

Gene ontology (GO) enrichment analysis is a method used to identify functional categories of genes that are overrepresented in a set of genes of interest, such as those that are differentially expressed in a particular experiment or that are associated with a disease. The GO database provides a standardized vocabulary of functional terms and their relationships to each other, which allows researchers to categorize genes based on their biological processes, molecular functions, and cellular components.

GO enrichment analysis involves comparing the set of genes of interest to the entire genome or a background set of genes to determine which GO terms are significantly overrepresented in the set of interest. This can be done using statistical tests such as the hypergeometric test or the chi-squared test. The resulting p-values indicate the significance of the enrichment of each GO term in the gene set of interest.

GO enrichment analysis can help researchers gain insights into the biological processes and molecular functions that are involved in a particular phenotype or disease. For example, if a set of differentially expressed genes is found to be enriched in a particular GO term related to immune response, it may suggest that the immune system is involved in the phenotype or disease being studied. GO enrichment analysis can also be used to identify potential therapeutic targets by identifying biological processes that are dysregulated in disease states.

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