

A Study Reveals Overlapping Gene Expression Profiles Affiliating Breast Cancer and Lung Cancer Metadata

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Abstract—Reconstruction of biological network for topological analysis helps in identification and correlation between various types of biomarkers. These networks have been vital parts of System Biology in present era. Genes are the basic physical and structural unit of heredity. Genes act as instructions to make molecules called proteins. Alterations in the normal sequence of these genes are the root cause of various diseases and cancer is the prominent example disease caused by gene alteration or mutation. These slight alterations can be detected by microarray analysis. The high-through put data obtained by microarray experiments helped the scientists to reconstruct the cancer specific gene regulatory network. The purpose of experiment performed is to find out the overlapping of the gene expression profiles of breast and lung cancer metadata, so that the common hub gene can be utilized as a drug target which could be used for the treatment of both the diseased condition. In this study, first the differentially expressed genes in a disease have been identified (lung cancer and breast cancer), followed by the filtration approach and most significant genes are taken using paired t-test and gene regulatory network between the identified genes has been computed depending on the absolute value of Pearson correlation coefficient. The obtained result has been checked and validated with the available databases and literatures.