Continuous and discrete time dynamics of regulatory networks

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Abstract

Regulatory networks in cell biology postulate monotonicity structure of interactions between genes and proteins, but not the specific forms of nonlinearities. What types of models are able to provide predictions and insights in this severely underdetermined situation?

Rather than examining individual solutions of particular ODE models, one is drawn to examination of coarse descriptors of dynamics that persist over large sets of parameters and are exhibited by a robust set of nonlinearities. At the same time, since the models of interest have at least 5-15 coupled nonlinear ODEs, these descriptors should be combinatorial, so they can be computed without the need for sampling of parameters or initial conditions.

We discuss one approach to this problem that is based on global approximation of the dynamics of ODE models by models with piece-wise constant functions. We discuss how such approximation yields a finite collection of models for each network, where each model is characterized by a multilevel discrete map which are closely related to monotone Boolean models. Our approach, named DSGRN, provides a direct connection between ODE dynamics and Boolean models.

We examine briefly some consequences of this connection by discussing lattice structure of monotone Boolean functions, algebraic topology that links dynamics predictors computed from discrete and continuous time models, and a potential for combinatorial characterization of bifurcations.

References

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