Abstract

Most of the existing methods in literature have used proximity measures in the construction of co-expression networks (CEN) consisting of functional gene modules. This work describes the construction of co-expression network using mutual information (MI) as a proximity measure which preserves non-linear correlation. Functionally enriched network modules over full space are then extracted from this network. Further, subspace network modules that are defined over a subset of samples are extracted. This methodology has been tested on several publicly available datasets and the subspace network modules so obtained have been validated in terms of p and Q values. The effectiveness of the method is established over a number of gene expression data while comparing it with its existing counterparts. The topological properties of such modules have also been compared with that of some real biological network to prove its biological significance.

Keywords: mutual information, co-expression network, network modules, topological property