Homework

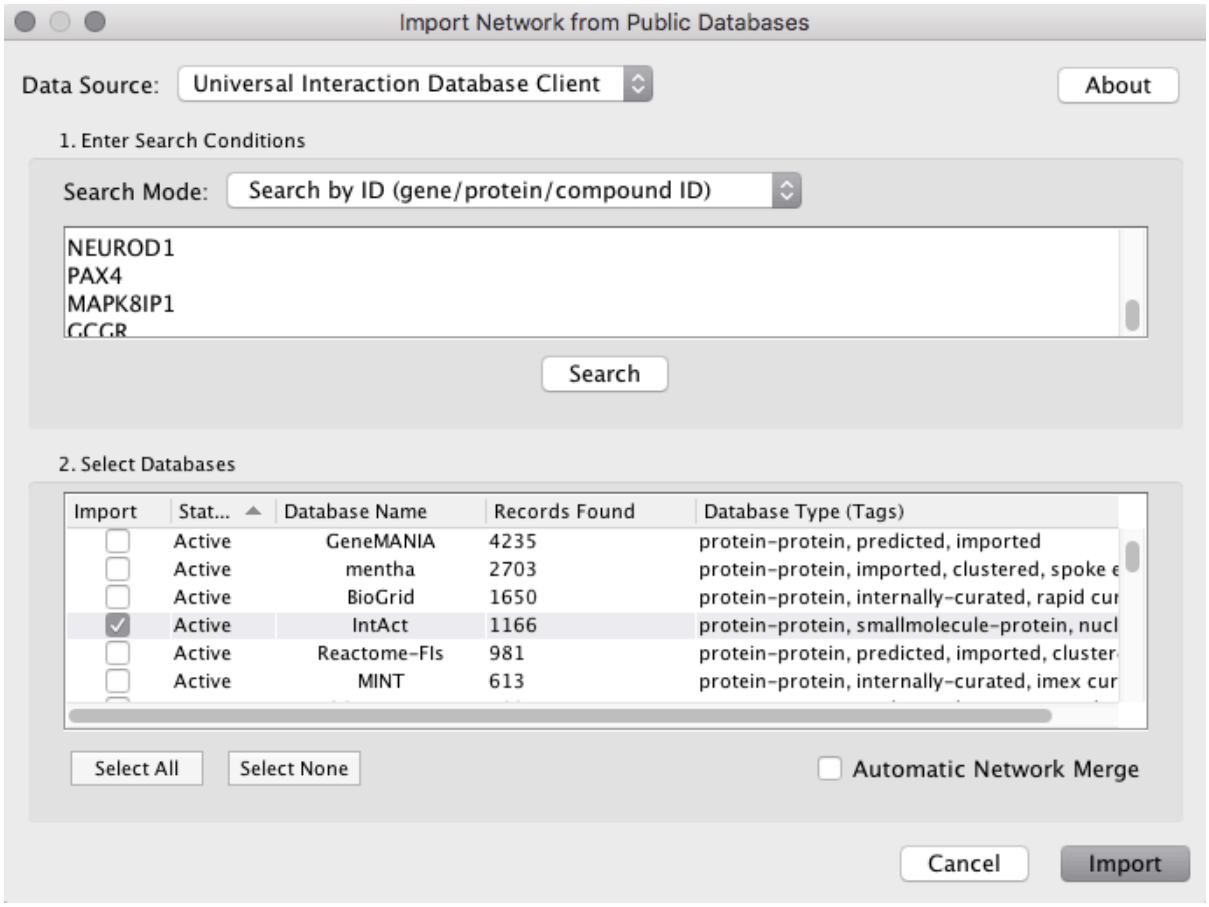
Introduction to Biological Network Visualization (Due 5/12/2016)

