



iSEQ lunch seminar series

Talk:

Towards schizophrenia genes and pathways based on hypothesis-free analysis of GWAS data.

Speaker:

Tune H. Pers, PhD, Broad Institute of Harvard and MIT.

Venue: Merete Barker Auditory, The Lakeside Theatres

Time: Friday 6 June 2014 at 12.00 – 13.00

Abstract:

I will describe an unpublished method called Data-driven Expression-Prioritized Integration for Complex Traits (DEPICT), which we recently developed and is aimed towards systematically prioritizing the most likely causal genes at trait-associated genetic loci, highlighting enriched pathways, and identifying tissues/cell types where genes from associated loci are highly expressed.

We have applied DEPICT to unpublished genome-wide association study (GWAS) data from the Psychiatric Genomics Consortium and highlight multiple pathways significantly enriched for associations. In particular, we highlight pathways related to the function of postsynaptic structures, including the postsynaptic density (at false discovery rates below 1%).

DEPICT is already being widely used to help interpret the findings of GWAS. We and our colleagues have successfully used DEPICT to gain new biological insights in multiple GWAS for anthropometric traits (Locke et al., under revision in *Nature*, Shungin et al, under revision in *Nature* and Wood et al, under revision in *Nature Genetics*), and hypospadias (Geller et al., under revision in *Nature Genetics*).

Refreshments:

Sandwiches will be provided.

Therefore, please email Anne Hedemand (anneh@hum-gen.au.dk) no later than 4 June 2014, if you would like to participate.