AUSHANG

FREIE UNIVERSITÄT BERLIN
Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Montag, 10. Dezember 2018, 10:30

Ort: Max Planck Institute for Molecular Genetics,
Ihnestr. 73, Seminarraum One

Disputation über die Doktorarbeit von

Herrn Mohammadhossein Moeinzadeh

Thema der Dissertation:

De novo and haplotype assembly of polyploid genomes

Thema der Disputation:

Haplotype reconstruction for the human genome

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

Abstract:
The typical human cell has two sets of homologous chromosomes. The sequence of one chromosome is called a haplotype and haplotype information plays an important role in diverse contexts, such as disease association studies and population genetics. Computing haplotypes from sequencing reads is a challenging task. One strategy to achieve this is to reconstruct and assemble individual haplotypes from the mapping of reads to a reference genome. Sequencing technologies and protocols, such as PacBio, Nanopore, Hi-C and 10x genomics can be used for this purpose. Each technology has pros and cons in terms of read properties. In this presentation, I will present the computational problems and discuss a combinatorial approach to solve the haplotype reconstruction problem using reads from different sequencing platforms. The talk will be followed by a summary of my thesis entitled "*De novo* and haplotype assembly of polyploid genomes".

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