AUSHANG

FREIE UNIVERSITÄT BERLIN
Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Montag, 3. Juni 2013, 16.15 Uhr

Ort: Institut für Informatik, Takustr. 9, Raum 049, 14195 Berlin

Disputation über die Doktorarbeit von

Herrn Dipl.-Inf. David Weese

Thema der Dissertation:

Indices and Applications in High-Throughput Sequencing

Thema der Disputation:

Error-Correction Methods for High-Throughput Sequencing Data

Die Arbeit wurde unter der Betreuung von **Prof. Dr. K. Reinert** durchgeführt.

Abstract: High-throughput sequencing (HTS) technologies are revolutionizing genomics and systems biology by enabling high-coverage sequencing of whole genomes or transcriptomes at ever decreasing costs. Sequencing errors constitute one of the major problems in analyzing such data. Read error correction can have a large impact on the accuracy of genome assemblies and variation detection. In the last 4 years a dozen of reference-free error correction tools for the purpose of correction of DNA sequencing reads have been published.

In my presentation I will summarize the three major algorithmic techniques for reference-free error correction: the multiple read alignment, k-spectrum, and suffix tree based approach. I will further compare their assumptions, limitations, and performance on real data.

A data structure which is basis for many HTS applications, including all algorithms of my first talk, is the substring index. The second talk will cover the results of my PhD thesis in which I developed a generic substring index framework for HTS data and two applications utilizing it: a general approach for frequency based string mining and RazerS - a read mapper for full-sensitive alignment of sequenced reads to a reference genome.

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. K. Reinert