Understanding biological networks with the random walker's perspective

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We present a new method for analyzing networks and demonstrate its applications to biological networks. The networks we study are *modular*, meaning that they display a structure of dense communities connected by sparser formations. It has been observed that biological networks, such as protein-protein interaction networks, often exhibit this structure [1].

We propose an approach to reveal the organization of such networks. Unlike previous methods, that aim to identify a specific type of network element (community detection, hubs identification, etc.), our methods discover these individual elements as well as the connections between them: finding modules, identifying the important paths between them, and most importantly pinpointing the key nodes in the network, those that are the most vital to communication between the modules. Such nodes could, for example, be good candidates for drug targets.

We base our novel algorithms on the random walker approach to modular networks. Here the modules correspond to *metastable sets*: regions of the network where a random walker stays for a long time before exiting. We then associate the important paths and key nodes with those carrying the most flow in the sense of *transition path theory* [2], a rigorous framework with proven properties originally designed for the study of dynamical systems.

We demonstrate the effectiveness of our methods in recovering known structures in a well-known yeast protein interaction network.

References

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