Investigating the genetic control of complex traits

One of the grand challenges of biology is to dissect the genetic control of the complex traits that underpin variation of medical, evolutionary and commercial relevance. Indeed, almost all traits of importance are complex and influenced by the actions and interactions of many genes and environmental factors.

The advent of high-density SNP genotyping arrays has made it possible to derive marker based estimates of relationships between individuals. No longer are pedigrees required to estimate basic genetic parameters such as the heritability (the proportion of variance that is genetic) or to predict genetic merit or risk. These estimated relationships have a vital role in the investigation of the genetic architecture of a trait and the detection of causal loci. It has become apparent, however, that naive estimation of relationships may lead to erroneous results impacting on our ability to disentangle the sources of variation.

The broad aim of this project is to investigate how SNP information should be used to estimate relationships between individuals for the purposes of heritability estimation and the understanding of the genetic control of traits. Possible areas for investigation include the sensitivity to the SNPs selected for analysis, how to combine information from multiple SNPs and the effect of including close relatives. Use will be made of the large, human, data sets becoming available.

This project will provide training and experience in key areas of genomics combined with statistics and computation whilst tackling one of the most exciting scientific challenges of the 21st century. A background in biology is not essential and any student with a strong mathematical or computational ability and an interest in biological systems is encouraged to apply. Additional training in genetics and genomics is available through our MSc programme in Quantitative Genetics and Genome Analysis (http://qgen.bio.ed.ac.uk).

Background references

Powell JE *et al.* (2010) Reconciling the analysis of IBD and IBS in complex trait studies. *Nature reviews Genetics* **11** (11) p. 800-5.

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Hemani G *et al*. (2013) An Evolutionary Perspective on Epistasis and the Missing Heritability. *PLOS Genetics* **9**: e1003295