

How to get there

Schedule

Registration and coffee
Session I: Genetic and Epigenetic Variation
Poster session I and coffee break
Keynote talk: Prof Brian Charlesworth
Session II: Population Genomics and Adaptation
Lunch break
Keynote talk: Dr Nicole Soranzo
Session III: Gene Expression and Regulation
Poster session II and coffee break
Session IV: Disease Genomics and Complex Phenotypes
Post-conference drinks

Abstracts

Short and long talks
Posters

Participants Organisers

QG15 Conference Programme

■ Welcome to Quantitative Genomics 2015! ■

QG15 is a one-day event designed to bring together early-career researchers (Masters and PhD students) from around the world working at the forefront of mathematical and quantitative genomics. Students will present their work and discuss the hottest topics in the field in an informal environment to encourage the building of lasting networks.

The day will involve four sessions comprised of 15 or 5 minute student talks, keynote talks by Dr. Nicole Soranzo and Prof Brian Charlesworth, as well as two poster sessions. It will conclude with an informal drinks reception at a nearby pub.

The topics include mathematical, statistical, bioinformatic and computational approaches to population, evolutionary, quantitative and disease genetics and to genomics generally. The specific sessions are driven entirely by the submitted abstracts.

The event is “open for tweeting”, and we encourage the use of the hashtag #quantgen15. If you are one of the speakers please indicate on your first slide whether you want your talk to be ‘tweetable’.

We would be delighted to hear feedback (good and bad!) throughout the day, or afterwards in our follow up questionnaire. We look forward to seeing you in London!

Best wishes,
The QG15 Organisers

Conference venue

The conference venue is the Wellcome Trust Headquarters at Euston square in London. The venue is conveniently located close to Tottenham Court Road and Euston Road. It is a great venue with event spaces offering modern facilities ideal for a conference.

Wellcome Trust Headquarter (Gibbs Building)
215 Euston Road
NW1 2BE

The Wellcome Trust Headquarters is located next to Euston Square station or a short walk from Warren Street or Euston station:

from Kings Cross: Circle/Hammersmith City line to Euston station

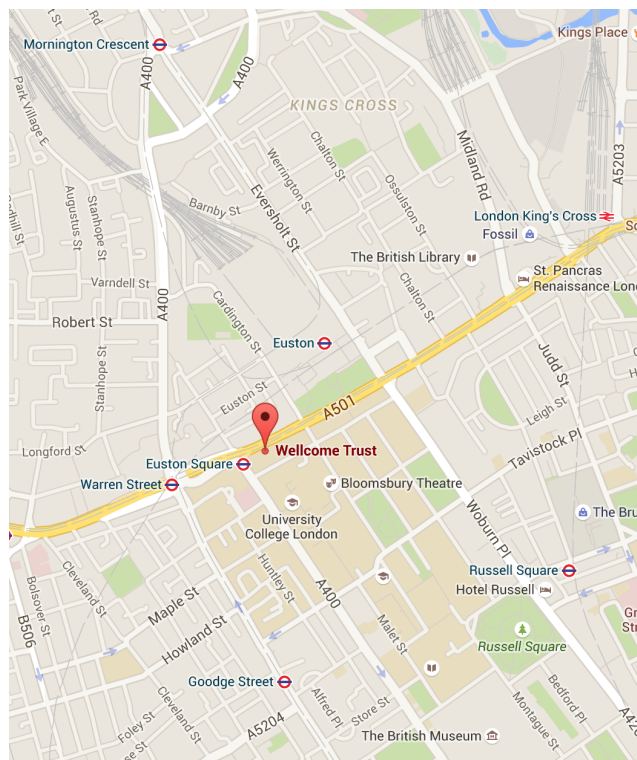
from Liverpool street: Circle/Hammersmith City line to Euston station

If you are travelling by bus, the stop outside the building (Euston Square Stop P) is served by the 10, 18, 30, 73, 205 and 390 bus routes. You can plan your journey on the [Transport for London website](#).

