

MCB course exercises ProMeTra• **1 Upload your maps to ProMeTra**

In this step, you will upload the pathway data you made using the kegg2sbml tool

- 1.1 login to the ProMeTra website (prometra.cebitec.uni-bielefeld.de)
- 1.2 Click on "Convert SBML files ..."
- 1.3 Chose a unique identifier for your map
- 1.4 Upload the 2 or more SBML files generated with the perl program kegg2sbml
- 1.5 Download and save the SVG file that is generated
- 1.6 Upload the SVG file to ProMeTra by clicking on "Import your own pathway maps"
- 1.7 Choose a (different than before) unique identifier for your map again

• **2 Prepare data for use with ProMeTra (microarray)**

Data can be used with prometra if they are in a certain format. During this exercise you will prepare the data sets and make them ready for use with ProMeTra. Unfortunately you will have to use Excel here.

- 2.1 open the microarray data set in J-Express (it's called "MA" dataset)
- 2.2 take out only the "leading edge" data points contained in some of the interesting pathways from GSEA analysis
note, that for now only metabolic pathways are supported
- 2.3 export data as a tab separated file
- 2.4 import into Excel without messing the gene symbols
To accomplish that, rember to set the identifier column types to text during import of tab separated files.
- 2.5 remove all columns from the sheet, **except** the *gene_symbol* and the numeric measurements (of course you want to keep these...)

• **3 Visualize microrarray data using prometra**

First we will try to visualize only one datasource, if that works out, we will try to integrate more sources.

- 3.1 Upload your data to ProMeTra using "*upload your data in CSV format*"
Use the Browse button and upload the file, don't copy paste here
- 3.2 select "*Protein*" as "*Data type*" and click "*Submit CSV file*"
- 3.3 Check your uploaded data by "*Review Dataset: Protein*"
- 3.4 Click "*Map data to pathway*"
- 3.5 In the pathway list choose the pathway map **you** have just uploaded
- 3.6 Don't change other options and click "*Process pathway map*"
- 3.7 Download the resulting SVG

• **4 Visualize proteomics data**

- 4.1 Repeat exercise 2 and 3 but:
- 4.2 Exchange the dataset and use "*Pro data*"

• **5 Visualize both data sources**

- 5.1 You should have already merged the two data sets in J-Express, if not do so now
- 5.2 Process the data in Excel as before
- 5.3 use search/replace in Excel to replace all "0" (zero) data entries with nothing (leave replace empty)
This step is for re-introducing the missing values. These were set to 0 during merging in J-Express. This step is a bit tricky, if you have real exact 0 values, but that will rarely be the case.
- 5.4 Visualize the merged data set as in exercise 3 and 4

• **6 Extra tasks (optional):**

- 6.1 : Create your own model using CellDesigner and add other proteins and metabolites
- 6.2 Add metabolite measurements to your data. You may use the ProMeTra built in data sources or create your own "measurements" :) using the upload data dialogue.
It will be useful to note or copy-pase some metabolite identifiers from the pathway maps to be able to create the table right.
- 6.3 Figure out how to use ProMeTra in a toponomics study
Toponomics means study of spatial localization of genes, proteins, compounds, etc. in a an organism