EUROPEAN MATHEMATICAL GENETICS MEETING 2015 - Brest, France

Thursday, April 16, 2015	
8:30-9:15	On-site registration and mounting of posters
9:15-9:30	Welcome
9:30-10:50	**SESSION 1 : Familial data**
9:30-9:50	**Suzanne Leal:** The collapsed haplotype pattern method for linkage analysis of next-generation sequencing data
9:50-10:10	**Stefan Böhringer** - Genotype imputation of family data
10:10-10:30	**Richard Howey** - Increased power for detection of parent-of-origin (imprinting) effects using haplotype estimation
10:30-10:50	**Renaud Tissier** - Secondary phenotype analysis in ascertained family designs: Application to the Leiden Longevity Study.
10:50-11:30	Coffee Break / Poster
11:30-12:30	**SESSION 2 : Interactions**
11:30-11:50	**Vitalia Schüller** - Extension of the One-Degree-Of-Freedom Test for Supra-Multiplicativity of SNP Effects in Logistic Regression Models
11:50-12:10	**Bathilde Ambroise** - Interactions analysis with covariates
12:10-12:30	**Christine Herold** - A Gene-Gene Interaction Meta-Analysis framework: Application to IGAP GWA studies
12:30-14:00	Lunch
14:00-16:00	**SESSION 3 : Population stratification and admixture**
14:00-14:20	**Dmitry Prokopenko** - Utilizing the Jaccard index to reveal population stratification in sequencing data: A simulation study and an application to the 1000 Genomes Project
14:20-14:40	**Marie-Claude Babron** - Population stratification in secondary genetic association studies
14:40-15:00	**Fabien Laporte** - Relatedness distribution estimation between individuals in multi-population panels
15:00-15:20	**Steven Gazal** - Estimating inbreeding in admixed population: application to the final phase of 1000 Genomes project
15:20-16:00	**Justo Lorenzo Bermejo** - Genetic Ancestry and Mortality in Chile
16:00-16:20	Coffee/Tea Break / Poster
16:20-17:40	**SESSION 4 : Fine mapping and causality inference**
16:20-16:40	**Holly Ainsworth** - Comparison of methods for inferring causal pathways between genotype and phenotype
16:40-17:00	**Anubha Mahajan** - Discovery and fine-mapping of EGFR susceptibility loci through trans-ethnic meta-analysis
17:00-17:20	**Iuliana Ionita-Laza** - Identification of disease risk genes in psychiatric diseases, using empirical Bayes models
17:20-17:40	**Warren Kretzschmar** - A predominantly European Haplotype Reference Panel of over 32,000 individuals

Friday, April 17, 2015
9:30-10:50 **SESSION 5 : Multi-phenotype analysis**
9:00-9:20   **Mariza Andrade** - Multivariate Phenotypes, Familial Data, and Pleiotropy
9:30-9:50   **Zitong Li** - Robust penalized regression for association mapping of multiple quantitative traits
9:50-10:10   **Saurabh Ghosh** - Allelic versus genotypic level tests for multivariate phenotypes
10:10-10:30   **Marika Kaakinen** - A novel method and software tool for genome-wide multi-phenotype analysis of rare variants
10:30-10:50   **Dragana Vuckovic** - MultiMeta: an R package for meta-analyzing multi-phenotype genome-wide association studies
10:50-11:30   Coffee Break / Poster
11:30-12:30 **SESSION 6 : Rare variants and association testing**
11:30-11:50   **Dmitriy Drichel** - Rare Variant Collapsing Test with Variable Binning
11:50-12:10   **Elodie Persyn** - A statistical association test for the identification of clustered disease risk variants.
12:10-12:30   **Pascal Roy** - Statistical method for Next Generation Sequencing pipeline comparisons
12:30-14:00   Lunch and Posters
11:30-12:30 **SESSION 7 : Longitudinal data analysis**
14:00-14:20   **Ben Francis** - Two-component mixture modelling approach integrating genetic and clinical variables in analysis of time to first seizure in epilepsy.
14:20-14:40   **Hamzah Syed** - Powerful methodology for the analysis of "time-to-event" data in pharmacogenetic studies.
14:40-15:00   **Jeanine Houwing-Duistermaat** - Statistical methods to analyze repeated measurements of overdispersed categorical data: an application in longitudinal microbiome data.
15:00-15:20   **Anne-Sophie Jannot** - Methodological considerations deriving from a PHeWAS and LaboWAS on UGT1A genotype
15:20-16:00   Prizes and Farewell with coffee / Tea
16:00-17:00 **SESSION 8 : Heritability and multi-marker analysis**
16:00-16:20   **Julian Hecker** - Heritability estimation from summary statistics using generalized estimating equations
16:20-16:40   **Claire Dandine-Roulland** - The impact of population stratification on genomic heritability estimation
16:40-17:00   **Wenjia Wang** - A Multi-Marker Genetic Association Test Based on the Rasch Model Provides New Insights into Genetics of Alzheimer's Disease