
META-ANALYSIS OF CANCER TRANSCRIPTOMES USING INDEPENDENT COMPONENT ANALYSIS

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Introduction: Independent Component Analysis (ICA) is a matrix factorization method for data dimension reduction. ICA has been widely applied for the analysis of transcriptomic data for blind separation of biological, environmental and technical factors affecting gene expression. This study aimed to analyze cancer data using the ICA for identification and comprehensive analysis of reproducible signaling pathways and molecular signatures in cancer.

Materials and Methods: In this study, four independent cancer transcriptomic datasets GSE26886, GSE69925, GSE32701 and GSE21293 (Affymetrix) from GEO databases were used. R Bioconductor and Matlab have been used for normalization. A bioinformatics tool «BiODICA - Independent Component Analysis of Big Omics Data» was applied to compute independent components (ICs). Gene Set Enrichment Analysis (GSEA) and ToppGene uncovered the most significantly enriched pathways. Construction and visualization of gene networks and graphs were performed using the OFTEN method, Cytoscape and HPRD database.

Results: The correlation graph between decompositions into 30 ICs was built with absolute correlation values exceeding 0.15. Clusters of components - pseudocliques were observed in the structure of the correlation graph. Top 500 most contributing genes of each ICs in pseudocliques were mapped to the PPI network to construct signaling pathways for gene interaction. Some cliques were composed of densely interconnected nodes and included components common to most cancer types, while others were common to some of them.

Conclusion: The results of this investigation may reveal potential biomarkers of carcinogenesis, functional subsystems in the tumor cells, and helpful in predicting the early development of a tumor.