Evening reception venue

The drinks reception will take place at a nearby pub, the Prince Arthur Pub. It is conveniently located a few minutes away from the Wellcome Trust Headquarters:

Prince Arthur Pub
80-82 Eversholt Street
London NW1 1BX



09:00 – 09:30**Registration and coffee****09:30 – 10:30****Session I: Genetic and Epigenetic Variation**

Chair: Sarah Morgan

09:30-09:45 Erik Garrison (Wellcome Trust Sanger Institute, Hinxton, Cambridge UK):*Resequencing against a human whole genome variation graph***09:45-09:50** Patrick K. Albers (Wellcome Trust Centre for Human Genetics, University of Oxford, UK): *Shared haplotype estimation using rare variants to identify tracts of common ancestry***09:50-10:05** Victoria Hore (Department of Statistics, University of Oxford, UK):*Sparse Bayesian latent factor decompositions for identifying trans-eQTLs***10:05-10:10** Charles E. Breeze (UCL Cancer Institute, University College London, London, UK): *eFORGE: a tool for identifying tissue-specific signal in epigenetic data***10:10-10:25** Vagheesh Narasimhan (Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK):*Human Knockout Project - Impact and architecture of naturally-occurring gene knock-outs in parentally-related fit adult humans***10:25-10:30** Sarah Marzi (Institute of Psychiatry, Psychology and Neuroscience, King's College London, London, UK): *Methylomic variation in adolescents exposed to severe early-life adversity***10:30 – 11:15****Poster session I and coffee break****11:15 – 12:00****Keynote talk: Prof Brian Charlesworth****Title: "Recombination, genome organisation and molecular evolution in *Drosophila*"**

Prof Brian is an evolutionary geneticist at the University of Edinburgh. He is concerned with the application of classical and molecular genetics to the study of evolution and natural variation. His group carries out both theoretical and experimental research, using theoretical ideas to motivate the experiments, and experimental data as stimulant for the development of theory. His recent research has focussed on three main areas: molecular evolution and variation, the evolution of genetic and sexual systems, and the quantitative genetics of life-history traits. He is currently especially interested in the nature of the evolutionary process in genomes or genomic regions with low rates of genetic recombination, and he is using theoretical models and studies of DNA sequence evolution and variation to study this problem. He is also interested in the problem of estimating the extent and intensity of selection on non-synonymous, synonymous and non-coding mutations.

12:00 – 13:00**Session II: Population Genomics and Adaptation**

Chair: Moisés Expósito-Alonso

12:00-12:05 Marie Lopez (Institut Pasteur, Paris, France):*Assessing the impact of demography on selection and adaptation in humans***12:05-12:20** Hilary C. Martin (Wellcome Trust Centre for Human Genetics, University of Oxford, UK): *Insights into sex chromosome evolution from whole-genome sequencing of platypus***12:20-12:25** Tom R. Booker (Institute of Evolutionary Biology, University of Edinburgh, UK): *Simulating genome evolution in the house mouse: understanding the contribution of Hill-Robertson interference to patterns of genetic diversity*

12:25-12:40 Ignacio Vázquez-García (Wellcome Trust Sanger Institute, Dep. of Applied Mathematics and Theoretical Physics, University of Cambridge, UK): *Transient dynamics of selection and adaptation in heterogeneous populations*

12:40-12:55 Thomas C. Nelson (Institute of Ecology and Evolution, Eugene, OR, USA): *Standing genetic variation drives rapid adaptation of the threespine stickleback*

13:00 – 14:00

Lunch break

14:00 – 14:45

Keynote talk: Dr Nicole Soranzo

Title: "Next generation association studies of complex traits"

Dr Nicole Soranzo is a leading researcher within the fields of genetics at the Wellcome Trust Sanger Institute in Hinxton, Cambridge. She uses genetic analysis of high-dimensional phenotypic and genetic datasets to unravel genetic predisposition to quantitative traits that are risk factors for cardiometabolic diseases, principally coronary artery disease and type 2 diabetes. The aim of this research is to advance understanding of biologic processes underlying disease etiology addressing genetic and physiologic influences, and to explore the use of this genetic information in clinical care.

14:45 – 15:45

Session III: Gene Expression and Regulation

Chair: Kaur Alasoo

14:45-15:00 Emma Pierson (Department of Statistics and Wellcome Trust Centre for Human Genetics, Oxford, UK): *New Statistical Methods for scRNA-seq Data*

15:00-15:05 Mitra Barzine (European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, Cambridge, UK): *Integration of independent human RNA-seq datasets - a feasibility study*

15:05-15:20 Davis McCarthy (Wellcome Trust Centre for Human Genetics and Department of Statistics, Oxford, UK): *Identifying quiescent stem cells from single-cell RNA-seq data with 'scatter'*

15:20-15:25 Christof Angermüller (European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, Cambridge, UK): *Machine learning for the combined analysis of scBS-Seq and scRNA-Seq data*

15:25-15:40 Kieran Campbell (MRC Functional Genomics Unit, University of Oxford, UK): *High-resolution pseudotemporal ordering of single-cell gene expression profiles*

