

# Setting up the first analysis

<https://www.evinet.org>

**ALWAYS** start from setting your project ID and the organism. Otherwise your analysis might use irrelevant data. Also note that EviNet currently supports only gene symbols and not other ID types. Type in 'project1' to see and try our example files.

The whole aim of network enrichment analysis (Alexeyenko et al., 2012) is characterization of certain genes or gene lists. Hence continue by submitting your altered gene sets (AGS) by either explicitly pasting gene symbols or uploading a file.

**Note: EviNet currently accepts only human and mouse gene symbols and AT\*G symbols in Arabidopsis.**

Once uploaded, a file might remain in your project space to be re-analyzed later.

**NOTE:** the file should contain at least two columns and you have to specify column roles and the column delimiter. An advantage of using files is that they might contain multiple AGSs (the AGS IDs should then appear in a special column). Our [example file](#) contains a few lists of differentially expressed genes "experiment" vs. "control". The same file can be seen in 'project1' (pressing button "Display file content" will help investigating its content). You can choose desirable AGS and proceed to the next two tabs.

Another file in 'project1' is [CPW\\_collection.hsa](#). It is one of the FGS files found in the third tab. Although, we can present any FGS (known pathway etc.) as a novel gene list and explore its functions. Note that gene symbols in this particular file are in col. 2, hence leaving the default col. 1 leads to submitting gene IDs in a wrong format (ENSEMBL – currently not supported).

Select a network. More detailed networks (FunCoup, STRING) are larger but less precise. Networks from curated resources like KEGG, CORUM, PhosphoSite are confident but much less comprehensive and hence might miss novel genes. You can investigate comparative efficiency of the networks by looking at the ROC curves (below the table). More sensitive and specific options must be higher and shifted to the left. Note also that for each individual analysis one can create unions of networks of different types ("Merged" is a pre-compiled example of such a union). Such merging is often beneficial.

Select a collection of functional gene sets, i.e. pathways or GO terms. They should be as close to your angle of view as possible. For example, for cancer it might be our [CPW\\_collection](#). (alternatively, you submit a general collection and then filter the output in the next tab). In most specific and important cases consider submitting your own pathway as a gene list in the text box.

Finally, click the button "Submit and calculate"! It might take time to get the job finished, thus we recommend starting from smaller networks (< 10000 links) and smaller FGS/AGS collections. In order to re-plot the results, you can return and click the button "Restore latest analysis". **NOTE:** options "Analyze ...individually" and "Employ statistic" can alter the output only if you press "Submit and calculate". As long as you try different options and parameters on your AGS files, executed analyses accumulate in your project directory and can be seen in the "Archive" tab. See [example analysis output](#) in 'project1'.

Check if the three components of the analysis correctly appear at the "Check and submit" tab. **NOTE: here you can only see them, but not edit.** For editing, return to respective tabs.

