AUSHANG

FREIE UNIVERSITÄT BERLIN
Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Freitag, 1. November 2019, 14:00 Uhr

Ort: Seminarraum II
(Max Planck Institute for Molecular Genetics, Ihnestr. 73, 14195 Berlin)

Disputation über die Doktorarbeit von

Frau Sabrina Verena Krakau

Thema der Dissertation:

Statistical models to capture protein-RNA interaction footprints from truncation-based CLIP-seq data

Thema der Disputation:

Detection of allele-specific protein-RNA interactions: recent advances and future perspectives

Die Arbeit wurde unter der Betreuung von **Prof. Dr. A. Marsico** durchgeführt.

Abstract: Genetic variants located in non-coding regions often affect post-transcriptional regulation, and can thus - just like their counterparts in protein-coding regions - cause a large range of different diseases or affect therapeutic responses. To understand the underlying disease causing pathways it is crucial to identify functional variants. Interactions between RNA and RNA-binding proteins (RBPs) play an important role in this context, as they can be disrupted by or newly arise from genetic variants. The analysis of allele-specific binding of an RBP using CLIP-seq data enables us to investigate the effect of such variants on protein binding under the same cellular and experimental conditions. Moreover, eCLIP datasets for already more than 150 different proteins are published by the ENCODE consortium and can be exploited for a large-scale analysis.

In my disputation talk I will introduce the main challenges in detecting allele-specific protein-RNA binding and present the recent advances in this field, with a focus on a method called BEAPR (Yang et al., 2019).

The core of BEAPR is based on an empirical Gaussian distribution to model the allelic mean count distributions, using a variance estimated based on a learned mean-variance relationship. This model will then be compared to edgeR (Robinson et al., 2010), a method widely used to detect differential expression based on read counts from RNA-seq data.

Lastly, another recently published method to detect allele-specific protein-RNA interactions called ASPRIN (Bahrami-Samani and Xing, 2019) and potential future improvements will be discussed.

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

Interessierte werden hiermit herzlich eingeladen

Die Vorsitzende der Promotionskommission
Prof. Dr. A. Marsico