

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

Montag, 19. Mai 2014, 14.00 Uhr

Ort: Raum 006, Takustraße 9, 14195 Berlin

Disputation über die Doktorarbeit von

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**Thema der Dissertation:
Contributions to Computing and Modeling
Multiple Whole-Genome Alignments**

**Thema der Disputation:
The SWIFT algorithm:
Filtering for local similarity in biological sequences**

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

Abstract: One of the most fundamental tasks in the analysis of biological sequences is the search for similarity. The immense amount of sequence data that has become available within the last two decades makes this search a challenging task - highly efficient but nevertheless accurate approaches are sought.

In the first part, I will discuss the SWIFT filter algorithm [1], a very efficient q-gram counting algorithm for finding high similarity regions in long sequences. The algorithm stands out from other efficient similarity search approaches by providing a guarantee for full sensitivity. This guarantee is achieved through elaborate calculation of algorithm parameters. At the end of this part, I will touch on the counterintuitive effects that the parameter calculation has on the filtering performance.

In the second part, I will briefly summarize the general strategy for computing multiple whole-genome alignments and cover the main contributions of my thesis to three aspects of this field: local alignment, representation in graphs, and genome rearrangement.

[1] Rasmussen KR, Stoye J, Myers EW. Efficient q-gram filters for finding all ϵ -matches over a given length. *J Comput Biol* 13(2):296-308, 2006.

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