15:40-15:45 Malcolm Perry (MRC Clinical Sciences Centre, Imperial College, UK): *Inferring long-range regulation from chromatin data*

15:45-16:30

Poster session II and coffee break

16:30 – 17:30

Session IV: Disease Genomics and Complex Phenotypes

Chair: Hannah Meyer

16:30-16:35 D. Leland Taylor (National Human Genome Research Institute, Bethesda, MD, USA, EMBL-European Bioinformatics Institute, Hinxton, UK): *The genetic architecture of metabolic response in skeletal muscle expression*

16:35-16:50 Nicola Roberts (Wellcome Trust Sanger Institute, Hinxton, Cambridge, United Kingdom): *Deciphering mutational signatures in cancer with the hierarchical Dirichlet process*

- 16:50-16:55** Jonas Zierer (Dep. for Twin Research KCL, UK, Ins. of Bioinformatics Systems Biology Helmholtz Zentrum München, Germany): *Integration of Multi-Omics Data in Ageing Research*
- 16:55-17:10** Annique Claringbould (Imperial College London, UK): *Multi-phenotype analysis of cardiometabolic traits through usage of multivariate analytical methods*
- 17:10-17:15** James Liley (Juvenile Diabetes Research Foundation, Dep. of Medical Genetics, University of Cambridge, UK): *Approaches to disease heterogeneity in genomic analysis*
- 17:15-17:30** Siobhan Connolly (Trinity College Dublin, Ireland): *Assortative Mating in Autism Spectrum Disorders*

17:30 – late

Post-conference drinks

Name	Surname(s)	Affiliation(s)
Agathe	Jouet	Sainsbury Laboratory
Alexander	Neumann	Erasmus MC
Alexander	Young	Wellcome Trust Centre for Human Genetics, University of Oxford
Alice	Stanley	Wellcome Trust Sanger Institute, University of Cambridge
Anders	Bergström	Wellcome Trust Sanger Institute, University of Cambridge
Anna	Ramond	University of Cambridge
Annabel	Stokkermans	NA
Annique	Claringbould	Imperial College
Anthony	Payne	Wellcome Trust Centre for Human Genetics, University of Oxford
Avalos	Pacheco	University of Oxford
Casper	Lumby	University of Cambridge
Charles E.	Breeze	University College London
Christina	Wesse	University Osnabrück
Christof	Angermüller	EBI, University of Cambridge
Cian	Murphy	University College London
Craig	Glastonbury	King's College London
Daniah	Trabzuni	University College London
Daniel	Greene	University of Cambridge
Daniel	Kunz	University of Cambridge
Daniel P.	Temko	University College London
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Elena	Loizidou	Imperial College London
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Emma	Pierson	University of Oxford
Erik	Garrison	Wellcome Trust Sanger Institute, University of Cambridge
Filip	Ruzicka	University College London
Hilary	Martin	Wellcome Trust Centre for Human Genetics, University of Oxford
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Jacek	Marzec	Queen Mary University London
James	Liley	University of Cambridge
John	Lees	Wellcome Trust Sanger Institute, University of Cambridge
Jonas	Zierer	King's College London
Joseph G.W.	McCarter	National University of Ireland
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Katrina	de Lange	Wellcome Trust Sanger Institute, University of Cambridge
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Kieran	Campbell	University of Oxford
Kurzawa	Nils	University of Heidelberg
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Liam	Shaw	University College London
Lucy	Burkitt-Gray	University College Dublin
Malcolm	Perry	MRC Clinical Sciences Centre, Imperial College
Marie	Lopez	Institut Pasteur
Mark	Hill	University College London
Mary	Fortune	JDRF and WT Diabetes and Inflammation Laboratory, Cambridge

Name	Surname(s)	Affiliation(s)
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Sarah	Marzi	King's College London
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Suchen	Jin	University of Oxford
Thomas C.	Nelson	Institute of Ecology and Evolution
Tom	Booker	Institute of Evolutionary Biology, University of Edinburgh
Vagheesh	Narasimhan	Wellcome Trust Sanger Institute
Victoria	Hore	University of Oxford
Yunfeng	Ruan	Bio-X Institute, Shanghai Jiao Tong University

The conference is designed and led by students from the University of Cambridge, UCL, Max Planck Institute, University of Oxford and King's College London. We would appreciate your feedback and suggestions, so do come and talk to us during the conference or email us at quantgen@damtp.cam.ac.uk. The organising committee members are:

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