Modularity and dynamical timescales in Boolean Networks

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July 16, 2013

Modularity refers to systemic organization characterized by the presence of weakly-coupled subsystems that are themselves tightly integrated internally. Modularity has been argued to be ubiquitous in real-world complex systems and to have important functional roles [4, 6]. However, the concept has been developed along different conceptual and formal lines in different fields. Our work aims toward a more unified definition of modularity that applies generally to multivariate dynamical models.

Modularity has received extensive attention in the domains of evolutionary biology, genetic algorithms, and other fields concerned with optimization or learning of functions in high-dimensional spaces. If the function of interest can be decomposed into nearly-independent contributions from separate subspaces, then the optimization problem can be broken down into simpler subproblems and solved much faster. We have previously developed a model of Bayesian learning of multivariate dynamics and shown how relative independence of modular subsystems can be exploited to accelerate learning, with the amount of data available controlling the 'resolution' at which modules are detected [1, 2].

This treatment of modularity suggests how to structure a learning algorithm in order to adapt optimally to a given cost function (for example, how to design crossover operators in a genetic algorithm). In this work, however, we are not interested in selecting a modular architecture to speed up convergence to an optimum, but rather in the reverse problem: given a dynamical system converging to an equilibrium, to infer the modular structure underlying its dynamics. It is particularly relevant in analyzing systems with functionally-meaningful equilibria, such as evolving populations and dynamical models of biological development.

We exploit the fact that in a dynamical system, modular organization – that is, stronger intra-modular than inter-modular interactions – reveals itself in a separation of dynamical timescales: intra-modular interactions dictate dynamics on short time scales, whereas inter-modular interactions dictate dynamics on longer time-scales [5, 3]. We detect multi-scale modular architecture with a formal method that identifies, at intermediate timescales, which subsystems are near local equilibrium, indicating the resolution of local constraints. We apply our method to Boolean networks (BNs) models, which are discrete-state,

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discrete-time dynamical systems that can display multiple equilibria, periodicity, and transient states, making them challenging but illuminating examples for this approach. More importantly, they are commonly used for modeling developmental and regulatory networks in computational biology, where questions of model decomposition and modularity are of central interest. We demonstrate our approach on several example networks.

References

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