Course on Statistical Analysis of Genetic Association Studies

Course Overview
This four day course provides guidance on how to undertake the statistical analysis of a genetic association study, with particular focus on genome-wide association studies (GWAS). It provides an overview of the key statistical issues to be aware of when analysing genetic association studies, and an introduction to software for conducting the analyses. The course is structured to include a combination of short lectures and computer practicals to ensure that attendees gain hands-on experience of analysing genetic association datasets.

Who should attend?
The course is aimed at NHS professionals, PhD students and academic staff as well as individuals working elsewhere e.g. in industry with an interest in learning how to analyse genetic association studies. A prior understanding of basic statistical concepts would be an advantage (e.g. please see our week-long course ‘Statistical issues in the design and analysis of research projects’).

What does the course cover?
- Introduction to R
- Introduction to format of genetic data
- Candidate gene association studies
- GWAS
- Linkage disequilibrium
- Genotype quality control
- Population substructure
- Genotype imputation
- Introduction to software packages e.g. PLINK, SNPtest

The course will also include a seminar on ‘Progress in defining the genetic basis of type 2 diabetes susceptibility’ by Professor Andrew Morris, to reflect on real-life application of the theoretical concepts being taught. Andrew Morris is Professor of Statistical Genetics and Wellcome Trust Senior Fellow in Basic Biomedical Science in the Department of Biostatistics, University of Liverpool, UK. He also has visiting appointments at the Wellcome Trust Centre for Human Genetics, University of Oxford, UK, and the Estonian Genome Center, University of Tartu, Estonia. The primary theme of his research is the development, evaluation and application of methodology for the analysis of genome-wide association and re-sequencing studies of complex human phenotypes, with a focus on type 2 diabetes and related metabolic traits, blood pressure, kidney function, women’s benign health disorders, and response to pharmaceutical drugs. His most recent research has focussed on “fine-mapping” complex trait association signals by aggregating genetic data from diverse populations to localise likely causal variants and genes, and to improve understanding of the molecular mechanisms by which they impact human disease. He currently co-leads analytical groups in international efforts to further understanding of the genetic architecture and pathophysiology of type 2 diabetes as part of the DIAGRAM and DIAMANTE Consortia, which have led to identification of more than 100 loci robustly associated with the disease. Within these efforts, his research has demonstrated that genetic association signals for type 2 diabetes are shared across ethnicities, and that specific signatures of transcription factor binding in disease-relevant tissues (pancreas and liver) are likely markers of causal variants.