Community Based Cancer Biomarker Identification from Gene Co-expression Network

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ABSTRACT

Finding the biomarkers of cancers and the analysis of cancer-driving genes that are involved in these biomarkers are essential for understanding the dynamics of cancer. Gene expression profiling has been widely used for cancer research, and its patterns, combined with statistical and computational techniques have been explored in many types of cancer. Genes having correlations in terms of expression may form complexes, pathways, or participate in regulatory and signaling circuits [1]–[3].

Clusters of genes in co-expression networks are commonly used as functional units. Gene co-expressed across multiple samples are more likely to correspond to functional groups. Analysis of gene co-expression networks of different types of cancer found that various cancers share common characteristics and functions and genes related to these characteristics were found in [4]–[6]. This work is based on the hypothesis established by previous works that the dense clusters or communities in the gene co-expression networks of cancer patients may represent functional units regarding cancer initiation and progression.

Gene co-expression networks were constructed from RNA-seq gene expression data of three cancers - Breast Invasive Carcinoma (BRCA), Colorectal Adenocarcinoma (COAD) and Glioblastoma Multiforme (GBM), using Pearson Correlation with a strict threshold. Then communities were found using seven renowned community detection algorithms. The permutation test was performed on these communities to find the ones that were conserved in all co-expression networks. Survival analysis based on the genes of conserved communities concludes that some of these could predict the survival risk of patients, which can be considered as the biomarkers of cancer.

The discovered biomarker communities were also validated using survival analysis of two different cancers – Glioma (GBMLGG) and Ovarian Serous Cystadenocarcinoma (OV) - which were not used in finding the communities.

KEYWORDS

Cancer Biomarkers, Community Detection, Gene Co-expression Network.

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