

Modular Structures of Protein-protein interaction networks

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Abstract

The random graph theory approach was employed to analyze the protein-protein interaction networks, in which a total of seven species were considered. Several global topological parameters were used to characterize the PINs for each species. Good evidence by correlation analysis supported the fact that the seven PINs are well described by scale-free networks [1].

In addition to the scale-free behavior, some networks also demonstrate a high degree of clustering (modularity). It is found that two of the PINs could be modeled by hierarchical networks. In particular, it is determined that the E. coli and the yeast PINs are well represented by the stochastic and deterministic hierarchical network models respectively [1]. The current fruit fly protein-protein interaction dataset does not provide convincing evidence in favor of the hierarchical network model. These results suggesting that the hierarchical network model is a better description for certain species' PINs, and it may not be an universal feature across different species.

There were concerns that large fraction of the protein-protein interaction data was false signals, which could possibly spoil the topological results. In order to test this point, we perturb PINs with four types of perturbations in order to investigate the network robustness issue. It is demonstrated that PINs are robust with respect to failure, attack, random rewiring and edge deletion perturbations [2].

References

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2. Ka-Lok Ng, Chien-Hung Huang, Po-Han Lee, Jywe-Fei Fang, Jeffrey J.P. Tsai. Modular Structures and Robustness of protein networks. (To be published)

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