

Invited Talk 1.4

PATHWAY MODELING IN METABOLIC NETWORKS

Stefan Schuster

Friedrich Schiller University of Jena, Germany

Abstract

The topological analysis of metabolic networks has attracted increasing interest in recent years in bioinformatics and systems biology. Dynamic mathematical modelling of large-scale metabolic and regulatory networks meets difficulties as the necessary mechanistic detail is rarely available. In contrast, structure-oriented methods such as metabolic pathway analysis only require network topology and information about the reversibility of reactions.

It is shown that the concept of elementary modes [1,2] is well-suited for determining routes enabling maximum yields of bioconversions and properly describes knockouts. Thus, it is well-suited for analysing redundancy and robustness properties of living cells [3,4]. The analysis is illustrated by several biochemical examples, such as the conversion of lipids into sugar [5].

Algorithms for computing these structural properties are outlined here as well. An earlier algorithm developed in our group is based on an algorithm for computing the edges of convex polyhedral cones [2]. Recently, an alternative algorithm based on the nullspace matrix to the stoichiometry matrix was proposed [6]. It empirically shows an even higher performance and has therefore been implemented in the program METATOOL [7].

1. S. Schuster, C. Hilgetag: On elementary flux modes in biochemical reaction systems at steady state. *J. Biol. Syst.* 2 (1994) 165-182.
2. S. Schuster, D.A. Fell, T. Dandekar: A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks. *Nature Biotechnol.* 18 (2000) 326-332.
3. J. Stelling, S. Klamt, K. Bettenbrock, S. Schuster, E.D. Gilles: Metabolic network structure determines key aspects of functionality and regulation. *Nature* 420 (2002) 190-193.
4. J. Behre, T. Wilhelm, A. von Kamp, E. Ruppin, S. Schuster: Structural robustness of metabolic networks with respect to multiple knockouts. *J. theor. Biol.* 252 (2008), 433-441.
5. S. Schuster, D.A. Fell: Modelling and simulating metabolic networks. In: *Bioinformatics: From Genomes to Therapies* (T. Lengauer, ed.), Vol. 2, Wiley-VCH, Weinheim 2007, pp. 755-805.
6. R. Urbanczik, C. Wagner: An improved algorithm for stoichiometric network analysis: theory and applications. *Bioinformatics* 21 (2005) 1203-1210.
7. A. von Kamp, S. Schuster: Metatool 5.0: fast and flexible elementary modes analysis. *Bioinformatics* 22 (2006) 1930-1931.

Biography

Since 2003, Stefan Schuster is head of the Chair of Bioinformatics in the School of Biology and Pharmacy at the University of Jena, Germany. He graduated from the Biophysics Department at Humboldt University in Berlin and received his PhD from the same department. He had post-doc positions at the University of Bordeaux II, with Professor Jean-Pierre Mazat, and at the Netherlands Cancer Institute, with Dr. Hans Westerhoff. From 1993-1997, he was a senior scientist and lecturer in Biophysics at Humboldt University, in the group of Reinhart Heinrich. From 1997-2003, he was a group leader at the Max Delbrück Center in Berlin and, in parallel, a reader at Humboldt University.

Professor Schuster's current projects include metabolic pathway analysis, the modelling of calcium oscillations, population dynamics of yeasts and bacteria studied from a game-theory perspective, and alternative splicing. An important scientific achievement is the development of the concept of elementary flux modes in metabolic networks and, thus, the promotion of structural approaches in that field.