

ABSTRACT:

A crucial part in understanding the bodily functions of living organism is the network of co-expressed genes. Existing techniques generally depend on proximity measures to draw the relationship between genes. In this work, pair-wise expression profiles of genes are compared, correlation are computed, and based on which gene-gene network is constructed. The genes in a network with high similarity form a coherent group that can encode proteins and take part in common biological processes. We applied the proposed approach on Subset of Yeast cell cycle dataset, Rat CNS dataset and Subset of Human Fibroblasts serum dataset to construct a gene-gene co-expression network. In this study, a novel correlation-based method is proposed to extract simple gene interaction networks from microarray data. The clustering technique adopted in this approach is independent of any constraints like number of clusters to be formed and produces clusters of good quality both in terms of visual representations and cluster validity measures. The Co-Expression Network formation method incorporated in this work searches for highly coherent genes having an association between them and thus forms the graph model representing the co-expression network. The network formation technique is free from the limitations of proximity measures. The proposed method has been tested on four real life datasets and experimental results on time series gene expression data from the various datasets are biologically validated based on standard tools.

Keywords: Gene expression, co-expression network, cluster, networks, homogeneity, gene expression profile, genetic network, undirected graph, correlation