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Identifying edge clusters in networks via edge graphlet degree vectors (edge-GDVs) and edge-GDV-similarities

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Inference of new biological knowledge, e.g., prediction of protein function, from protein-protein interaction (PPI) networks has received attention in the post-genomic era. A popular strategy has been to cluster the network into functionally coherent groups of proteins and predict protein function from the clusters. Traditionally, network research has focused on clustering of nodes. However, why favor nodes over edges, when clustering of edges may be preferred? For example, nodes belong to multiple functional groups, but clustering of nodes typically cannot capture the group overlap, while clustering of edges can. Clustering of adjacent edges that share many neighbors was proposed recently, outperforming different node clustering methods. However, since some biological processes can have characteristic "signatures" throughout the network, not just locally, it may be of interest to consider edges that are not necessarily adjacent. Hence, we design a sensitive measure of the "topological similarity" of edges that can deal with edges that are not necessarily adjacent. We cluster edges that are similar according to our measure in different baker's yeast PPI networks, outperforming existing node and edge clustering approaches.

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