

A U S H A N G

FREIE UNIVERSITÄT BERLIN

Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

D I S P U T A T I O N

Donnerstag, 22. April 2021, 14:00 Uhr

[WebEx](#)

Disputation über die Doktorarbeit von

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Thema der Dissertation:

**Genome-wide Determination Of Splicing Efficiency And Dynamics
From RNA-Seq Data**

Thema der Disputation:

**Intron-centric approach for identification and quantification of
alternative splicing events**

Die Arbeit wurde unter der Betreuung von **Prof. Dr. M. Vingron** durchgeführt.

Abstract: Eukaryotic genes are mostly composed of a series of exons intercalated by sequences with no coding potential called introns. These sequences are generally removed from primary transcripts to form mature RNA molecules in a post-transcriptional process called splicing. The alternative removal of introns and the combination of exons is central for many biological processes. This mechanism, called alternative splicing (AS), increases diversity between organisms, and it has been estimated that a range from 35% to as high as 95% of human pre-mRNAs undergo AS. Isoform variation and aberrant transcript processing can impact cell regulatory processes and even lead to disease. RNA-seq has become the main technology for studying these events. However, the accurate quantification of relative transcript abundances and AS events identification is statistically challenging due to RNA-seq limitation to place reads into overlapping genomic coordinates without ambiguity. The existing methods for splicing quantification fall basically into three categories: the isoform abundance estimation in which reads are probabilistically assigned to a known set of isoforms to estimate their abundances; the Percent Spliced In that applies the ratio of normalized read counts indicating the inclusion of an exon over the total normalized reads for that event; and the intron-centric approaches that aim to quantify intron usage rates rather than exons. In my talk, I will focus on an intron-centric approach for the identification and quantification of AS. It will cover: (i) an introduction to splicing and the commonly used approaches for studying AS from short-read RNA-seq data; (ii) an intron-centric suite of methods for identification and quantification of novel and known AS and differential AS events, and its underlying Dirichlet-multinomial generalized linear model; and (iii) the application of this method to identify differential AS among GTEx brain and heart tissues. The second talk will be dedicated to the contents of the dissertation.

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
Prof. Dr. M. Vingron