



iSEQ lunch seminar series

Talk:

De Novo Full-Length Transcriptome Analysis by a Hybrid Sequencing Approach

Speaker:

Dr. Wei Chen, Berlin Institute for Medical Systems Biology, Max-Delbrück-Center for Molecular Medicine

Venue: Merete Barker Auditory, The Lakeside Theatres

Time: 5 March 2014 at 12.00 – 13.00

Abstract:

I will present a hybrid sequencing approach based transcriptome analysis pipeline that reports high quality transcripts in their full length independent of reference genome sequences. Using full-length cDNA libraries in conjunction with Single Molecule Read-Time (SMRT) DNA sequencing technology, we can directly capture the full-length transcripts, but with low sequencing accuracy. To report high quality transcriptome, we then developed a novel computational tool, IPEC (Illumina Pacbio Error Correction), which utilizes the high quality Illumina sequencing data to correct the random errors generated in the SMRT sequencing. Our method can be widely applied in different organisms, especially those without genome reference sequences.

Refreshments:

Sandwiches will be provided.

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