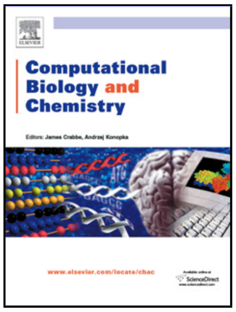

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An Efficient Strategy for Identifying Cancer-related Key Genes based on Graph Entropy

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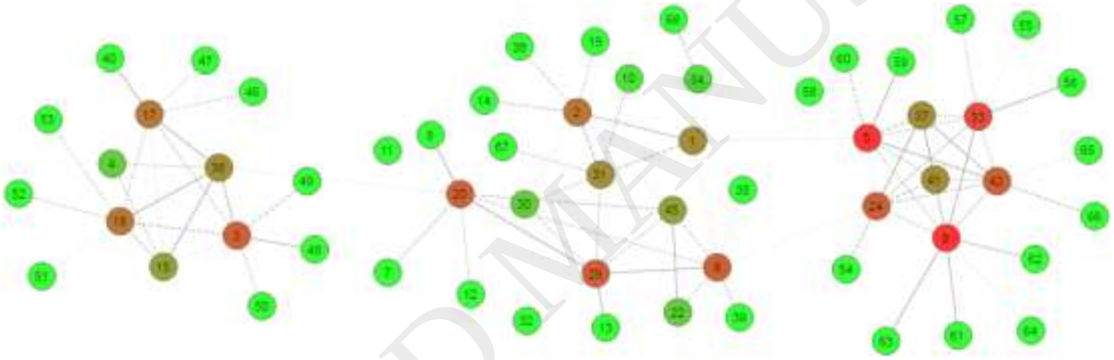
Graphical abstract



Highlights

- Use gene expression data to construct gene network.
- Use the algorithm of parallel maximal cliques for quickly obtaining a series of subgraphs.
- We introduce a novel metric that combine graph entropy and the influence of upstream gene mutations information to measure the impact factors of genes.
- The strategy is effective and easy to identify new genes that can be used as potential markers for prognosis prediction

Abstract

Gene networks are beneficial to identify functional genes that are highly relevant to clinical outcomes. Most of the current methods require information about the interaction of genes or proteins to construct genetic network connection. However, the conclusion of these methods may be bias because of the current incompleteness of human interactome. In this paper, we propose an efficient strategy to use

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