Unraveling biological networks

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A new approach to disentangling the complexities of biological networks, such as the way in which proteins interact in our body's cells has been developed by researchers in China. The team's algorithm could allow biologists and biomedical researchers to unravel new clues about how cells work and what goes awry with such networks in various diseases, such as Alzheimer's disease and cancer.

We find networks everywhere in technology, in nature, in our bodies. They are ubiquitous in countless fields of research from [electronic circuitry](#) to social networks from transportation systems to biological systems. Researchers have demonstrated that although networks may superficially be very disparate in nature they nevertheless share many global properties, such as "small world" and "scale free" characteristics. This means that understanding one kind of network can help us understand another.

However, to dig deeper still into the universal characteristics of networks requires us to understand the basic structural elements present in a particular - the so-called network "motifs". Motifs are patterns of interconnections between the nodes in a network, whether transistors, neurons Facebook users, or in [molecular biology](#), proteins. Motifs that occur in significantly larger numbers in real networks than in randomised networks can be used to characterise local features of even the most complex networks. With high-throughput analytical techniques, molecular biologists are beginning to uncover network motifs in protein systems, and likewise in metabolism, the brain, the spread of pathogens and many other areas of interest.

Computer scientists Guimin Qin and Lin Gao of Xidian University in Shaanxi, China, have devised an efficient algorithm for detecting motifs in protein networks. The algorithm first searches for specific non-tree-like sub-structures in a network that are not so commonly found in random networks. It then classifies these sub-structures and clusters them hierarchically to reveal the presence of recurring motifs in the network. The team has applied the algorithm to a network of protein-protein interaction (PPI) for the well-studied bacterium Escherichia coli and the yeast Saccharomyces cerevisiae.

"Our experimental results show that the algorithm can efficiently discover motifs, which are consistent with current biology knowledge," the team says. Importantly, however, the approach has also revealed several novel motifs previously unrecognised. "Our algorithm can detect several consensus motifs with a given size, which may help biologists go further into cellular process," the team adds.

More information: "An algorithm for network motif discovery in biological networks" in *Int. J. Data Mining and Bioinformatics*, 2012, 6, 1-16

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