

Consistent Dissection of the Protein Interaction Network by Combining Global and Local Metrics

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Abstract

We propose a new network decomposition method to systematically identify protein interaction modules in the protein interaction network. Our method incorporates both a global metric (Betweenness) and a local metric (Commonality) for balance and consistency in network Decomposition (BCD Method). We compare the performance of our method with several earlier approaches on both simulated and real datasets using different criteria, and show that our method is more robust to network alterations and more effective at discovering functional protein modules.