Università di Cagliari

Universität Heidelberg

European Mathematical Genetics Meeting 2018
Cagliari, Italy, April 18th to 20th

The event is sponsored by and organized under the auspices of the University of Cagliari

Conference Site	Università di Cagliari, Facoltà di Scienze Economiche, Giuridiche e Politiche Via Sant'Ignazio 76, Cagliari
Opening and Lectures	Room B0-A
Poster Area	next to Room B0-A
Course	Computer Room LISS-D

Organizing Committee

Francesco Cucca	Università di Sassari and Istituto di Ricerca Genetica e Biomedica at the National Research Counsil of Italy
Marcella Devoto	University of Pennsylvania and Università Sapienza di Roma
Christine Fischer	Universität Heidelberg
Justo Lorenzo Bermejo	Universität Heidelberg

Local Organizing Committee

Claudio Conversano	Università di Cagliari
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Wednesday 18th

8:30 – 9:00	**Registration**
9:00 - 14:00	**Preconference course "Introduction to population genetics"** Benjamin Peter (Leipzig), Christine Fischer, Justo Lorenzo Bermejo (Heidelberg)
16:30 - 17:00	**Conference Registration**
17:00	**Opening**
17:15-18:15	**Keynote lecture: Genetic Architecture of Sardinians** Francesco Cucca (Sassari)
19:00	**Welcome Reception**

Thursday 19th

9:00 - 10:30	***Population stratification and admixture,*** Chairs: Justo Lorenzo Bermejo, Hui Guo	
	Jonas Meisner	Inferring population structure and admixture proportions in low depth next-generation sequencing data
	Edmund Gilbert	Shared genetic ancestry of Scotland and Ireland reveals fine scale structure
	Heidi Hautakangas	Effect of reference panel in LD score regression analysis of lipid traits in the Finnish population
	Mart Kals	Population-specific imputation reference panel as a tool for GWAS analysis
	Regina Brinster	Optimal selection of genetic variants for adjustment of population stratification in European association studies
10:30 - 11:00	Coffee break	
11:00 - 12:30	***Results of association studies,*** Chairs: Inke König, Svetlana Cherlin	
	Peter K Joshi	The genomic basis of human lifespan
	Zoltán Kutalik	A joint analysis of adiposity genetics unravels subtypes with different metabolic implications
	Erin Macdonald-Dunlop	Genome-wide association analysis of 225 metabolites in isolated populations
	Marika Kaakinen	Genome-wide association study of 1,124 protein levels in pulmonary arterial hypertension patients identifies a novel trans-pQTL at ELK2AP for death receptor
	Eleonora Porcu	Mendelian randomization combining GWAS and eQTL data reveals new loci, extensive pleiotropy and genetic determinants of complex and clinical traits
12:30 - 14.00	Lunch and posters	Thursday poster authors are at their posters 13:15 - 14:00
14:00 - 15:30	***Autozygosity Polygenic Risk Scores, and more,*** Chairs: Michael Nothnagel, Peter Joshi	
	James F Wilson	Sex-specific inbreeding depression in humans
	Krista Fischer	Integration of polygenic risk estimates into personalized risk prediction algorithms – experience from the Estonian biobank
	Svetlana Cherlin	Prediction of treatment response from genome-wide SNP data in rheumatoid arthritis patients
	Sini Kerminen	Evaluating robustness and geographic differences in polygenic risk in Finland
	Amke Caliebe	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans
15:30 - 16:00	Coffee break	
16.00 - 17:20	***Methods for Pedigree Data,*** Chair: Marcella Devoto	
	Suzanne M. Leal	A rare variant nonparametric linkage method for nuclear and extended pedigrees with application to late onset Alzheimer's disease whole genome sequence
	Alexandra Lefebvre	An Elston-Stewart algorithm for computing exact derivatives of the likelihood in pedigrees
	Mohamad Saad	Comparison and assessment of family- and population-based genotype imputation methods in large pedigrees
	Renaud Tissier	Ascertainment corrections for secondary phenotypes analysis in family studies
17:20 - 17:30	Future EMGMs	
20:00	**Conference Dinner**	A'mare (c/o Il Lido), Viale Poetto 41 Cagliari

