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Update of ProteINSIDE: an online tool for proteome data mining

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1. Introduction

We previously presented the ProteINSIDE tool to the scientific community [1,2]. ProteINSIDE was developed to mine results from large lists of proteins or genes, and thus to extract meaningful biological knowledge from “omics” datasets. The first version of ProteINSIDE gave 4 types of analyses or results: (1) identifiers conversion plus an overview of the biological information stored in public databases (NCBI and UniProt), (2) Gene Ontology enrichment analysis, (3) proteins that are predicted as secreted by mammalian cells, (4) protein protein interactions. Since then, we have improved this tool on many points, including an increase in the number of organisms considered, new functional enrichments (in addition to the GO ones) and the search for quantitative trait loci.

This new version of ProteINSIDE is available at the following address:

https://umrh-bioinfo.clermont.inrae.fr/ProteINSIDE_2/

2. Improvements

The workflow now uses the g:profiler API (Application Programming Interface) [3] for the conversion module (g:convert) and enrichment module (g:GOS). The second version of ProteINSIDE analyzed lists of identifiers from more than 600 organisms rather than those from the 6 species previously targeted by the first version. Functional enrichment analysis previously focused on GO is now complemented by functional enriched analysis to find over-representation of information from several databases: (Human Proteome Atlas, Human Phenotype Ontology, Kegg, miRTarBase, Transfac, Reactome and WikiPathways).

A new functionality for protein protein interactions was added: the comparison between multiple lists experiments. For this, a user sends several lists of proteins. Then, ProteINSIDE, with the help of Psicquic [4], searches for any interactions between the proteins in these lists. The results are downloadable and can also be displayed on a network.

A complete overhaul of the tool was carried out in order to have a simplest interface and best optimization, in particular by parallelizing the calculations. Now the modules are independent of each other to allow the user to choose which one to launch, in order to access to the results as soon as possible without waiting for all the modules to finish running. For the visualization of networks, cytoscape web Flash was no longer supported and has been replaced by its Javascript version [5].

Finally, we added a fifth module, to search for quantitative trait loci using AnimalQTLdb [6] for the bovine species only.

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