Structure Detection: Finding Hierarchies in Enormous Networks

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Abstract

Many complex systems possess hierarchical network structures. For such networks without an intuitive framework—particularly biological networks (e.g. protein interactions)—specific groupings can only be found through computation without imposing unreasonable human bias. Current methods for determining or extracting these hierarchical structures generally rely on maximizing a measure of modularity over all partitions of a network. In particular, a partition with high modularity has the property that any module contained within has more connections than are expected in a random network of the same size. However, such methods can be prone to imprecision. The goal of this presentation is to instead analyze and expand upon a method of matrix shuffling in which a cost function, defined by an affinity matrix for a given network and an appropriate weighting function, is minimized over all possible partitions of the network.

 $^{^1\}mbox{\sc "Extracting the hierarchical organization of complex systems."}$ Sales-Pardo, et. al., PNAS, September 2007.