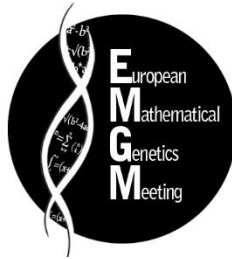


## European Mathematical Genetics Meeting 2022 Thursday 21<sup>st</sup> & Friday 22<sup>nd</sup> April



### Programme

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

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

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

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

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.