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**Detection of Prostate Cancer Related Genes using Modified Ford-Fulkerson Algorithm in Protein-to-Protein Interaction Network**

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**Abstract**

Prostate cancer is a malignancy cancer that affects prostate epithelial cells. Presently, prostate cancer is the second leading cause of cancer-related death in men. In this research, a new computational system was proposed for determining the prostate cancer related genes with the shortest path methodology in a Protein to Protein Interaction (PPI) network. Here, a weighted PPI network was constructed on the basis of PPI data from Search Tool for the Retrieval of Interacting Genes/Proteins (STRING) database. Totally, eighteen prostate related genes were extracted from the STRING database by using Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway. Then, the shortest path between eighteen genes was identified using modified Ford-Fulkerson algorithm. Generally, the conventional Ford-Fulkerson algorithm was very effective in detecting the shortest path between the prostate cancer-related genes, but the elapsed time was high when the PPI network has more number of genes. In order to reduce the elapsed time, the modified Ford Fulkerson algorithm was developed by eliminating the invalid path in gene connection. In the experimental section, the proposed shortest path approach reduced the elapsed time up to 0.025-0.002 seconds compared to the existing shortest path methodologies.

**Keywords:**

Modified Ford-Fulkerson algorithm, prostate cancer, protein to protein interaction, and shortest path.

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