



The Bioinformatics of Mutant Mouse Resources: *A two-day hands-on introduction*

Training objectives

At the end of this training, participants will be able to find their favourite genes, understand their gene structures in detail, as well as the underlying experimental data supporting the annotation. They will gain basic understanding and usability of comparative genomics and be able to observe the synteny surrounding their regions of study. They will also be introduced to non-specialist data mining skills.

Participants will be able to find mutant mouse resources for their genes of interest using the IKMC (International Knockout Mouse Consortium) and similar resources. They will gain basic understanding of the different alleles available from various pipelines, identifying their strengths and weaknesses for different applications. They will be able to judge the quality of the KO strategies offered, draw their own vector maps and find key elements for the targeting strategy and genotyping.

Participants will be able to search IMPC (International Mouse Phenotype Consortium) phenotypic databases of IKMC mouse mutants such as EuroPhenome, gain an understanding of the high-throughput phenotype data generated and the statistical approaches required to analyse it. They will also be able to compare and interpret this data with other phenotype data sources and identify mouse models of relevance to their clinical domain of interest.

Program Overview :

Day 1 (26th June 2011) Genome Browsing and datamining

Overview of Mouse gene datasets available. How these are derived, reliability, completeness and biotypes. (WTSI and MGI)

An introduction to Ensembl Genome browser. Examining comparative genomics, variation and whole genome alignments (including hands on exercises). (EBI)

Datamining using Biomart: From GWAS data to mouse protein sequences and domains (EBI)

Day 2 (27th June 2011) Mutant mouse resources

IKMC resource overview: Partners and pipelines. Knock out strategies available: traps, deletion and conditional alleles. Visualising knockouts in the genome browsers, downloading and drawing vector maps (WTSI)

Making the most of EUCOMM resources: Modular tools for targeting mouse genes (WTSI)

Mining phenotype databases, to identify mouse models of clinical relevance: interpretation and statistical analysis of high throughput phenotypic data. (MRC-Harwell)

Each sessions will include detailed “hands on” exercises requiring each participant to bring his/her laptop to the workshop.