Universität Regensburg

FAKULTÄT
MEDIZIN
Institut für Funktionelle Genomik
Lehrstuhl für Statistische Bioinformatik

Regensburg Lectures in Medical Bioinformatics

"Model reduction and symbolic dynamics of biological and chemical networks using methods from tropical geometry"

Andreas Weber

Institut für Informatik
Professur für Bioinformatik
Universität Bonn

Introduction

Model reduction of bio-chemical networks relies on the knowledge of slow and fast variables. We provide a geometric method, based on the Newton polytope, to identify slow variables of a bio-chemical network with polynomial rate functions.
The gist of the method is the notion of tropical equilibration that provides approximate descriptions of slow invariant manifolds.
Compared to numerical algorithms such as the intrinsic low dimensional
manifold method, our approach is symbolic and utilizes orders of magnitude instead of precise values of the model parameters.
Application of this method to a large collection of biochemical network
models supports the idea that the number of dynamical variables in minimal models of cell physiology can be small, in spite of the large number of molecular regulatory actors.
Moreover, the the computed solution polytopes can be related to
metastable regimes allowing to describe the qualitative dynamics of chemical reactions

Wednesday, 02.05.2018, 5 p.m.

Seminarraum DE._0.133 (Westliche Naturwissenschaften, EG)

Host: Prof. Dr. Rainer Spang