

# 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

**Mittwoch, 17. Dezember 2014, 14.15 Uhr**

**Ort: Arnimallee 2 (Villa) Raum 01, 14195, Berlin**

**Disputation über die Doktorarbeit von**

**Herrn Jialu Hu**

**Thema der Dissertation:  
Algorithms to Identify  
Functional Orthologs And Functional Modules  
from High-Throughput Data**

**Thema der Disputation:  
Network Topology Strengthens Our Biological Knowledge**

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

Abstract: In the aspect of molecular medicine, the living system is regarded as a complex molecular network. All biochemical processes are connected as a whole network by molecular interactions. Highthroughput technologies enable us to screen all protein-protein interactions (PPI) of a cell in one test. The emerging challenge is to understand the function of the network components, answer the question about network evolution and how the network responds to diseases such as cancers. To come up with these problem, network alignment provides a promising framework to test hypotheses, identify functional orthologs and predict protein functions by using diverse high-throughput data.

This talk will be organized in two parts. In the first part, I will introduce a global network alignment algorithm IsoRank [1] and its improved version IsoRank-N [2] which integrate sequence information and network topology into one similarity measure. Incorporating network topology data in ortholog prediction results in improvements over existing sequence-only approaches and over predictions from local alignments of the yeast and fly networks. In the second part, I will briefly summerize the results and the contributions of my thesis.

[1] Rohit Singh, Jinbo Xu, and Bonnie Berger, Global alignment of multiple protein interaction networks with application to functional orthology detection PNAS 2008 105 (35) 12763-12768; published ahead of print August 25, 2008, doi:10.1073/pnas.0806627105

[2] Chung-Shou Liao, Kanghao Lu, Michael Baym, Rohit Singh, and Bonnie Berger. (2009) IsoRankN: Spectral methods for global alignment of multiple protein networks, Bioinformatics, 25:i253-i258

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