### THE CAMBRIDGE STATISTICS DISCUSSION GROUP

## Thursday 7th April 2016 7:15 for 7:45

The Large Seminar Room, Institute of Public Health, University Forvie Site, Robinson Way, Cambridge, CB2 0SR

# Genome-wide association studies: in search of common and low frequency variants in complex traits

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Abstract: Genome-wide association studies (GWAS) have transformed the field of complex trait genetics over the past 7 years. A number of scientific achievements made GWAS feasible, for example the availability of large sample sizes, better understanding of human genome sequence variation, high-throughput genotyping technologies, and the development of methodological and analytical approaches to analyze and interpret genetic data. Traditionally, GWAS have focused on common-frequency single nucleotide polymorphisms (SNPs) (minor allele frequency (MAF)  $\geq$  0.05) and have typically been powered to detect modest/small effect sizes. Genome-wide meta-analysis, facilitated by imputation of untyped genetic variants, has been used as a robust framework within which to synthesize data across studies and genotyping platforms, thus increasing power and leading to further novel discoveries. Although these findings have improved our understanding of the genetic basis of many complex traits, for most traits they explain only a fraction of genetic heritability. This observation supports the long established idea that low frequency and rare variants may play an important role in common diseases. This hypothesis has shifted the complex trait genetics field towards low frequency (MAF between 0.01 and 0.05) and rare variation (MAF less than 0.01). I will introduce key principles and analytical issues when conducting GWAS and discuss current and impending extensions in the field of complex disease genetics employing the next generation of chips, whole genome sequencing, and a wide array of populations.

**Speaker:** I graduated from the University of Thessaloniki in Greece with a BSc in Mathematics and gained an MSc in Statistics at University College London. I then undertook a PhD in Bioinformatics at Imperial College London, also gaining a MSc in Bioinformatics. I gained a PhD in Statistical Genetics in 2008 followed by a Career Development Fellowship at the MRC Biostatistics Unit in Cambridge. I have been a Statistical Geneticist at the WellcomeTrust Sanger Institute since 2011. My research is in the genetic etiology of common disease. Currently I am analyzing genome sequence data for metabolic related traits and developing statistical methodology and software for the discovery of disease susceptibility loci. Other research: fine-scale mapping, sequence studies and rare variants analysis, multivariate analysis of sequence data, Bayesian survival analysis, Bayesian inference and model selection.

**Directions:** (From Central Cambridge) Turn right off Hills Road into the Addenbrooke's site then turn left at the hospital roundabout onto Robinson Way. Follow Robinson Way until you see an access road on the left signed 'Forvie Site' (but note that the sign is on your right). Turn into the access road and follow signs - first to the Institute and then to the Large Seminar Room. There is ample car parking. The front doors will be locked at 7:45. Arrivals after 7:45pm can gain admittance by contacting the secretary on 07761769436.

#### **Provisional Next Meetings:**

28th April – Lisa Pennells (Department of Public Health and Primary Care);

11th October – Katrina Gore (Pfizer Neusentis)

21st November – Nick Galwey (GlaxoSmithKline) on 'Use of historical information to supplement a future study: opportunity and difficulty'.

2nd February 2017 – David Excell (Featurespace) on 'What can gambling machine data tell us about betting behaviour?'

Supper: Some members eat regularly in the University Centre before each meeting at 5-45pm. Feel free to join them.

**Subscriptions:** of 1 pound are now due for attending the 2015-2016 session.

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Slides and .mp3 files of old talks: http://www.mrc-cbu.cam.ac.uk/people/peter.watson/csdg.html