The dynamics of multilayer network community structure

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By accounting for the complex and diverse nature and scales of clinical and molecular data, biomedical multilayer networks offer a range of research challenges that still require substantial investigation, while providing the means to achieve a comprehensive view of human diseases. Biomedical multilayer networks have proven striking analytical advantages for heterogeneous data integration [1], especially the effective detection of communities of genes to infer functional associations and drug targets based on multiple evidence. Nevertheless, community structure determination in networks is an open problem to such an extent that the preferred formulations of network communities are often domain-specific [2]. We implement several approaches to study the community structure of biological multilayer network, with special emphasis on the detection of stable partitions at different scales of modularity resolution. Modules of genes that are consistently found in such partitions can be deemed functionally related as supported by the multiple association evidence of the multilayer network. We examine this approach to the study of multilayer community structure of multi-omics data in rare diseases, namely Congenital Myasthenic Syndromes [3] and medulloblastoma [4].

References and useful liks

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