

Dynamical analysis and design of biochemical kinetic networks

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Abstract

Systems Biology is an emerging field that uses a global and integrative perspective to capture and understand the behavior of complex living organisms. The study of metabolic networks, the set of chemical processes and reactions occurring in a cell, represents nowadays a topic of intense interest in the scientific community, a fact which is a reflection of its expected impact on several areas such as biotechnology and medicine. The complete quantitative dynamic characterization of biochemical networks remains an open problem, due to their intrinsic non-linearity and high number of parameters to be inferred. A multidisciplinary approach, involving the optimal integration of mathematical formulation and experimental data, is especially promising. In particular, one major challenge is to estimate the parameters of the systems of non-linear differential equations that better adjust experimental multivariate time-series of metabolite concentrations. This step constitutes a bottleneck of the modeling procedure; due to the existence of local minima, there is no straightforward procedure that guarantees convergence to a unique, global solution. Other problems include the change of the network graph through gene mutations in order to maximize fluxes and optimize the production of desired products. Project DynaMo is a three-year project that will address some of these problems and will involve a multidisciplinary team with several partners and collaborations.

*Supported by project DynaMo (PTDC/EEA-ACR/69530/2006 - FCT, Portugal).