Part 1: Creating custom visualization for public data sets

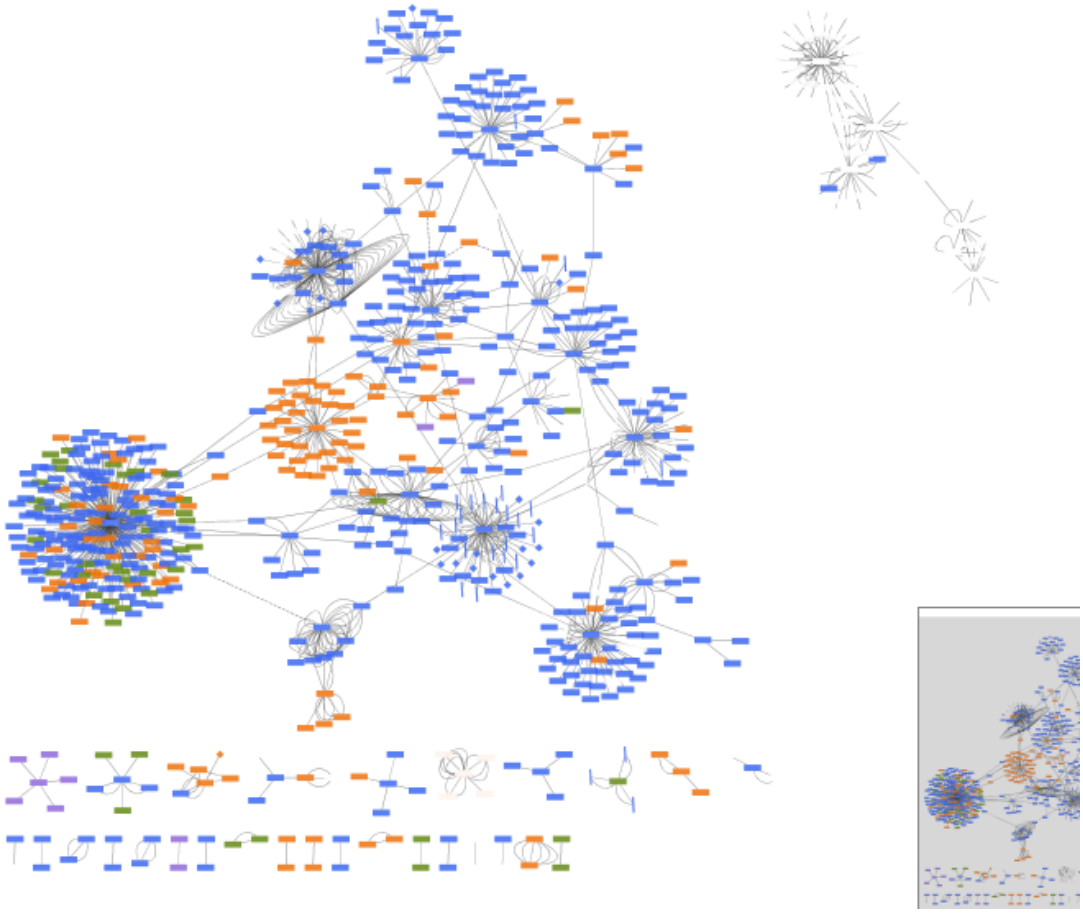
1. Import known interactions from public database

```
PPARG
TCF7L2
RETN
IRS1
HNF1A
HNF4A
KCNJ11
GCK
LIPC
PTPN1
ABCC8
ENPP1
HNF1B
HMGA1
AKT2
WFS1
IRS2
SLC30A8
PDX1
MTNR1B
IGF2BP2
CDKAL1
SLC2A2
NEUROD1
PAX4
MAPK8IP1
GCGR
GPD2
```

- Choose ***File—> Import —> Network—> Public databases…***
- Copy & paste the gene list above to the search box
- Click ***Search***



- From the result, choose *IntAct*
- Click ***Import***
- It will take some time to import the data from the server in UK…
- You will get the network like the following:

