



Mining topological structures of protein-protein interaction networks for human brain-specific genes

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ABSTRACT. Compared to other placental mammals, humans have unique thinking and cognitive abilities because of their developed cerebral cortex composed of billions of neurons and synaptic connections. As the primary effectors of the mechanisms of life, proteins and their interactions form the basis of cellular and molecular functions in the living body. In this paper, we developed a pipeline for mining topological structures, identifying functional modules, and analyzing their functions from publically available datasets. A human brain-specific protein-protein interaction network with 1482 nodes and 3105 edges was built using a MapReduce based shortest path algorithm. Within this, 7 functional cliques were identified using a network clustering method, 98 hub proteins were obtained by the calculation of betweenness and connectivity, and 5 closest relationship to clique connector proteins were recognized by the combination scores of topological distance and gene ontology similarity. Furthermore, we discovered functional modules interacting with TP53 protein, which involves several fragmented research study conclusions and might be an important clue for further *in vivo* or *in silico* experiments to confirm these associations.

Key words: Brain-specific genes; Functional cliques; GO similarity; Betweenness; Hub protein