We are awash with whole genome sequencing data from normal tissues and cells from a very wide variety of organisms from bacteria to humans. In addition, there are equally large sets of data derived from human clinical samples. We have learnt that sequence variation between individuals may be associated with differences in gene expression which in turn can lead to changes in phenotype and to disease. However, most of this variation is not currently interpretable because, apart from changes affecting the tiny fraction of the genome that codes for proteins, we do not understand the functional significance of most genome variation.

Our challenge is to distinguish functional from non-functional variants, and to understand how they cause changes in phenotype between individuals and throughout evolution. This meeting brings together scientists using genetics, genomics, computational, cell and developmental biology to discuss how to identify functional elements in the non-protein-coding portion (99%) of the genome and to determine how they affect gene expression. Such elements include distal regulatory elements driving spatial and temporal gene expression and non-coding RNAs. Speakers at the meeting will be chosen to draw on examples from multiple plant and animal species.

Confirmed Speakers
- Daniel Bauer, Harvard, USA
- Barak Cohen, Washington University of St Louis, USA
- Emma Farley, Princeton University, USA
- Anna Gloyn, Wellcome Trust Centre for Human Genetics, UK
- Nuria Lopez-Bigas, University Pompeu Fabra, Barcelona, Spain
- Javier Caceres, University of Edinburgh, UK
- Ben Neale, Broad Institute, USA
- Eric Miska, Gurdon Institute, University of Cambridge, UK
- Caroline Dean, John Innes Centre, UK

Scientific Organisers
- Wendy Bickmore, University of Edinburgh, UK
- Doug Higgs, University of Oxford, UK
- Chris Ponting, University of Edinburgh, UK
- Martin Taylor, University of Edinburgh, UK
- Richard Flavell, Ceres Inc, USA

Award Speakers
- Felicity Jones, Max Planck Institute, Germany (Balfour 2016)
- Duncan Odom, Cancer Research UK (Mary Lyon 2016)
- Ben Lehner, Center for Genomic Regulation, Spain (Balfour 2015)

for registration, visit www.genetics.org.uk