EMGM BREST 2025 PROGRAM

TUESDAY 8th April	
8.00 - 8.45	**Registration**
8.45 - 9.00	**Welcome Introduction**
9.00 - 10.30	**Session 1 – Haplotype-based inference** **Chairs: Anthony Herzig and Heike Bickeböller** Invited speaker: Garrett Hellenthal, *Leveraging haplotype sharing patterns to infer overlapping admixture events among populations* Robin Hofmeister, *Parent-of-Origin inference and its role in the genetic architecture of complex traits: evidence from ~265,000 individuals* Yoann Seeleuthner, *Detection of mosaic uniparental disomy from whole-exome and whole-genome sequencing data of single patient* Sidonie Foulon, *Detecting rare recessive variants involved in multifactorial diseases: validation and power of the Fantasio method*
10.30 - 11.00	**Coffee Break**
11.00 - 12.00	**Session 2 – Complex Traits** **Chairs: Florian Privé and Mohamad Saad** Ana Luiza Arruda, *The effect of stratified type 2 diabetes genetic liability on non-cardiometabolic comorbidities* Merli Koitmäe, *Using Genomic Structural Equation-Based Polygenic Scores to Improve Type II Diabetes Management* Martin Tournaire, *PRISM: a pleiotropy-driven framework to disentangle the effects of genetic variants in complex traits* Margot Derouin, *Using multiomic integration to improve blood biomarkers of major depressive disorder: a case-control study*
12.00 - 12.30	**Poster Highlights** **Chair: Gaëlle Marenne** Matthieu Pluntz, Hanna Julienne, Sohane Aissa, Sebastian Sendel, Kelly Larissa Vomo-Donfack, Vidhi Vidhi
12.30 - 14.00	**Lunch**
14.00 - 15.15	**Session 3 – Ancient DNA** **Chairs: Aude Saint Pierre and Michael Nothnagel** Invited speaker: Céline Bon, *Using Ancient DNA to Unveil the Genetic Diversity of Neolithic Populations in the Paris Basin: Interactions Between Farmers and Hunter-Gatherers* Guillaume Laval, *Deep Bayesian estimation of the intensity and timing of selection from a thousand ancient genomes of East Eurasians* Christian Dina, *Integrating Temporal and Spatial Dimensions in Genetic Selection Analysis: A Comprehensive Approach to Detecting Positive Selection in Human Genomes*
15.15 - 16.30	**Posters & Coffee**
16.30 - 17.15	**Session 4 – Evolution and Selection** **Chairs: Amke Caliebe and Arthur Frouin** Ferdinando Insalata, *Mutational signatures of deterministic and noise-induced evolutionary mechanisms* Elise Lucotte, *Characterizing the evolution and phenotypic impact of ampliconic Y chromosome regions* Mihaela Diana Zanoaga, *Triangulating evidence to detect signatures of stabilizing selection acting on molecular traits in humans*
17.15 – 17.30	**Plans for the EMGM2026**
19.30 - 22.00	**Gala Dinner**, Ateliers des Capucins, Brest

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WEDNESDAY 9th April	
9.00 - 10.30	**Session 5 – Statistical Modelling and non-Human studies** **Chairs: Hervé Perdry and Emmanuelle Génin** Invited speaker: Beatriz C. D. Cuyabano, *The challenges of variance components estimation in the multi-omic era* Arthur Frouin, *ChoruMM: a versatile multi-components mixed model for bacterial-GWAS* Emil Pedersen, *A robust liability-scale R-squared* Louis Le Nezet, *Search of the genetic predisposition for Hip Dysplasia, using the dog model through leveraging One Health and Open Science*
10.30 - 11.00	**Coffee Break**
11.00 - 12.15	**Session 6 – Multi-Omics** **Chairs: Ozvan Bocher and Ana Luiza Arruda** Li Yiran, *Joint plasma pQTL analysis in the UK Biobank with efficient Bayesian inference* Adriaan Van Der Graaf, *Summary Statistic-Derived Metabolite Ratio QTL Analysis Identifies 427 Otherwise Missed Loci and Reveals Catalyzing Enzymes* Amandine Santini, *Epigenetic signatures in developmental disorders: can signature patterns disclose enriched information on phenotypes?* Raphaël Malak, *K-mer-based-genome-wide association studies of the gut microbiome* Mohamad Saad, *Integrating Multi-Omics and Machine Learning through Polygenic Risk Scores in Middle Eastern Populations for Cardiometabolic Traits*
12.15 - 13.30	**Lunch**
13.30 - 14.30	**Session 7 – Modelling ancestry** **Chairs: Christian Dina and Gaëlle Marenne** Fiona Pantring, *Characterisation of diverse global ancestries within participants of the UK Biobank* Florian Privé, *Improved ancestry and admixture detection using principal component analysis of genetic data* Maël Guivarch, *Comparing the performance of clustering methods to understand fine-scale genetic structure using simulated data* Siru Wang, *Multi-ancestry fine-mapping accounting for ancestral and environmental heterogeneity improves resolution*
14.30 - 15.15	**Posters & Coffee**
15.15 - 16.15	**Round-table panel discussion** **Chairs: Anthony Herzig and Hervé Perdry** 10 years on from the EMGM2015 in Brest: Headway, shift changes, atavism? Françoise Clerget-Darpoux Paul McKeigue Yves Moreau Amke Caliebe
16.15 - 16.45	**Closing remarks, Awards**