AUSHANG

FREIE UNIVERSITÄT BERLIN
Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Freitag, 15. Dezember 2017, 14.00 Uhr

Ort: Tower 3, Raum: SR I, Max-Planck-Institut für molekulare Genetik, Ihnestr. 63-73, 14195 Berlin

Disputation über die Doktorarbeit von

Herrn Matthew Robert Huska

Thema der Dissertation:

Using Machine Learning to Predict and Better Understand DNA Methylation and Genomic Enhancers

Thema der Disputation:

Kernel Methods and String Kernels for Computational Biology

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

Abstract: Methods from the field of machine learning have proven themselves to be invaluable to the modern computational biologist. In particular, "kernel methods" such as support vector machines are especially well suited to working with biological data which is not naturally represented numerically, such as DNA sequences or protein or gene networks.

The concept of adapting existing machine learning methods from using explicit features to using similarity measures, defined by functions called kernels, is presented. The advantages of being able to substitute different kernels depending on biological knowledge of the problem is also discussed, and several common string kernels are presented along with the motivation for using each of them on a specific biological problem. Lastly the impact the choice of kernel has on computational runtime and memory usage is highlighted.

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