



Home assignment 3

1. Identify within String-DB the interactome of your identified proteins.
2. Examine all proteins (original and identified in step 1). in Pathways databases (e.g. KEGG or Reactome). Identify the most important pathways and common pathways in your proteins of study
 - a. Cytoscape may be used to complement the network analysis of the metabolic interactions between your proteins and others within the cell.
3. Search the ArrayExpress database or the relevant literature for one appropriate study where either: a) the study is related to your problem or, in the case of no study being found, b) your selected proteins may be a key factor:
 - a. Use the protocols defined in class for discovering the relevant genes on the study (over- and under-expressed) Are the results reached what was expected?
 - b. With the genes discovered, identify the most relevant GO Terms with GO enrichment analysis
 - c. Input your array relevant results into Reactome. Describe the coherent and relevant pathways found. Can you find any meaningful relationship emerging from the expressed pathways?
4. Are there any relevant drug-based therapies for your problem disease? Where do they act? Can you find any relationship between existing therapies and the pathways and biological processes identified?
 - a. Use ChEMBL and other repositories for other potential analogues or potential therapies related to your problem

Present a report with no more than 8 pages with the student name, number and major on the first page

Deadline: May 29, 2017
The submission will be made online in a PDF file using FCUL's Moodle