Global regulation of gene expression

This lab is studying global aspects of gene regulation by combining genome-wide experimental and computational techniques. In particular, this lab is interested in deepening our understanding of mouse embryonic development through the generation of high-resolution data sets on the expression of transcripts isoforms and short RNAs.

Breakthroughs in genome sequencing techniques are now allowing the sequencing of complete transcriptomes in short time and in cost-effective manners. Using Solexa technology, it is now possible to obtain over 20 million short sequence reads from a single RNA preparation from a tissue or cell population. By analyzing where the sequence reads map to the genome and annotated protein and non-coding genes we can profile the complex transcriptome in an unbiased fashion and also ask novel questions about different levels of regulation that has never been possible before. In addition to finding genes with different expression levels (i.e. transcriptional regulation) this data can be used to identify post-transcriptional regulation e.g. generated by alternative splicing and poly(A) site regulation that regulates gene expression through developmental stages.

This is a very exciting area of research where general aspects of gene regulation can be discovered!

We are looking for students interested in studying gene regulation using global data sets generated within the lab together with public data.

Contact me by email (rickard.sandberg@ki.se) for more information and check the lab web page (http://web.mit.edu/~sandberg/www/sandberglab/) for more information.

Lämplig för:
Molekylär bioteknik och bioinformatik

Typ av projekt:
Examensarbete, 20 p

Typ av arbete:
Laborativt

Plats:
Institution

Rickard Sandberg
Group Leader,
Department of Cell and Molecular Biology (CMB)
Karolinska Institutet
SE-171 77 Stockholm
phone: +46-8-5248 3986
email: rickard.sandberg@ki.se