


For this demo, we will use Cytoscape (a Java tool) to visualize and calculate topological properties for a yeast protein-protein interaction network

Getting the data and software

1. Cytoscape can be downloaded from <https://cytoscape.org/>. Java will be automatically installed if not already present on your computer.
2. Data files are provided on class website:
 - a. Network (.sif) https://github.com/cmb-chula/comp-biol-3000788/blob/main/demo/gal_network.sif
 - b. Node annotation (.csv) https://github.com/cmb-chula/comp-biol-3000788/blob/main/demo/gal_node.csv
 - c. Edge annotation (.csv) https://github.com/cmb-chula/comp-biol-3000788/blob/main/demo/gal_edge.csv
3. More tutorials on Cytoscape: <https://github.com/cytoscape/cytoscape-tutorials/wiki>

Understanding Cytoscape file formats

1. The network format for Cytoscape (.sif) is just a tab-separated text file. The first and third columns contain node names and the middle column contain user-defined interaction name (e.g., pp = protein-protein interaction).

 gal_network.sif - Notepad

File	Edit	Format	View	Help
YDR277C	pp		YDL194W	
YDR277C	pp		YJR022W	
YPR145W	pp		YMR117C	
YER054C	pp		YBR045C	
YER054C	pp		YER133W	
YBR045C	pp		YOR178C	
YBR045C	pp		YIL045W	
YBL079W	pp		YDL088C	
YLR345W	pp		YLR321C	

2. The node annotation file is a tabular text file. Each row corresponds to a node (gene) and each column contains information for that gene, such as gene symbol, expression level, etc.

	A	B	C	D	E	F	G	H
1	genesymbol	gal1RGexp	gal1RGsig	gal4RGexp	gal4RGsig	gal80Rexp	gal80Rsig	name
2	GCN3	-0.154	9.12E-04	-0.501	3.57E-06	0.292	0.011229	YKR026C
3	NAB2	0.174	8.73E-04	0.02	0.61707	0.187	0.0059966	YGL122C
4	CRM1	-0.018	0.61381	-0.001	0.9794	-0.018	0.80969	YGR218W
5	SRM1	0.16	0.0021913	-0.23	0.0022461	0.008	0.93826	YGL097W
6	DED1	-0.033	0.39944	-0.056	0.31268	-0.91	8.35E-16	YOR204W
7	YEF3	-0.39	2.71E-08	-0.394	0.04747	-0.769	0.035939	YLR249W
8	TEF1	-0.138	9.87E-04	0.009	0.89728	-0.278	6.78E-04	YPR080W
9	TEF2	-0.074	0.053125	-0.063	0.15497	0.044	0.54556	YBR118W

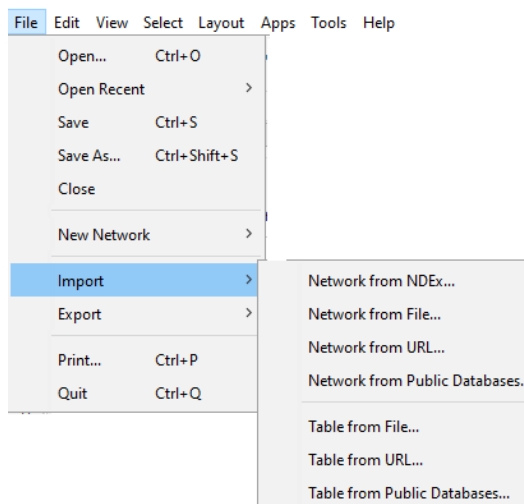
3. The edge annotation file is also similarly structured. Here, the protein-protein interaction strengths (from experiment or prediction) are provided.

	A	B	C
1	interaction strength	interaction	name
2	0.89	pp	YKR026C (pp) YGL122C
3	0.12	pp	YGL122C (pp) YOL123W
4	0.57	pp	YGR218W (pp) YGL097W
5	0.46	pp	YGL097W (pp) YOR204W
6	0.32	pp	YLR249W (pp) YPR080W
7	0.77	pp	YLR249W (pp) YBR118W


Running the demo

1. These files can be imported into Cytoscape using the **File → Import**

For network, use [Network from File](#) option. For node and edge annotations, use [Table from File](#) option.



2. You will then be asked to specify whether the data is for Node Table or Edge Table and which column should be used to map the node or edge name ([Key Column for Network](#)). This is also visualized with a [key symbol](#) in the columns below.

 Import Columns From Table
 ✕

Target Table Data

Where to Import Table Data: To a Network Collection

Select a Network Collection

Network Collection: gal_network.sif

Import Data as: Node Table Columns

Key Column for Network: shared name

Case Sensitive Key Values: ☒

Preview

Click on a column to edit it.

EdgeBetweenness	interaction	name
496.0	pp	YKR026C (pp) Key - String
988.0	pp	YGL122C (pp) YOL123W
6.0	pp	YGR218W (pp) YGL097W
6.0	pp	YGL097W (pp) YOR204W
4.0	pp	YLR249W (pp) YPR080W
4.0	pp	YLR249W (pp) YBR118W
4.0	pp	YPR080W (pp) YAL003W
4.0	pp	YBR118W (pp) YAL003W
6.0	pp	YLR293C (pp) YGL097W
496.0	pp	YMR146C (pp) YDR429C

3. More Cytoscape features will be explored in class.