AUSHANG

FREIE UNIVERSITÄT BERLIN

Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Freitag, 19. Oktober 2018, 15:30

Ort: Seminarraum 046
(Fachbereich Mathematik und Informatik, Takustr. 9, 14195 Berlin)

Disputation über die Doktorarbeit von

Frau Martina Fischer

Thema der Dissertation:

Computational Methods and Statistical Models for improving Quantification Accuracy of High-throughput Omics Data

Thema der Disputation:

Modeling quantification uncertainty in differential expression analysis

Die Arbeit wurde unter der Betreuung von **PD Dr. B. Renard** durchgeführt.

Abstract:
High-throughput sequencing technologies, such as DNA-Seq or RNA-Seq, provide quantitative outputs in the form of read count data. One main interest lies in comparing gene or transcript expression between different samples and conditions. Aim of most differential analysis studies is to identify significant and biologically relevant expression changes and separate them from technically and experimentally provoked changes. However, multiple sources within the quantification process, from sample preparation to sequencing and computational expression inference, cause bias in final quantitative estimates. The different arising variances lump together and contribute to an overall variance observed between samples. Thus, a crucial challenge for bioinformatics methods is to carefully quantify and decouple these variances to capture expression changes of interest. Many statistical models, such as LIMMA (Smyth 2004), DESeq (Anders & Huber 2010), and edgeR (Robinson & Smyth, 2008), have been developed for differential analysis, however mostly exclusively focus on modeling variances from sample replicates.

The disputation talk will address the diversity of variances in a high-throuput omics experiment impacting differential expression analysis. Focus of the presentation will be the recently published tool sleuth (Pimentel et al. 2017) with its new modeling strategy on decoupling variances for differential analysis of RNA-Seq data. Sleuth proves superior performance to existing approaches with further promising advances for isoform-specific differential analysis.

Die Disputation besteht aus dem o. g. Vortrag, danach der Vorstellung der Dissertation einschließlich jeweils anschließenden Aussprachen.

Interessierte werden hiermit herzlich eingeladen

Der Vorsitzende der Promotionskommission
PD Dr. B. Renard