

iSEQ lunch seminar series

Wednesday 24 February 2016 at 12.00 – 13.00



Oliver Stegle

European Bioinformatics Institute (EMBL-EBI),
Wellcome Genome Campus,
Cambridge

Talk:

Statistical approaches to exploit high-dimensional phenotype data in association genetics.

Abstract:

The genetic analysis of correlated high-dimensional traits is hampered by a large multiple testing burden. In this talk, I will discuss different computational strategies to fully exploit large high-dimensional datasets, thereby testing for genetic effects that are shared across traits or are specific to some. In the first part of the talk I will outline how computationally efficient multi-variate linear mixed models can be used to identify genetic associations between genomic regions and multiple correlated traits. This approach scales to large cohorts with hundreds of thousand individuals and up to tens of traits, while simultaneously correcting for population structure and non-genetic sources of trait correlations. The presented method offers both power advantages as well as improved interpretation when dissecting genotype-environment interactions.

In the second part of the talk I will discuss approaches to map the determinants of gene expression levels and other molecular intermediates. These large-scale expression datasets are often compromised by hidden structure between samples. In the context of genetic association studies, this structure can be linked to differences between individuals, which can reflect their genetic makeup (such as population structure) or be traced back to environmental and technical factors. I will discuss statistical methods to reconstruct this structure from the observed data to account for it in genetic analyses. By incorporating principles from causal reasoning, we show how these methods can be extended to circumvent critical pitfalls of falsely explaining away true biological signals.

Venue:

Merete Barker Auditory, The Lakeside Theatres, Aarhus University, Bartholins Allé 3, 8000 Aarhus C.

Refreshments:

Sandwiches will be provided. Therefore, please email Anne Hedemand (anne@biomed.au.dk) no later than 22. February 2016, if you would like to participate.