EMGM 2021

Thursday, 22 April

All times are Paris time, CEST / UTC+2. Last updated 20 April 2021 18:00

08:45	09:00	Welcome & VC instructions	
09:00	09:40	**Invited Speaker :** Ele Zeggini - The genomic aetiology of osteoarthritis	**Chair:** Emmanuelle Génin
		Long talk session 1 (4 talks 15min+5min questions) **GWAS AND IMPUTATION**	**Chair:** Jennifer Asimit and Doug Speed
09:40	10:00	L1 - Sahar GHASEMI - Assessment of significance of conditionally independent GWAS signals	
10:00	10:20	L2 - Anthony HERZIG - Can imputation in a European country be improved by local reference panels? The example of France	
10:20	10:40	L3 - Simone RUBINACCI - A systematic evaluation of low-coverage whole genome sequencing imputation across human populations	
10:40	11:00	L4 - Albert ROSENBERGER - I'am hiQ : A Novel Accuracy Index for Imputed Genotypes	

Break (30 min)

Short talks	Population Genetics		Association test and disease models	
	Chair : Anne-Louise Leutenegger and Céline Bellenguez		**Chair :** Hervé Perdry and Claire Dandine	
11:30	S1 - Fine scale population structure in France and its implications on whole-genome association tests	Ozvan Bocher	S7 - Flexible framework for gene-based association studies using GWAS summary statistics	Nadezhda Belonogova
11:35	S2 - Native American Ancestry, Genetic Susceptibility to critical Covid-19, and Covid-19 Case-Fatality Rates in Chile	Felix Boekstegers	S8 - A Binomial Regression Model For Genetic Association Mapping Combining Population-based And Family-based Designs	Saurabh Ghosh
11:40	S3 - Pigmentation prediction in admixed Latin Americans	Kaustubh Adhikari	S9 - Leveraging on gene interaction networks to explore digenic patterns of inheritance in rare diseases	Gaelle Marenne
11:45	S4 - Efficient multiple changepoint procedure for the detection of local signatures of selection	Tristan Mary-Huard	S10 - The effect of synaptic plasticity gene variants on working memory in mentally healthy individuals under gene-by-environment interactions	Anastasiya Kazantseva
11:50	S5 - Stabilization of cultural innovations depends on population density: the case of rock art	Anders Eriksson	S11 - Pgainsim: A method to assess the mode of inheritance for quantitative trait loci in genome-wide association studies	Nora Scherer
11:55	S6 - The Impact of Cross-Species Gene Flow on Species Tree Estimation	Xiyun Jiao	S12 - grmsem: R Package for Genetic Modelling	Mariska Barendse
12:00	12:30		Questions & Answers	

Lunch break (1h30)

14:00	14:40	**Invited Speaker :** Hugues Aschard - Multitrait analyses using GWAS summary statistics	**Chair:** Anne-Louise Leutenegger
		Long talk session 2 (4 talks 15min+5mn questions) **COMPLEX DISEASES**	**Chair:** Nabila Bouatia-Naji and Zoltan Kutalik
14:40	15:00	L5 - Liudmilla ZUDINA - Shared Genetic Susceptibility between Type 2 Diabetes and cancer	
15:00	15:20	L6 - Pradeep ERANTI - Identification of gene modules shared by childhood-onset asthma and Immunoglobulin-E levels by integrated network analysis of multi-omics data	
15:20	15:40	L7 - Catherine SCHRAMM - Penetrance estimation of SORL1 LOF variants using a family-based strategy adjusted on APOE genotypes suggests a non-monogenic inheritance	
15:40	16:00	L8 - Ariana LANDINI - Same role but different actors: genetic regulation of post-translational modification of two different proteins	

Break (30 min)

Short talks	Complex Traits Modeling		Bioinformatics	
	Chair : Emmanuelle Génin and Amke Caliebe		**Chair :** Hugues Roest Crollius and Ozvan Bocher	
16:30	S13 - SNP Fine-Mapping and Gene Prioritisation in the PGC3-Schizophrenia Study	Antonio Pardinas	S19 - Reconstructing KIR haplotypes taking ambiguous and missing data into account	Lars Van Der Burg
16:35	S14 - Probabilistic inference of genetic architecture, functional enrichment, and improved prediction of complex traits and common disease age-at-onset.	Matthew Robinson	S20 - COMET: an R package to identify sample cross-contamination in whole genome sequencing studies.	Alexandre Thiery
16:40	S15 - Assessing the impact of the non-Gaussian dependence structure in the REML estimation of the multivariate genetic model	Tom Rohmer	S21 - BactGWAS: a new R package to perform GWAS for bacteria	Fabien Laporte
16:45	S16 - Genetically independent phenotype analysis identifies LPA and VCAM1 as drug targets for human ageing	Paul Timmers	S22 - Enhanced SpliceMap and RNA-seq from clinically accessible tissues improves outlier prediction for non-accessible tissues	Nils Wagner
16:50	S17 - Large scale genomic data identifies common biological mechanisms of cardiometabolic traits	Yanina Timasheva	S23 - SNPs tagging structural variations help to reveal widespread role of CNVs in complex traits and gene expression	Maarja Lepamets
16:55	S18 - Increasing the Efficiency of SNP Haplotype Regional Heritability Mapping: joint mapping of common and rare variation affecting complex traits	Eilidh Fummey	S24 - Set-based testing of proteomic features with large portions of missing values - a bootstrapping approach with optimal data usage	Birgit Debrabant
17:00	17:30		Questions & Answers	

