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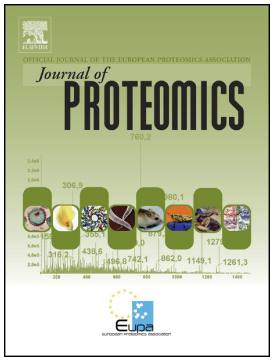

Comprehensive functional analysis of large lists of genes and proteins

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Comprehensive functional analysis of large lists of genes and proteins

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Abstract

The interpretation of high dimensional datasets resulting from genomic and proteomic experiments in a timely and efficient manner is challenging. ClueGO software is a Cytoscape App that extracts representative functional biological information for large lists of genes or proteins. The functional enrichment analysis is based on the latest publicly available data from multiple annotation and ontology resources that can be automatically accessed through ClueGO. Predefined settings for the selection of the terms are provided to facilitate the analysis. Results are visualized as networks in which Gene Ontology (GO) terms and pathways are grouped based on their biological role. Many species are now supported by ClueGO and additional organisms are added on demand. ClueGO can be used together with the CluePedia App to enable the visualization of protein-protein interactions within or between pathways.

Introduction

With today's high-throughput technologies a continuous large amount of data is generated. The rapid advancement of DNA and RNA next generation sequencing, microarrays as well as mass spectrometry based proteomic technologies [1] facilitates the investigation of global aspects of health and disease. Studies of gene expression levels reveal expression patterns in particular cell types and how these change at particular stages of development or in the context of disease [2]. On the other hand, proteomic techniques interrogate the entire repertoire of proteins of an organism and can underline interactions of proteins involved in diverse cellular functions [3]. Biological processes are in fact multidimensional, with multiple informational levels including genes that code for several proteins. These proteins are involved in multiple pathways and can be further post-translationally modified in complex ways. The interpretation of such high dimensional datasets

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