

Titel:

Leveraging differential transcript usage analysis of (single-cell) RNA-seq data with DTUrtle

Abstract:

High throughput gene expression profiling via RNA-seq has been a major driver of biological insight in the last decade, recently boosted by the so called “single-cell revolution”. Most RNA-seq studies focus on gene level differences, although the measured data is inherently on transcript level. As a great amount of genes are expressed in different transcript isoforms, and these isoforms are major drivers of various genetic diseases, we propose to perform a differential transcript usage (DTU) analysis alongside a commonly used differential gene expression (DGE) analysis. By combining these two analyses, the potential of a RNA-seq data set is exploited more thoroughly.

In a DTU analysis, changes in a genes transcript composition are compared, i.e. changes of each transcripts contribution to the total gene expression. This talk presents DTUrtle, the first DTU calling and visualization pipeline for bulk and single-cell RNA-seq data. DTUrtle utilizes transcriptomic quantification results, which are also suitable for DGE analysis, and incorporates well with standard single-cell analysis toolkits like Seurat.