Jost Neigenfind
Max-Planck Institute of molecular plant physiology, potsdam, germany
e-mail: Neigenfind@mpimp-golm.mpg.de
Zoran Nikoloski
Max-Planck Institute of molecular plant physiology and institute of biochemistry and biology, university of potsdam, potsdam, germany
e-mail: Nikoloski@mpimp-golm.mpg.de

Structural Sources of Robustness in Biochemical Reaction Networks Using a Simplified Analytical Method

Robustness is a property of a biological system which enables maintenance of systemic functionality in presence of external and internal perturbations. Here, we investigate the concept of robustness for the metabolite concentration profiles and its effects on the robustness of the system as a whole: Given a metabolic network operating in steady state, we are interested in characterizing and identifying those metabolites whose concentration assumes only one value under the given internal conditions (specified by the reaction rates). This concept has recently been termed absolute concentration robustness (ACR) [1], since the metabolite with such property has the same concentration in every positive steady state the system might admit. Note that a metabolic network in which some metabolites have the ACR property requires smaller extent of regulation to maintain a given steady state, rendering the entire system more robust. Moreover, Shinar and Feinberg have shown that metabolites endowed with ACR can be elegantly determined with the apparatus of the Chemical Reaction Network Theory (CRNT) [1].

Metabolic networks often show switching behavior related to multistationarity of metabolite concentrations [2]. Moreover, metabolic network states, characterized by the distribution of fluxes and metabolite concentrations, may exhibit intrinsic flux and concentration couplings. Therefore, for metabolic networks, the study of robustness should encompass the interplay between reaction fluxes and the resulting metabolite concentration profiles. To capture the interplay between multistationarity and couplings in the metabolic state, we generalize the concept of ACR to a family of robustness types for the concentration of metabolites. Unlike the CRNT-based approach, we present an analysis based on commutative algebra and algebraic geometry that helps to understand the qualitative properties of metabolic networks that included elements endowed with the proposed robustness types. The concepts are illustrated on paradigmatic network models as well as existing metabolic pathways.

References

[1] G. Shinar, M. Feinberg, *Structual sources of robustness in biochemical reaction networks* Science **327** 1389–1391.

[2] S. Grimbs, A. Arnold, A. Koseska, J. Kurths, J. Selbig, Z. Nikoloski, *Spatiotemporal dynamics of the Calvin cycle: Multistationarity and symmetry breaking instabilities* Biosystems **103** 212–223.