SYSTEM AND METHOD FOR CONSTRUCTING PATHWAY NETWORKS OF TWO OR MORE PATHWAYS FOR A SET OF GENES OR PROTEINS

Abstract

The present invention provides systems and methods for constructing pathway networks of two or more pathways for a set of genes or proteins, wherein a single pathway contains one or more genes or proteins that are grouped based on one or more commonality of all the genes or proteins within the pathway, and wherein the set of genes or proteins are identified by differential gene expression profiling. More particularly the invention uses computer-implemented methods and systems to analyze gene expression profiling dataset by identifying a set of genes or proteins that are responsive in coordination to one or more effecters, constructing a secondary pathway database by mining primary databases, identifying the pathways that contains one or more genes or proteins of the set of genes or proteins, and constructing a pathway network of the identified pathways by using a single source maximum pathways algorithm. The constructed pathway networks can be visualized and compared to obtain common and non-common pathways.

FIG 4A