Group-Directed Biasing Effects on Topological Properties of PPI Networks

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Abstract

Complex networks have increasingly been used for representing and analyzing biological systems such as protein-protein interaction, metabolism, and gene regulation. However, most these networks are substantially incompletely sampled as a consequence of experimental difficulties. So, it becomes important to investigate to which extent such incompleteness can bias the network representations, especially regarding the estimation of several topological properties. Though some related studies have been reported in the literature, they mostly focus on uniform sampling biases, therefore not including situations in which one or more groups of nodes or edges are, by their biological nature, differently affected by sampling. This case is henceforth called group-directed biasing. Indeed, this situation is commonly found in biology, such as in the case of proteins with high content of exposed apolar amino acids bias effect on yeast two-hybrid (Y2H) assays. The present work aims at investigating such situations, by using simulations. More specifically, we build diverse model networks which are biologically more plausible (e.g. Barabási-Albert) in Protein-Protein Interaction (PPI) networks, select subgroups of nodes and/or edges which may or may not share topological characteristics, and derive respective sampled versions of these networks with sampling biasing specific to groups of nodes. Then, several topological measurements are obtained for these networks and compared to the original models. In this way, we provide insights about the effect of different types of group-directed biasing on the accuracy of the estimation of topological features of complex networks.

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