

Genomics paper

-A Streamlined Approach to Pathway Analysis from RNA-Sequencing Data

-Task two / Related Works

-Related works

- The main contributions of our work to the problem of Pathway Analysis is to Use already and previously existing researches and tools and combine them to approach a more streamlined pathway analysis we use The Pathway Interaction Database and Gene Annotation and Pathway Mapping in KEGG and FunRich: An open access standalone functional enrichment and interaction network analysis tool , KEGG Orthology-Based Annotation System, DAVID Bioinformatics Resources, ConsensusPathDB, Cytoscape, BioGRID and many more!