

MODEL-DEPENDENT AND MODEL-INDEPENDENT CONTROL OF BIOLOGICAL NETWORK MODELS

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Abstract: Network models of cell signaling and regulation are ubiquitous because of their ability to integrate the current knowledge of a biological process and test new findings and hypotheses. An often asked question is how to control a network model and drive it towards its dynamical attractors (which are often identifiable with phenotypes or stable patterns of activity of the modeled system), and which nodes and interventions are required to do so. In this talk, we introduce two recently developed network control methods - feedback vertex set control and stable motif control - that use the graph structure of a network model to identify nodes that drive the system towards an attractor of interest (i.e., nodes sufficient for attractor control). Feedback vertex set control makes predictions that apply to all network models with a given graph structure and stable motif control makes predictions for a specific model instance, and this allows us to compare the results of model-independent and model-dependent network control. We apply these methods to various biological network models and discuss the aspects of each method that makes its predictions dependent or independent of the model. In addition, and if time permits, I will talk about some of the mechanistic models of oncogenic signaling I have worked on (the epithelial-to-mesenchymal transition in liver cancer and drug resistance in breast cancer) and the insights we have learned from them.