



54th European Mathematical Genetics Meeting: Programme

Tuesday 14 April

8.15 – 9.00	Registration
9.00 – 9.15	Welcome and introduction
9.15 – 11.00	Session 1 – Genome-wide association studies Chairs: Cristian Riccio and Heather Cordell <u>Invited speaker</u> : Timothy Frayling, <i>Using genomic structural equation models, genome-wide association study data and simple clinical measures to provide an improved metric of obesity</i> Jasper Hof, <i>Improving GWAS power by exploiting phenotype severity</i> Stefanie Muff, <i>Limitations and alternatives for genome-wide association studies (GWAS) for complex traits</i> Leonhard Kohleick, <i>Evaluating generalizability of causal gene prioritisation with biologically informed datasets</i> Poster highlights: Chia-Yi Chu, Carola Di Meo
11.00 – 11.15	Group photo
11.15 – 11.45	Coffee break
11.45 – 12.30	Session 2 – Fine-mapping Chairs: Adriaan van der Graaf and Ekaterina Maksimova Poster highlights: Rachael Harkness, Richard Howey, Ali Movasati Martin Tournaire, <i>Deconvoluting linkage disequilibrium to refine GWAS associations</i> Poster highlights: Cathal Ormond, Maria Pieczarka, Leyi Zhang
12.30 – 13.30	Lunch
13.30 – 15.00	Poster session
15.00 – 16.30	Session 3 – Rare variants Chairs: Nicholas Toda and Davide Greco <u>Invited speaker</u> : Joelle Mbatchou, <i>Using large language models for rare variant association testing in large-scale biobanks</i> Dominic Sayers, <i>Identifying shared genetic associations in fibrosis: a multi-organ rare variant analysis</i> Jack Murzynowski, <i>Rare variant burden tests in the Fenland cohort</i> Mihaela-Diana Zanoaga, <i>Inferring stabilising selection acting on protein levels using rare variant associations</i>
16.30 – 16.45	Plans for the 55th EMGM in 2027
19.00 – 20.45	Conference dinner , Restaurant STAU, Davos

Wednesday 15 April

9.00 – 10.45	<p>Session 4 – Mendelian randomisation and genetic epidemiology</p> <p>Chairs: Vivian Link and Adriaan van der Graaf</p> <p><u>Invited speaker:</u> Eleonora Porcu, <i>Omics and Mendelian randomisation: a journey into biological mechanisms</i></p> <p>Théo Cavinato, <i>Rare variant burden Mendelian randomisation provides orthogonal evidence for protein causal effects</i></p> <p>Tabea Schoeler, <i>Separating social influence from shared geographic environments in complex traits: a spatial Mendelian randomisation approach</i></p> <p>Koitmäe Merli, <i>Large-scale mapping of polygenic risk to disease phenotypes in the Estonian Biobank</i></p> <p>Wei-Yu Lin, <i>Genetic features that predict susceptibility to immune-mediated diseases also predict ability to control viral load of chronic infections</i></p>
10.45 – 11.15	<p>Coffee break</p>
11.15 – 12.30	<p>Session 5 – Pleiotropy and heritability</p> <p>Chairs: Amra Dhabalia Ashok and Sebastian Schönherr</p> <p>Anna O'Carroll (née Hutchinson), <i>A phenome-wide map of pleiotropy: connecting genetic signals to disease mechanisms and drug discovery</i></p> <p>Suzanne Leal, <i>Leveraging cis- and trans-variants to improve protein expression level prediction for proteome-wide association studies</i></p> <p>Leona Knüsel, <i>Decoding the genetic basis of nurture using untransmitted parental alleles</i></p> <p>Silvia Di Maio, <i>Integrating variable number tandem repeats into association and fine-mapping reduces missing heritability: a framework for lipoprotein(a)</i></p> <p>Ekaterina Maksimova, <i>Estimating the genetic basis of quantitative traits across populations</i></p>
12.30 – 13.30	<p>Lunch</p>
13.30 – 14.30	<p>Session 6 – Survival modelling and causal inference</p> <p>Chairs: Pascal Schlosser and Théo Cavinato</p> <p>Jakub Bajzik, <i>Improved biomarker selection and disease onset prediction in proteomics survival models via vector approximate message passing</i></p> <p>Jean-Josué Tokpo, <i>A comparison of the Cox mixed and Andersen-Gill models for the genome-wide analysis of recurrent events: malaria data and a set of simulated data</i></p> <p>Zulema Rodríguez Hernández, <i>PMCN: an R package for phenome-wide molecular causal inference network analysis at biobank scale</i></p> <p>Sydney Fleming, <i>18 Perturb-seq experiments as a source of causality orthogonal to genetic methods</i></p>
14.30 – 15.00	<p>Coffee break</p>
15.00 – 16.30	<p>Session 7 – Multi-omics</p> <p>Chairs: Andreas Ziegler and Silvia Di Maio</p> <p><u>Invited speaker:</u> Marylyn Ritchie, <i>Too many omics? There's an app (algorithm) for that</i></p> <p>Takiy-Eddine Berrandou, <i>Multi-trait, gene-based and multi-omics integration broadens spontaneous coronary artery dissection biology and prioritises arterial-wall pathways for follow-up</i></p> <p>Maarja Jõeloo, <i>Integration of metabolome-wide CNV-GWAS and PacBio long-read sequencing uncovers a complex, high-impact protective LDLR multiplication</i></p> <p>Mario Favre-Moiron, <i>Identifying sub-threshold trans-pQTLs via data-driven protein clustering using rank-rank hypergeometric overlap</i></p>
16.30 – 16.45	<p>Awards and closing</p>