:30 – 14:00 | Peter Foster |
| | *Modelling compositional and exchange rate changes over time* |

| 14:00 – 14:30 | Ana Serra Silva |
| | *Is the deuterostome clade real?* |

| 14:30 – 14:35 | Mattes Mrzik |
| | *Scalable phylogenetic inference with long indels* |

| 14:35 – 14:40 | Nathan Clark |
| | *Inferring niche shifts from phylogenies and species distributions* |

14:40 – 15:10   Coffee break

Day 2, Session 3 – Cancer Evolution & Genomics, and Others
Chair: Paul Kirk

| 15:10 – 15:40 | Nathaniel Mon Père |
| | *The dynamic fitness landscape of ageing haematopoiesis through clonal competition* |

| 15:40 – 16:10 | Elisa Scanu |
| | *Modelling the evolutionary dynamics of multiple extrachromosomal DNA types in cancer* |

| 16:10 – 16:40 | Julie Fendler |
| | *Dual clustering approaches for pathway discovery and risk stratification using longitudinal high-dimensional biomarker data* |

| 16:40 – 16:45 | Thomas Chen |
| | *Jointly Modelling RNA-Seq and Legacy Microarray Data for Improved Power in Biomarker Discovery* |

| 16:45 – 16:50 | Isabel Poetzsch |
| | *Dynamic Adaptive Sampling for Human Trio Sequencing* |

| 16:50 – 16:55 | Jeffrey Pullin |
| | *Flexible and efficient count-distribution and mixed-model methods for eQTL mapping with quasar* |

17:00 – 17:30   Closing