

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. nodes.csv, edges.csv
 2. Importing networks from files:
 - 2.1. Import the *edges.csv* file as a network, keep all the columns. File→Import→Network→File...
 - 2.2. Import the attributes 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. Create a net network from the selected nodes! Control Panel→Select→Column filter→Node: Taxonomy ID→9606
File→New→Network→From selected nodes, all edges
Delete the existing mapping settings from the Style
 6. Create a clear style for the nodes and edges.
 7. Visualize your chosen protein and their first neighbours with different shapes. To do that, look for your chosen protein with the search bar on top, then select its first neighbours and set a *Bypass* style for them. Select→Nodes→First Neighbors of Selected Nodes→Undirected
 8. Save the Cytoscape Session file! We are going to use it next week.
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9. Delete the nodes that are not connected to the main component. Select them by clicking on them and delete
 10. Using the *Network Analyzer* calculate the main parameters of the network, then close the results panel of the *Network Analyzer*. Tools→NetworkAnalyzer→Network Analysis→Analyze Network
 11. Set the colour of the nodes based on their degrees.