

**A U S H A N G**

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**FREIE UNIVERSITÄT BERLIN**  
**Fachbereich Mathematik und Informatik**

Promotionsbüro, Arnimallee 14, 14195 Berlin

**D I S P U T A T I O N**

**Freitag, 20. Juli 2018, 10:00**

**Ort: SR 1 (Turm 3), MPI**

**Disputation über die Doktorarbeit von**

**Herrn Edgar Steiger**

**Thema der Dissertation:**

**Efficient Sparse-Group Bayesian Feature Selection for Gene Network Reconstruction**

**Thema der Disputation:**

**Gene Network Reconstruction with Frequentist Feature Selection Methods**

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

**Abstract:**

A gene regulatory network is a graphical model of the interplay between genes (respectively their proteins). For large networks with thousands of genes, the number of possible interactions or edges in the network is vast, while the actual number of true interactions is much smaller. This needs to be taken into account by methods which try to reconstruct gene networks from gene expression data. Under the general assumption of a Gaussian graphical model, this sparsity problems translates directly to the problem of estimating a sparse inverse covariance matrix or equivalently feature selection in regression. Here I will present and discuss the "neighborhood selection" approach by Meinshausen and Bühlmann (2006) and compare it to other alternatives. The talk will be followed by a summary of my PhD thesis entitled "Efficient Sparse-Group Bayesian Feature Selection for Gene Network Reconstruction".

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