European Mathematical Genetics Meeting 2022
Thursday 21st & Friday 22nd April

Programme

Day 1 (Thursday 21st April)		
08:30	**Registration and Refreshments**	
09:00	**Welcome from Organising Chair:** Dr Jennifer Asimit, MRC Biostatistics Unit, University of Cambridge	
09:10	**Session 1: Characterising phenotypic sub-populations** Chair: Dr Chris Wallace, MRC Biostatistics Unit, University of Cambridge	
	Eleanor Sanderson, University of Bristol	*Estimation of causal effects of a time-varying exposure at multiple time points through multivariable Mendelian randomization*
	Sven Erik Ojavee, University of Lausanne	*Estimating age-specific effects for age-at-onset phenotypes*
	Vasileios Karageorgiou, University of Exeter	*Weak and pleiotropy robust Sex-stratified Mendelian Randomization in the one sample and two sample settings*
	Samvida Venkatesh, University of Oxford	*Genetic architecture of longitudinal obesity trajectories in primary care electronic health records*
10:30	**Refreshments Break**	
10:50	**Session 2: Population genetics and family-based analyses** Chair: Prof Antonis Antoniou, University of Cambridge	
	Daniel Malawsky, Wellcome Sanger Institute	*Consanguinity and disease in British Individuals with South Asian Ancestry*
	Trevor Cousins,	*Inference of ancestral population structure from*

	University of Cambridge	*a single diploid sequence*
	Cathal Ormond, Trinity College Dublin	*A Bayesian framework to model co-segregation in pedigrees using next-generation sequencing data*
	Heather Cordell, Newcastle University	*Quantifying the evidence for pathogenicity in the context of digenic inheritance with respect to a skeletal muscle myopathy phenotype*
12:10	**Lunch**	
13:00	**Virtual Networking via WonderMe (for in-person & virtual delegates)**	
13:40	**Session 3: Detecting and exploiting pleiotropy** Chair: Dr Elena Vigorito, MRC Biostatistics Unit, University of Cambridge	
	Ichcha Manipur, University of Cambridge	*CoPheScan: A Bayesian approach to PheWAS*
	Chiara Auwerx, University of Lausanne	*The individual and global impact of copy number variants on complex traits and common diseases*
	Feng Zhou, University of Cambridge	*Flashfm-ivis: interactive visualisation for fine-mapping of multiple quantitative traits*
	Oliver Pain, King's College London	*Using Local Genetic Correlation Improves Polygenic Score Prediction Across Traits*
15:00	**Refreshments Break**	
15:20	**Invited Talk: Prof Inês Barroso, University of Exeter** *The genomic architecture of glycaemic traits across multiple ancestries*	
16:30	**Poster Session 1 (in-person and virtual) with drinks**	
17:30	**Walk along backs of colleges in Cambridge**	
19:00	**Conference Dinner at Old Courts Main Hall, Gonville & Caius College**	

Day 2 (Friday 22nd April)		
08:30	**Registration and Refreshments**	
09:00	**Session 4: Bias and Technical Effects** Chair: Dr Hélène Ruffieux, MRC Biostatistics Unit, University of Cambridge	
	Ninon Mounier, University of Lausanne	*Bias correction for inverse variance weighting Mendelian randomization*
	Malthe S. Rasmussen, University of Copenhagen	*Improved Estimation of the Site Frequency Spectrum from Low-Depth Sequencing Data*
	Apostolos Gkatzionis, University of Bristol	*Using instruments for selection to adjust for selection bias in Mendelian randomization*
	Ashish Patel, University of Cambridge	*Conditional inference in cis-Mendelian randomization using weak genetic factors*
10:20	**Refreshments Break**	
10:40	**Session 5: Advancing genome-wide analysis** Chair: Dr Jennifer Asimit, MRC Biostatistics Unit, University of Cambridge	
	Daniel Crouch, University of Oxford	*Enhanced genetic analysis of type 1 diabetes by selecting variants on both effect size and significance, and by integration with autoimmune thyroid disease*
	Guillermo Reales, University of Cambridge	*Genetic feature engineering using blood cell traits to assess the differential genetic architecture of immune-mediated diseases*
	Erandee Robertson, Walter and Eliza Hall Institute of Medical Research	*A Hidden Markov Model to Identify Inherited Disease-Causing Variants Using Shared Genetic Markers*
	Takiy Berrandou, Aarhus University	*LDAK-GBAT - a powerful and efficient tool for gene-based analysis of GWAS data*
12:00	**Lunch**	
12:50	**Poster Session 2 (in-person and virtual)**	
13:50	**Session 6: Detecting disease mechanisms through multi-omics integration** Chair: Dr Paul Newcombe, AstraZeneca	

	Nikhil Milind, Wellcome Sanger Institute	*Multi-omics integration to characterise mechanisms of molecular QTL from a sepsis cohort*
	Alan O'Callaghan, University of Cambridge	*Optimising eQTL discovery with BaseQTL using a screening approach*
	Ralf Tambets, University of Tartu	*Using the central dogma to quantify the precision and recall of colocalisation methods*
	Kaido Lepik, University of Lausanne	*Assessing omics-based mediation of the impact of cardiometabolic risk factors on disease*
15:10	**Refreshments Break**	
15:30	**Invited Talk: Prof Vincent Plagnol, Genomics PLC** *The potential for genomics to empower a new prevention-first agenda for healthcare*	
16:40	**Awards**	
16:50	**Future EMGMs and Farewell**	

The European Mathematical Genetics Meeting (EMGM) 2022 is organised and hosted by the MRC Biostatistics Unit at the University of Cambridge, and is kindly sponsored by Genomics PLC.