



## **iSEQ lunch seminar series**

**Talk:**

Bioinformatic approaches to study high-throughput data in novel ways.

**Speaker:**

Jan Gorodkin, PhD, Professor, Center for non-coding RNA in Technology and Health, IKVH.

**Venue:** Merete Barker Auditory, The Lakeside Theatres

**Time:** 1 October 2014 at 12.00 – 13.00

**Abstract:**

High-throughput technologies are generating data at an increasing speed in numerous aspects of biology. Here, I will present two approaches we have taken to analyze such data. In the first approach we have developed the tool RNAsnp to detect the impact of single nucleotide variation (SNV) on RNA structure and to apply it to SNVs in UTRs from a cancer data set. In the second approach the tool, deepblockalign, is applied to the detection of novel miRNAs in small RNAseq data through comparison of their profiles appearing from the mapping of reads to the genomic sequence. This type of comparisons was further used to discover differential and coherent processing profiles appearing from processing of small RNAseq data.

**Refreshments:**

Sandwiches will be provided. Therefore, please email Anne Hedemand ([anne@biomed.au.dk](mailto:anne@biomed.au.dk)) no later than 29 September 2014, if you would like to participate.