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Friday, 23 April

08:30	09:10	**Invited Speaker :** Catherine Bourgain - Genetic prediction in the clinic	**Chair**: Hervé Perdy	
		Long talk session 3 (4 talks 15min+5mn questions) GWAS AND PREDICTION	**Chair:** Heike Bickeboller and Nicola Pirastu	
09:10	09:30	L9 - Valentin HIVERT - Estimating non-additive genetic variation in human complex traits from a large sample of unrelated individuals		
09:30	09:50	L10 - Fanny MOLLANDIN - Evaluating the interpretability of SNP effect size classes in Bayesian genomic prediction models		
09:50	10:10	L11 - Saswati SAHA - A two-stage approach to identify high-order epistatic interactions - An application to cardiac ageing in Drosophila		
10:10	10:30	L12 - Françoise CLERGET-DARPOUX - Can disease risk prediction hold its promises		

Break (30 min)

Short talks	**Complex Traits**		**Beyond GWAS**	
	Chair: Edith Le Floch and Anthony Herzig		**Chair :** Gaëlle Marenne and Stefan Boehringer	
11:00	S25 - Genetic factors driving immune differences between monozygotic twins clinically discordant for multiple sclerosis	Marisol Herrera Rivero	S32 - Retro-prospective modelling of recurrent events	Gaëlle Munsch
11:05	S26 - Polygenic patterns of susceptibility to multiple sclerosis	Yanina Timasheva	S33 - A Genome-Wide Association Study of the Longitudinal Course of Executive Functions	Bernadette Wendel
11:10	S27 - Shared risk alleles with discordant polygenic effects: Disentangling the genetic overlap between ASD and ADHD	Ellen Verhoef	S34 - Advanced Bayesian meta-analysis methods for investigating pleiotropy effect	Pierre-Emmanuel Sugier
11:15	S28 - Polygenic analysis of the complex genetic markers of longevity	Vera Erdman	S35 - A benchmarking of univariate pleiotropy detection methods, with an application to epilepsy phenotypes.	Oluyomi Adesoji
11:20	S29 - PathWAS analysis sheds a new light on the biology of complex traits	Sebastian May-Wilson	S36 - Genetic validation of Heart Failure drug targets using Mendelian randomisation	Claire Baudier
11:25	S30 - Dissecting the shared genetics between type 2 diabetes and depression using a multi-phenotype GWAS approach	Jared Gichohi	S37 - Is systolic blood pressure a causal risk factor for intraocular pressure?: a Mendelian randomisation study.	Denis Plotnikov
11:30	S31 - Multi-trait analysis of multiple related cardiovascular traits identifies novel loci for fibromuscular dysplasia.	Takiy Berrandou	S38 - The singleton missense variant found in a rare adult-onset cancer- SDHB/SDHD as an exemplar for quantifying phenotypic specificity.	Chey Loveday
11:35	12:10		Questions & Answers	

Lunch break (1h20)

13:30	14:10	**Invited Speaker : Ernest Turro - Statistical approaches for identifying the genetic determinants of rare diseases**	**Chair :** Hugues Roest Crollius	
		Long talk session 4 (4 talks 15min+5mn questions) OMICS	**Chair :** Matthew Robinson and Florence Demenais	
14:10	14:30	L13 - Heike DEULTELMOSER - Robust Huber-LASSO improves prediction of protein, metabolite and gene expression levels from individual genotype data		
14:30	14:50	L14 - Franklin DELEHELLE - An assessment/comparison of ground truth datasets for the identification of non-coding variants using machine learning		
14:50	15:10	L15 - Eleonora PORCU - Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome		
15:10	15:30	L16 - Abel JANSMA - Complex gene regulation: higher-order interactions in single cell expression data		

Break (30 min)

Long talk session 5 (4 talks 15min+5mn questions) VARIOUS STATISTICAL & BIOINFORMATIC APPROACHES		**Chair :** Philippe Broët and Heather Cordell	
16:00	16:20	L17 - Ninon MOUNIER - Correction for sample overlap, Winner's curse and weak instruments bias in two-sample Mendelian Randomization	
16:20	16:40	L18 - Judith LAMBERT - Identifying association between genotypes and patient care trajectories using patients' networks	
16:40	17:00	L19 - Cathal ORMOND - Converting single nucleotide variants between genome builds: from cautionary tale to solution	
17:00	17:20	L20 - Pingzhao HU - Computational prediction of the pathogenic status of cancer-specific somatic variants	
17:20	17:40	**Discussion on next meeting venue - EMGM2022 & EMGM2023**	
17:40	18:00	**SFBI and SFGH Awards & Farewell**	