Friday 20th

9.00 - 10:50	***Multiple Phenotypes and Imputation,*** Chairs: Zoltan Kutalik, Marika Kaakinnen	
	Andrew T. DeWan	A comparison of univariate and multivariate GWAS methods for analysis of multiple dichotomous phenotypes
	Harmen Draisma	Multi-phenotype epigenome-wide association analysis of fasting glucose and insulin in 1,105 Finnish individuals
	James J. Fryett	Improving gene expression prediction accuracy in transcriptome-wide association studies
	Saurabh Ghosh	Association mapping of multivariate phenotypes in the presence of missing dataa
	Richard Howey	Imputation of missing data for Bayesian network analyses of complex biological data
	J. Asimit	A Bayesian joint fine mapping approach that shares information between related autoimmune diseases increases accuracy and identifies novel associations
10:50 - 11:20	Coffee break	
11:20 - 12:30	***Heritability***	Chair: Heike Bickeböller
	Arthur Frouin	Quantify genomic heritability through a prediction measure
	Anthony F. Herzig	What insights can be gained through comparisons of broad-sense heritability estimates in isolated and outbred populations?
	Nicola Pirastu	The exposural landscape of coronary artery disease gives new insight in its aetiology and missing heritability
	Xia Shen	High-definition likelihood inference for heritability and genetic correlation using GWAS summary statistics
12:30 - 14.00	Lunch and posters	Friday poster authors are at their posters 13:15 - 14:00
14:00 - 15:30	***Software, platform, and more,*** Chairs: Stefan Böhringer, Reedik Mägi	
	Emil Jørsboe	fastNGSadmix: Admixture proportions and principal component analysis of a single low-depth sequencing sample
	Iuliana Ionita-Laza	A semi-supervised approach for predicting cell type/tissue specific functional consequences of non-coding variation using massively parallel reporter assays
	Mauro Pala	3. The eQTLs Catalog and LinDA browser: a platform for determining the effects on transcription of GWAS variants
	Adam Waring	Beyond burden testing – association analysis of ultra-rare variants
	Hui Guo	Genetic causal pathways: Mendelian randomization, fine-mapping and colocalization
15:30 - 16:00	Coffee break	
16:00 - 17:30	***Statistical methods and modeling,*** Chairs: Heather Cordell, Eleonora Porcu	
	Märt Möls	A statistical method for alignment-free analysis of sequencing reads with applications in copy number determination and plasmid integration detection
	Stefan Böhringer	Exact model comparisons when determining parent-of-origin effects
	Zheng Ning	A selection operator for summary association statistics reveals allelic heterogeneity of complex traits
	Michael Nothnagel	Impact of pathway structures on allelic spectra of diseases
	Stephan Seifert	Combining surrogate variables and minimal depth variable importance
17:30	**Awards & Farewell**	

Poster discussion with authors: odd numbers on Thursday and even numbers on Friday; 13:15 - 14:00

1	David Almorza	Principal components analysis in the phenotypic selection of inbred lines
2	Mila D. Anasanti	Modern approaches to address missing data in multi-phenotype genome-wide association studies
3	Felix Boekstegers	Pleiotropic effects of genetic variants on gallstone disease and gallbladder cancer in Europeans and Chileans
4	Stefano Calza	Cell-specific somatic mutation detection from single-cell RNA-sequencing
5	Valentina Cipriani	An improved bioinformatics tool for rare disease variant prioritization: the Exomiser 9.0.1 in clinical practice
6	Claire Dandine-Roulland	Genome-wide data manipulation, association analysis and heritability estimates in R with GASTON 1.5
7	Mariza de Andrade	An efficient test for gene-environment interaction in generalized linear models with family data
8	Damian Gola	Classification of CAD status using machine learning approaches
9	Rosa González Silos	Allele counts: a good alternative for testing genetic association in next generation sequence data
10	Katherine A. Kentistou	Assessing novel anthropometric indices and their predictive efficacy over metabolic health and disease
11	Kristi Läll	Comparison of genetic risk scores in the Estonian biobank cohort
12	Maarja Lepamets	New quality measure for CNV: a multi-omics approach
13	Reedik Mägi	How well does parental genetic risk predict early menopause genetic risk in offspring?
14	Merli Mändul	A cluster-randomized trial on personalized feedback on genetic risks: effects on treatment compliance of patients with hypertension
15	Ninon Mounier	Bayesian genome-wide association study to discover novel lifespan-associated loci
16	Carlos Pinto	Comparison of the performance of polygene scores and artificial neural networks in the classification of disease status
17	Linda Repetto	Investigating pleiotropic architecture of plasma proteins using multivariate methods
18	Albert Rosenberger	Genetic modifiers of radon induced lung cancer risk - a genome-wide interaction study in former uranium miners
29	Sina Rüeger	Drugs for specific diseases tend to target genes whose expression is causally linked to those diseases
20	Sanni Ruotsalainen	Phenome wide scan of *ANGPTl*4 e40k mutation reveals new insights for future drug development
21	Kristina Schlicht	Genetic imbalance affects functional outcome after ischemic stroke
22	Gulnara Svishcheva	Region-based association analysis of summary statistics using principal components and functional linear regression models
23	Nele Taba	Empirically derived dietary patterns – characteristics, phenotypic background, and associations with NMR metabolites and health outcomes in the Estonian biobank cohort
24	Tõnis Tasa	External evaluation of population pharmacokinetic for vancomycin in neonates with DosOpt
25	Hande Topa	Searching for genetic variants matching a given multivariate target profile
26	Viola Tozzi	Coverage of the Oncoarray
27	Steffen Uebe	Combined CNV and SNP ancestry analysis
28	Maren Vens	Is the healthy migrant effect heritable? Population structure and demographic history of resettlers and the autochthone German population
29	Jonathan Sulc	Genetic subtypes of obesity and their impact on health