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Computational modeling of biochemical networks

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Recent developments shift the traditional biological point of view from a reductionistic approach towards a systemic view on processes and cellular components. For long time, enormous effort was successfully put into the description of individual, isolated molecules or reaction pathways in molecular biology. The growing knowledge in this field of research leads to the questions of how all these elements interact, how the interplay of all components proceeds at a higher level. Computer models of biological processes that quantitatively predict the behavior of biological systems as a whole have therefore become an important area of research. However, the construction of these models is difficult, laborious, and highly error-prone. In this talk approaches will be discussed that lead from knowledge bases of biochemical reactions towards quantitative descriptions of these systems in terms of ordinary differential equation systems. Methods for efficient simulation and parameter estimation will be introduced and discussed. Finally, a new algorithm will be shown that incorporates thermodynamic constraints into the model and reduces the need for human interaction during the model building to a minimum.

Biography

Andreas Draeger grew up in Germany. In 1999 he finished his high-school diploma with honors and started his studies of bioinformatics at the Martin Luther University Halle-Wittenberg in 2000. He worked as an intern at the Max Planck Institute for Molecular Genetics, Berlin, in 2001 and at the University of Illinois at Chicago in 2004. After achieving his university diploma in 2006, he became a Ph.D. student in the group of Prof. Zell at the Center for Bioinformatics of the University of Tuebingen. During his Ph.D. time, he spent three month as a visiting research student at Keio University in Yokohama, Japan, in the group of Prof. Funahashi. After the successful defense of his Ph.D. thesis in 2011, Faculty of Science of the University of Tuebingen awarded his thesis as the most outstanding work of the year. In July 2013, he became a self-funded research scholar at the University of California, San Diego (UCSD) in the laboratory of Prof. Palsson with an NIH-funded graduate student and volunteers as an associate editor of the journal BMC Systems Biology.

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