MSc thesis project: A model for statistical inference of gene expression changes in *in vivo* RNA labeling experiments

Background

Analysis of gene expression with methods of Next Generation Sequencing (https://en.wikipedia.org/wiki/RNA-Seq) is a key research tools in biomedical research and depends heavily on data science. Typical transcriptome sequencing data produces negative binominal-distributed gene counts [1]. However, more optimal models are required for newly developed methods, for example to account for data (multi)dimensionality or variables that cannot be empirically obtained from a biological system.

Required student background

MSc thesis project for a person keenly interested in applying statistical inference to big data in biomedical reasearch. Basic knowledge of biology and familiarity with transcriptome sequencing data (Next Generation Sequencing) will be an advantage, but is not required.

Research objectives

- Develop a statistical model for inferring gene expression changes from count data obtained using in *in vivo* RNA labeling experiments such as SLAM-seq (thiol (**SH**)-**l**inked **a**lkylation for the **m**etabolic **seq**uencing of RNA) [2,3].
- To improve inference in *in vivo* experiments, such as those perfomed using Tagger transgenic mouse line [4], different labeling kinetics models will be considered to account for changing label concentration (concentration of any drug in a biological system will change with time, except in cases when a steady state is reached). Other relevant literature, describing the current statistical frameworks used in similar kind of experiments, includes [5–7].

Short data description

- **Data type:** RNA (transcriptome) sequencing data and nucleotide (https://en.wikipedia.org/wiki/RNA) conversion rates (count data, see: https://kasperdanielhansen.github.io/genbioconductor/html/Count_Based_RNAseq.html)
- **Tentative data volume:** Approx. total volume of currently available data is 10^8 sequencing reads x 300 bases x 30 samples. For this project a subset of data may be used to reduce computation time. Also, if need be, it is possible to access an HPC cluster

Contact person

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References

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