Data integration with Cytoscape - Practice

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1. Download the files from the webpage of the Genetics Department and open a New Session in Cytoscape. In Cytoscape 3.7 New Session is not required! — nodes.csv, edges.csv

2. Importing networks from files:

   2.1. Import the *edges.csv* file as a network, keep all the columns. Then you will get the "Giant component"! — File→Import→Network→File...

   2.2. Import the atributes of the nodes from the *nodes.csv* file, keep all the columns. — File→Import→Table→File...

3. Importing networks from online databases:

   3.1. Import a network of the first neighbours of your chosen protein from *IntAct and MINT* databases. — File→Import→Network→Public Databases...

4. Merge the previously downloaded networks *IntAct and MINT Merged Network* and the imported network *edges.csv* based on the Uniprot Accession. Make sure that in the *Matching columns* table you choose that column from each networks' *Node table*, which contains the Uniprot Accession! — Tools→Merge→Networks... / edges.csv: name, IntAct és MINT: uniprot_accession

5. Create a filter, which highlights the human proteins only. — Control Panel→Select→Column filter→Node: Taxonomy ID→9606

6. Create a net network from the selected nodes! — File→New→Network→From selected nodes, all edges

7. Create a clear style for the nodes and edges. — Delete the existing mapping settings from the Style

8. Visualize your chosen protein with different and bigger shape. To do that, look for your chosen protein with the search bar on top and set a *Bypass* style for it. Furthermore, edit the nodes and edges of the network like this:

   - Delete all of the points which are not connected to the "Giant component"!
   - Label should be protein names!
   - Size (width, height - if the size is not available) should be equal!
   - Colour of the nodes should be according to the pathways!
   - And make more and more changes to the network will be visually beautiful and nice!

9. Save the Cytoscape Session file! We are going to use it next week.