Titel:

Exploring transcript composition changes in RNA-seq data with the DTU-pipeline DTUrtle

Abstract:

The commonly used differential gene expression (DEG) analysis of RNA-seq data uses gene quantification counts to detect significant expression changes. Since the rise of fast and reliable transcriptomic quantifiers, these gene counts are often computed as the sum of the individual transcript counts of the genes transcripts. Complementary to the DEG-analysis proportional changes in the transcript composition of a gene would be of great interest for many research questions, such as analysis of differential splicing. These transcript composition changes can be quantified with a differential transcript usage (DTU) analysis.

This talk will gently introduce you to this topic and will show you some preliminary results of the upcoming DTU-pipeline DTUrtle.