EARLY-CAREER RESEARCHERS CONFERENCE

QUANTITATIVE GENOMICS

14 June 2018

University College London (UCL)

PROGRAMME

09:00-09:30 Registration and Coffee

09:30-10:30 **Session 1: Complex traits, heritability and genetic association**

09:30-09:45	The genetics of the human face	Daniel Crouch
09:45-10:00	Estimating heritability without environmental bias	Alexander Young
10:00-10:15	From pixels to SNPs: adapting neural-networks from image classification to complex disease prediction	Martin Kelemen
10:15-10:20	Extracting stability increases the SNP heritability of emotional problems in young people	Rosa Cheesman
10:20-10:25	Exploring broad-sense heritability estimation in isolated and outbred populations	Anthony Francis Herzig
10:25-10:30	Impact of a fine-scale population structure on rare variant association tests	Elodie Persyn

10:30-11:30 Poster session and coffee

11:30-12:15 **Keynote talk 1**

Genomic and expression signatures of glycaemic traits

Dr Inês Barroso, Wellcome Sanger Institute

12:15-13:00 **Session 2: Methods**

12:15-12:30	Micro-exons: from discovery to quantitative analyses using RNA-seq data	Guillermo Parada
12:30-12:45	Pandora - lifting the lid on genetic variation discovery across the pan-genome using long or short reads	Rachel Colquhoun
12:45-13:00	Addressing the missing data issue in multi-phenotype genome-wide association studies	Mila Desi Anasanti

13:00-13:45 Lunch

13:45-14:30 **Keynote talk 2**

Mapping the genetic architecture of common human diseases from routine healthcare data

Professor Gil McVean, Nuffield Department of Medicine, Oxford Big Data Institute

14:30-15:05 **Session 3: Cancer**

14:30-14:45	The origins and vulnerabilities of two transmissible cancers in Tasmanian devils	Max Stammnitz
14:45-14:50	Somatic evolution of an ancient infectious cancer	Adrian Baez-Ortega
14:50-14:55	Palaeogenomics of an ancient transmissible tumour	Máire Ní Leathlobhair
14:55-15:00	Clonality analyses of structural variation reveals how rearrangements influence tumour development and progression	Ruben Drews
15:00-15:05	Mutational signatures as interplay between DNA damage and repair	Nadezda Volkova

15:05-15:30 Coffee break

15:30-16:25 **Session 4: Common and rare disease genetics**

15:30-15:45	Quantifying the contribution of recessive coding variation to developmental disorders	Hilary Martin
15:45-16:00	HLA-DQA1 Contributes to the Development of Antibodies to Anti-TNF Therapy in Crohn's Disease	Aleksejs Sazonovs

16:00-16:05	BDNF Val66Met and childhood adversity on response to physical exercise and internet-based cognitive behavioural therapy in depressed Swedish adults	Md Shafiqur Rahman
16:05-16:10	The Role of the Microbiome in Rheumatoid Arthritis	Philippa Wells
16:10-16:15	Bootstrapping allele specific expression signals from human brain demonstrates significant enrichment of risk loci for neurological disorders and splicing	Karishma D'sa
16:15-16:20	Genetic variation in the Major Histocompatibility Complex (MHC) and association with depression	Kylie Glanville
16:20-16:25	Genetic risk factors influence the severity of SLE in a quantitative not a qualitative manner	Lingyan Chen

16:25-16:45 Short break

16:45-17:40 **Session 5: Developmental and molecular genetics**

16:45-17:00	Prevalence, tissue-specificity and age-dependent heritability of skewed X-inactivation	Antonino Zito
17:00-17:15	Charting the diversification of mammalian cells at whole organism scale	Jonathan Griffiths
17:15-17:30	Regionalization of the nervous system requires axial allocation prior to neural lineage commitment	Sebastian Steinhauser
17:30-17:35	Evolutionary origins of taxonomically restricted genes in Drosophila genus	Karina Zile
17:35-17:40	Exploring the characteristics and functions of RNA duplexes bound in vivo by Staufen	Anob M. Chakrabarti