

## Biological network analysis tools using sum of squares

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Mathematical modeling is a key tool in Systems Biology. Modeling and analyzing biological networks presents a number of mathematical and computational challenges, as the models that are considered are usually complicated nonlinear differential equations with several time-scales and unknown parameters. In this talk, we discuss a number of issues related to biological network modeling and analysis. We first present a 3-stage iterative method to elucidate biological system structure, consisting of: (1) Development of various biochemical reaction network models that can explain wild-type experimental data; (2) Designing the “best” new experiment with the aim of differentiating between possible models; and (3) Invalidating some of these models, and proposing new ones for further study. The chemotaxis network in *R. sphaeroides* will be used as an example. Once an adequate model has been obtained, we then present mathematical and algorithmic tools to quantify its robustness - both the deterministic stability and performance in the presence of parametric uncertainties but also its stochastic behavior in the presence of noise. These tools are rooted in robust control and dynamical systems theory, but use recent developments in the theory of positive polynomials. At the same time, they have great practical promise and relevance, which we explore through a series of biologically meaningful examples.