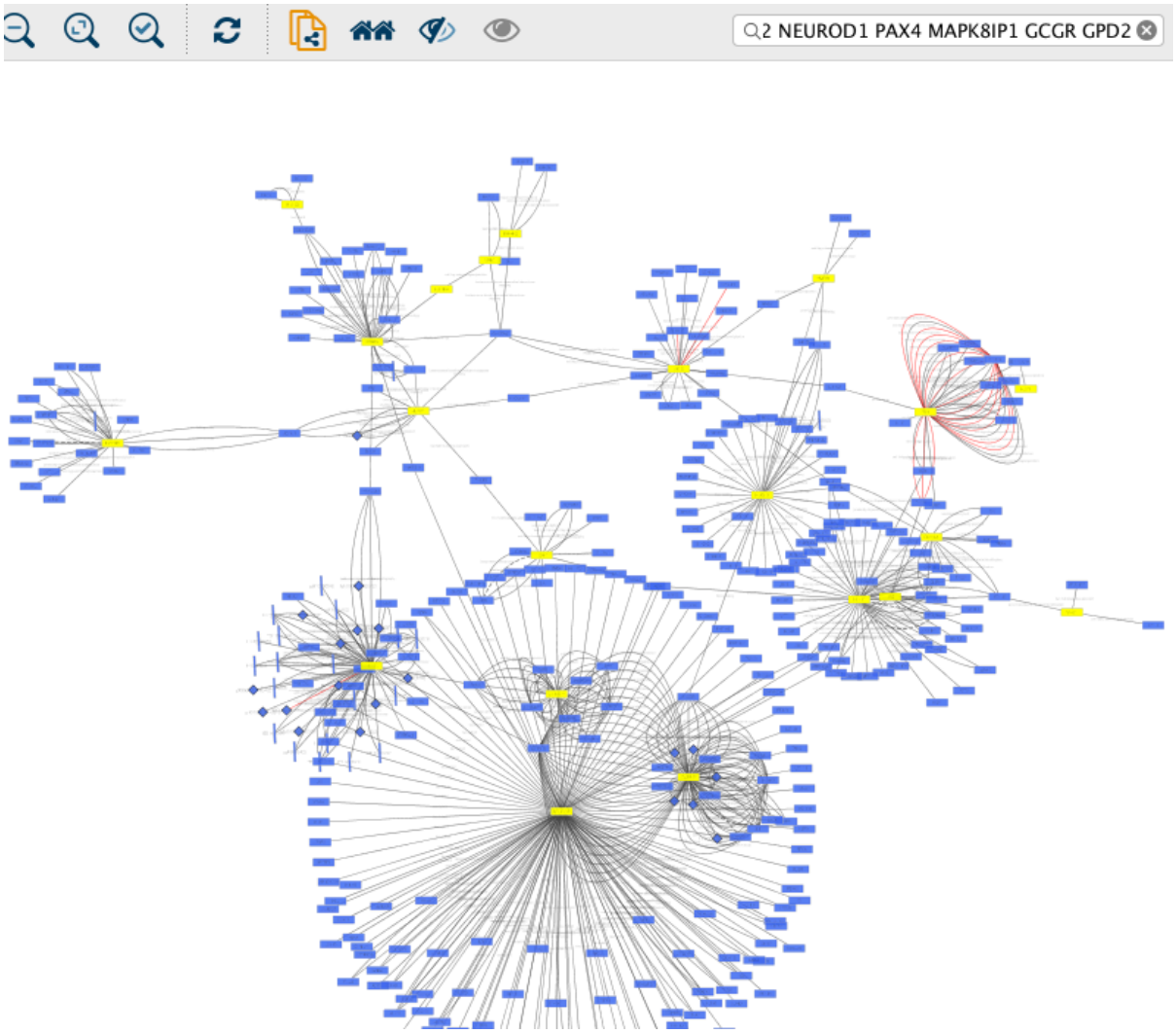


2. Filtering and Subnetworks

- Click Select tab
- Create a new Filter:
  - Click **+** and create new Column Filter
  - Select *Node: Taxonomy Name*
  - Enter *human* as query
- From the selection, create a new subnetwork: ***File—>New—> From Selected nodes, all edges***
- Apply yFiles organic layout: ***Layout —> yFiles Layouts —> Organic***

3. Creating new data column for nodes

- Copy the original gene list
- Paste the list to the search box and press enter
- Now all of the genes in the original query are highlighed:

