

Identifying Network Subgraph-Associated Essential Genes in Molecular Networks

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Abstract : Essential genes play an important role in the survival of an organism. It has been shown that cancer-associated essential genes are genes necessary for cancer cell proliferation, where these genes are potential therapeutic targets. Also, it was demonstrated that mutations of the cancer-associated essential genes give rise to the resistance of immunotherapy for patients with tumors. In the present study, we focus on studying the biological effects of the essential genes from a network perspective. We hypothesize that one can analyze a biological molecular network by decomposing it into both three-node and four-node digraphs (subgraphs). These network subgraphs encode the regulatory interaction information among the network's genetic elements. In this study, the frequency of occurrence of the subgraph-associated essential genes in a molecular network was quantified by using the statistical parameter, odds ratio. Biological effects of subgraph-associated essential genes are discussed. In summary, the subgraph approach provides a systematic method for analyzing molecular networks and it can capture useful biological information for biomedical research.

Keywords : biological molecular networks, essential genes, graph theory, network subgraphs

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