

Genetic sensitivity to the environment

Supervisors: Sara Knott, Institute of Evolutionary Biology and Chris Haley, IGMM and Roslin Institute

One of the major 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. With dense SNP genotypes or sequence data we can dissect this variation and investigate how individual genes act and interact with the environment.

Although current analytical approaches have been successful in identifying genes involved in trait control, only a small proportion of the genetic variation in a trait is generally explained. One explanation is the ignorance of the effect of small scale environmental variation and interactions between this and the genotype. Definition and measurement of environmental factors relevant to particular traits is often challenging making classic models explicitly modelling the interaction between environment and genotype intractable and alternative approaches that reduce this requirement desirable.

This project will investigate and develop analytical approaches modelling genetic sensitivity to the environment to identify causative variants and understand how they contribute to the phenotype. One exciting prospect is to consider that the environment is determined by other, possibly related, individuals and investigate to what extent the genes of others, through their contribution to the environment, could affect an individual's phenotype.

This project will provide training and experience in key areas of genomics combined with statistics and computation (relevant to all species) whilst tackling one of the most exciting scientific challenges of the 21st century. The project is relevant to students with a background in statistics, informatics or computational sciences as well as those with training in quantitative or population genetics and related subjects and would suit a student with strong mathematical and/or computational abilities and an interest in biological systems. 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

- Thomas, D. (2010) Gene-environment-wide association studies: Emerging approaches. *Nature Reviews Genetics* **11**: 259-272.
- Powell, J.E. *et al.* (2011) Optimal use of regression models in genome-wide association studies. *Animal Genetics* **43**: 133-143
- Nagamine, Y. *et al.* (2012) Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. *PLoS ONE* 7(10): e46501.