54th European Mathematical Genetics Meeting: Programme

As of 9 March 2026

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 Invited speaker: Timothy Frayling, *Using genomic structural equation models, genome-wide association study data and simple clinical measures to provide an improved metric of obesity* Jasper Hof, *Improving GWAS power by exploiting phenotype severity* Stefanie Muff, *Limitations and alternatives for genome-wide association studies (GWAS) for complex traits* Leonhard Kohleick, *Evaluating generalizability of causal gene prioritisation with biologically informed datasets* Poster highlights: Ali Mosavati, Carola Di Meo, Cathal Ormond, Chia-Yi Chu
11.00 – 11.30	**Coffee break**
11.30 – 12.30	**Session 2 – Fine-mapping** Chairs: Adriaan van der Graaf and Ekaterina Maksimova Poster highlights: Dany Mukesha, Dominic Sayers, Leyi Zhang, Maria Pieczarka Jian Zeng, *Genome-wide fine-mapping improves identification of causal variants* Martin Tournaire, *Deconvoluting linkage disequilibrium to refine GWAS associations* Poster highlights: Mario Favre-Moiron, Rachael Harkness, Richard Howey
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 Invited speaker: Joelle Mbatchou, *Using large language models for rare variant association testing in large-scale biobanks* Mohamad Saad, *Rare variant analysis in a large consanguineous Middle Eastern cohort identifies novel genes for cardiometabolic traits* Jack Murzynowski, *Rare variant burden tests in the Fenland cohort* Mihaela-Diana Zanoaga, *Inferring stabilising selection acting on protein levels using rare variant associations*
16.30 – 16.45	**Plans for the 55th EMGM in 2027**
18.30 – 20.45	**Conference dinner**, Restaurant STAU, Davos

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Wednesday 15 April

9.00 – 10.45	**Session 4 – Mendelian randomisation and genetic epidemiology** Chairs: Vivian Link and Adriaan van der Graaf Invited speaker: Eleonora Porcu, *Omics and Mendelian randomisation: a journey into biological mechanisms* Théo Cavinato, *Rare variant burden Mendelian randomisation provides orthogonal evidence for protein causal effects* Tabea Schoeler, *Separating social influence from shared geographic environments in complex traits: a spatial Mendelian randomisation approach* Koitmäe Merli, *Large-scale mapping of polygenic risk to disease phenotypes in the Estonian Biobank* Wei-Yu Lin, *Genetic features that predict susceptibility to immune-mediated diseases also predict ability to control viral load of chronic infections*
10.45 – 11.15	**Coffee break**
11.15 – 12.30	**Session 5 – Pleiotropy and heritability** Chairs: Amra Dhabalia Ashok and Sebastian Schönherr Anna Hutchinson, *A phenome-wide map of pleiotropy: connecting genetic signals to disease mechanisms and drug discovery* Suzanne Leal, *Leveraging cis- and trans-variants to improve protein expression level prediction for proteome-wide association studies* Leona Knusel, *Decoding the genetic basis of nurture using untransmitted parental alleles* Silvia Di Maio, *Integrating variable number tandem repeats into association and fine-mapping reduces missing heritability: a framework for lipoprotein(a)* Ekaterina Maksimova, *Estimating the genetic basis of quantitative traits across populations*
12.30 – 13.30	**Lunch**
13.30 – 14.30	**Session 6 – Survival modelling and causal inference** Chairs: Aleksejs Sazonovs and Pascal Schlosser Jakub Bajzik, *Improved biomarker selection and disease onset prediction in proteomics survival models via vector approximate message passing* Jean-Josué Tokpo, *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* Zulema Rodríguez Hernández, *PMCN: an R package for phenome-wide molecular causal inference network analysis at biobank scale* Sydney Fleming, *18 Perturb-seq experiments as a source of causality orthogonal to genetic methods*
14.30 – 15.00	**Coffee break**
15.00 – 16.15	**Session 7 – Multi-omics** Chairs: Andreas Ziegler and Silvia Di Maio Invited speaker: Marylyn Ritchie, *Too many omics? There's an app (algorithm) for that* Takiy-Eddine Berrandou, *Multi-trait, gene-based and multi-omics integration broadens spontaneous coronary artery dissection biology and prioritises arterial-wall pathways for follow-up* Maarja Jõeloo, *Integration of metabolome-wide CNV-GWAS and PacBio long-read sequencing uncovers a complex, high-impact protective LDLR multiplication*
16.15 – 16.45	**Awards and closing**