

Identifying metabolic pathway within microarray gene expression data using combination of probabilistic models

Abstract

Extracting metabolic pathway that dictates a specific biological response is currently one of the important disciplines in metabolic system biology research. Previous methods have successfully identified those pathways but without concerning the genetic effect and relationship of the genes, the underlying structure is not precisely represented and cannot be justified to be significant biologically. In this article, probabilistic models capable of identifying the significant pathways through metabolic networks that are related to a specific biological response are implemented. This article utilized combination of two probabilistic models, using ranking, clustering and classification techniques to address limitations of previous methods with the annotation to Kyoto Encyclopedia of Genes and Genomes (KEGG) to ensure the pathways are biologically plausible.