Abstract

Biomedical area of research has grown dynamically for identification of various diseases and prediction of disease, among the most cancer is vital and critical disease caused from various sources of gene mutation. Cancer is one of the most common diseases in the developed world. Cancer arises from the mutation of a normal gene. Mutated genes that cause cancer are called oncogenes. The Lung cancer is one of the leading causes of cancer mortality worldwide. The main types of lung cancer are small cell lung cancer (SCLC) and non small cell lung cancer (NSCLC). In this work, a computational method was proposed for identifying lung-cancer-related genes with a shortest path approach in a protein-protein interaction (PPI) network using R tool to set the computation. Based on the PPI data from STRING, a weighted PPI network was constructed. 54 NSCLC- and 84 SCLC-related genes were retrieved from associated KEGG pathways. Then the shortest paths between each pair of these 54 NSCLC genes and 84 SCLC genes were obtained with Dijkstra’s algorithm. Some of the shortest path genes have been reported to be related to lung cancer. Intriguingly, the candidate genes identified from the PPI community contained extra most cancers genes than the ones recognized from the gene
expression profiles. Furthermore, these genes possessed greater purposeful similarity with the recognized cancer genes than those identified from the gene expression profiles. This work proved the performance of the proposed technique and showed promising consequences.

References


Index Terms

Computer Science  Networks

Keywords
Data related to Proteins, Weighted PPI Data, Computational algorithm, Resultant Protein information.