

Introduction to Cytoscape

Bioinformatics 2 Lab Session

Running Cytoscape on DICE

- Goto <http://www.cytoscape.org/download.html>
- Fill in the required information and proceed to download page.
- Download the archive named “GZIP Archive (for Mac/Unix Systems)”.
- Un-zip this archive file to a directory (`tar xzf filename.tar.gz`).
- Open the directory in the terminal.
- Run the script `cytoscape.sh` in the terminal by typing “`./cytoscape.sh`”.

About Cytoscape

- An open-source package for the visualization and analysis of biological network data.
- Core functions are:
 - Automated graph layout
 - Integrating network data with expression data
 - Visual analysis of node and edges
- Cytoscape also offers open plug-in architecture.

Demo: Simple Biological Scenario

- Step # 1: Get the data files (network.sif & data.mrna).
- Step # 2: Load the network data from .sif file (File → Import → Network (Multiple file types)).
- Step # 3: Load the expression data (.mrna) file (File → Import → Attribute/Expression matrix)

Visualization/Layouts

- Once the network file is loaded, different layouts can be used to visualize the network.
- Cytoscape data panel is used to display the attributes of selected nodes and edges.
- Nodes in the network can be selected in many ways e.g. by name/ID or the neighbours of the node.
- Nodes can also also be selected using filters as described later.
- Demo

Expression Analysis

- In Cytoscape, expression data is primarily used for setting the visual attributes of nodes.
- Nodes are usually coloured as follows:
 - Red for large negative values
 - Pink for small negative values
 - Light green for small positive values
 - Bright green for large positive values
- Demo

Filtering

- Filter are used to select edges and nodes based on some criterion.
- Main types of edges/interactions are
 - Protein-DNA interactions (pd)
 - Protein-Protein interactions (pp)
- Demo

Lab Work

- Load the network data (See references for dataset location).
- Change the layout to 'Spring Embedded'.
- Create a filter to select protein-protein (pp) interactions/edges from this network.
- Select all the nodes connected by selected edges.
- Delete the selected pp interactions and connected nodes.
- Load the expression data (data.mrna).
- Use VizMapper to change the colour of the nodes in the network based on expression data.
- Filter out the genes that are over-expressed using filters and mRNA expression values.

References:

Dataset: <http://www.homepages.inf.ed.ac.uk/s0976841/bio2/>

Cytoscape manual: Available in download folder

Cytoscape tutorial(http://www.cytoscape.org/documentation_users.html)