Keynote Speech - 1

Identifying Functional Modules using MST-based Weighted Gene Co-Expression Networks

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Abstract

This study proposes an effective method for identifying functional modules of the weighted gene co-expression network using a minimum spanning tree (MST) approach coupled with network neighborhood connectivity. The MST-based gene co-expression network was reconstructed to serve as the backbone of gene co-expression network. Highly connected hub genes were identified based on the connectivity of the backbone network. All sub-networks were extracted by expanding from the hub genes to their neighborhood genes. Finally, functional modules were identified by integrating sub-networks with similar gene expression profiles. We tested the method with both simulated and autism spectrum disorder microarray data sets. The results show that our approach is better in highlighting the hub genes and can effectively identify functional modules with highly enriched pathways.