Topological analysis of co-expression networks in neoplastic tissues

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Motivations

Gene expression data carry important information for the study of the complex response patterns of a biological system to cell state modifications. Consequently, gene co-expression networks are useful models to enlighten the coordinated expression of groups of genes that are functionally co-regulated in order to provide the adaptive response to the system modification. In this framework, topology-based approaches to network analysis have yielded unexpected insights of the global properties of biological systems that could not be unveiled with one-gene approaches. The key idea is that topological differences can critically emerge from the comparison between normal and cancer networks and can identify those non-differentially expressed genes which are involved in the onset and progression of the specific disease.

Results

In this work, we introduce a novel method for the characterization of disease genes, based on the study of topological differences of co-expression networks inferred from microarray expression profiling of neoplastic and normal tissues. Moreover, we assess the statistical significance associated with the variation of topological observables in the two phenotype conditions. The analysis, that has been focused on different human solid tumors, provides crucial evidences of common characteristics in the response patterns of gene co-expression networks in neoplastic tissues.