

ABSTRACT

Discovering cancer-associated proteins is a major challenge in cancer research. Recently various techniques have been developed to identify novel cancer-associated proteins. Protein-protein interaction network and also protein clustering approaches are good predictors for cancer proteins. In this study, we implemented two different network clustering approaches on lung cancer protein-protein interaction network in order to identify novel lung cancer-associated proteins. Firstly, we adopted K-Means clustering technique to identify novel lung cancer associated proteins, and secondly, the Molecular Complex Detection approach (MCODE) was applied in this research work to detect significant proteins which related to lung cancer formation.

Enriched biological functions and KEGG pathways are determined, and results strongly suggest that most of predicted proteins involve in lung cancer formation. Also, based on the assumption that cancer proteins tend to interact with cancer proteins, we have identified several putative lung cancer proteins. It is expected that the approach developed in this work should be of value for identifying cancer-associated and cancer proteins.

