

A U S H A N G

FREIE UNIVERSITÄT BERLIN

Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Montag, 18. November 2019, 11:00 Uhr

Ort: Seminarraum T2 (1.4.03)
(Fachbereich Physik, Arnimallee 14, 14195 Berlin)

Disputation über die Doktorarbeit von

Frau Christine Jandrasits

Thema der Dissertation:

Computational Pan-genomics for Detection of Transmission Clusters in Molecular Surveillance with Application in the Epidemiology of Tuberculosis

Thema der Disputation:

Improved genomic analyses using sequence graphs

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

Abstract:

Genetics research is based on linear reference genomes and annotation of functional features and variations built on them. Increased use of next generation sequencing (NGS) technologies in genetics research and resequencing initiatives such as the 1000 Genomes Project [The 1000 Genomes Project Consortium] led to availability of vast amounts of genomic data. As it is the foundation of human genetics, including oncology and investigation of genetic diseases, the human genome is being constantly updated since its first assembly [Church et al. 2011]. Known variations are annotated in additional databases and recent versions of the human genome include additional "alternate locus" sequences for very diverse regions of the genome [Novak et al. 2019]. Nevertheless, in its linear form the human genome does not represent the diversity found in human populations and complex variations cannot be annotated easily.

The disputation talk will address concepts for representing several genomes or a linear genome with additional sequences and variations in one composite structure for joint analysis. Focus of the presentation will be variation graph (vg) [Garrison et al. 2019], a recently developed toolkit for composite analysis of all variation in a genome. Linear genomes at the scale of the human genome and their annotations are represented in a sequence graph that can be used for improved mapping based analysis of newly sequenced individuals.

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. B. Renard