生物信息学研究中心
Center of Bioinformatics

学术报告

题　　目： Dynamic centrality measures and adaptation of networks in crisis

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Abstract: Determination of centrality became a key question of the network-description of complex systems. Former studies highlighted the importance of local measures (such as degree) discriminating hubs, and of global measures (such as betwenness centrality) often identifying bridges or bottlenecks. We recently developed a modularization method, called ModuLand ([1], www.linkgroup.hu/moduland.php), which detects extensively overlapping network communities, and determines community centrality, i.e. a mesoscopic measure summing up the total influence of all network segments to a given node or link. Community centrality proved to be useful to identify the cores of modules, i.e. those few nodes, which form the center of the module. Analysis of the role of module core nodes proved to be a very good predictor of the function of the entire module in biological systems. Similar influence-like centralities can be derived using our recently developed Turbine algorithm to follow the propagation of perturbations in real world networks (www.linkgroup.hu/Turbine.php).

Based on our earlier studies on spatial games (*showing that memory plus randomness not only promote cooperation, but also make the outcome quite independent of the network structure*) [2], we constructed NetworGame (www.linkgroup.hu/NetworGame.php), which is a versatile program package to model any types of two-agent games (with 2 to 5 strategies) in any real world, or model networks using any types of strategy update rules, update dynamics and starting strategies. The NetworGame program allowed the definition of game centrality as the ability of a networked agent (or a link of two agents) with a single initial defective strategy to change an overall initial starting cooperation to defection (and vice versa: a cooperative strategy of a linked node-pair/triangle changing overall defection to cooperation). Spatial games can also be rationalized in networks of non-conscious agents, such as amino acids, or proteins [3]. Our game centrality measures correctly identified the major decision makers of social cooperation in benchmark networks, such as the Zachary karate club network or Michael's strike network, and pinpointed key 'actors' determining the cooperation of biological networks.

As an example of general messages of the dynamic behavior of biological systems, we observed a partial decoupling of yeast protein-protein weighted interaction network modules after stress. This rearrangement is beneficial to the cell, because it allows better focusing on vital functions, thus sparing resources, and localizes damage to only the most sensitive modules. It also reduces the propagation of noise throughout the network, allows the individual modules a larger degree of freedom for exploring different adaptation strategies, and helps reduce inter-modular conflicts during a period of major intra-modular changes. Several key proteins of the cellular stress response served as residual or newly induced overlaps and bridges of the yeast interactome. De-coupling/re-coupling cycles emerged as a general model of adaptation and learning of complex systems [4].

References

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