

## **Abstract**

A complex disease such as breast cancer has a multigenic involvement in disease mechanism. To discover breast cancer specific genes, it needs much laborious effort and time. Therefore, it is a good idea to identify an appropriate initial set of genes, before perform laboratory experiments. This will save time and effort.

This work was conducted to use candidate genes in order to identify inferred genes using gene-gene interactions. Literature based gene-gene interaction identification was carried out manually to extract gene interactions from PubMed abstracts. Then, gene interaction network was visualized using Cytoscape visualization tool. Gene ranking was done using network analysis. Gene-gene interaction network used as a base for development of interactive web based module to access to necessary gene information.

Using breast cancer candidate genes, gene interactions were discovered and visualized gene interaction network. Breast cancer related genes were ranked.

Visualization of gene-gene interaction network and network centrality analysis are important methods to identify disease specific genes and ranking discovered genes.