OMICS.NET (https://www.omicsnet.ca/)
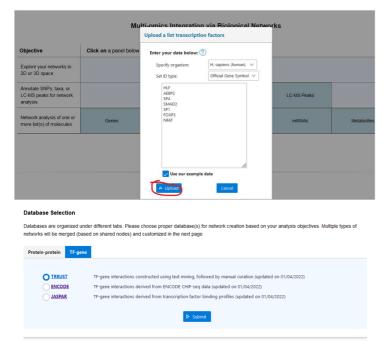
Data mining tool to identify potential **upstream regulators of the DE genes** in the list generated in the lecture 7 (I guess). Thus, Omics.net identifies transcription factors inducing the changes in transcription of those genes. It is an R-based tool.

You basically load the list of your genes (their symbols) and you can choose between different kinds of analysis. We are interested in TF-gene interaction and for this the most used database is TRRUST.

There are various subnetworks of TF. Possible to visualize them. In the node explorer there's the number of nodes associated to each gene, i.e. the genes associated to that TF (regulated by that TF).

The same node can be also investigated with different databases. For example, if we use the reactome database we can see which are the paths where our DE genes, regulated by the selected TF, are involved. We could also colour the TF based on the function.