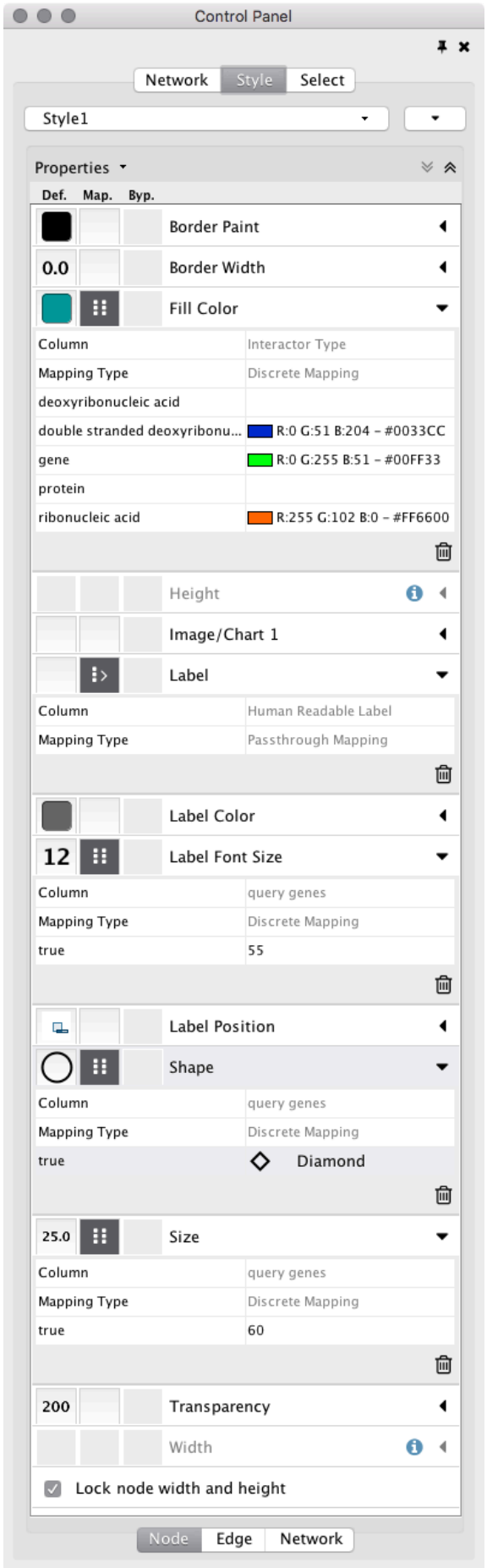


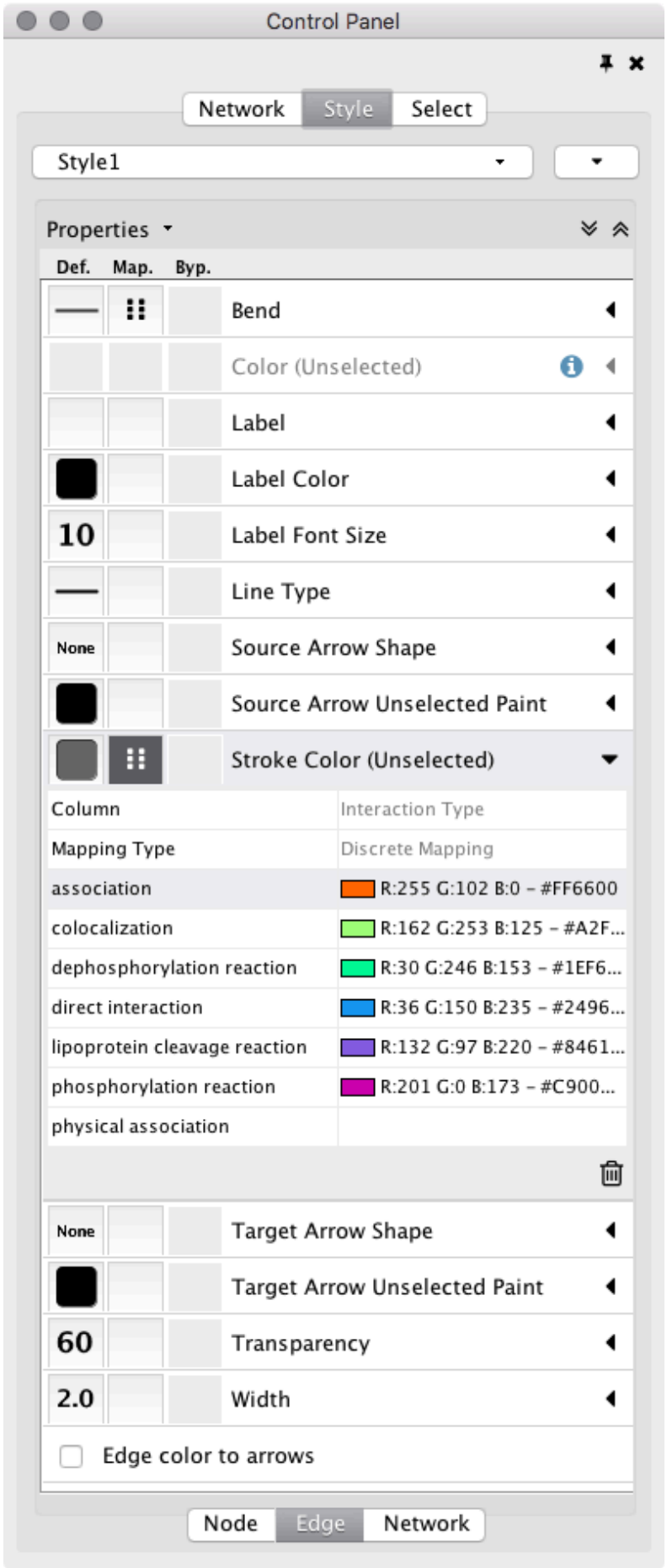
- Click + icon on the Table Panel
- Create new **Single Boolean Column**
- Name it ***query genes***
- Click any of the cell under the query genes column in the table browser
- Type true and press enter
- Right-click the cell
- Select ***Apply to selected nodes***

Now all of the genes in the original query list have special property “query genes” and you can use this for custom visualization.

4. Creating Visual Style

- Apply edge bundling: Layout—>Bundle Edges —> All nodes and edges
- Click Style tab
- Create new visual Style by clicking the triangle icon next to current style name
- Create your custom Visual Style: Use the following as a template but be creative!


Control Panel
Network
Style
Select
Style1
Properties
Def.
Map.
Byp.
Border Paint
0.0
Border Width
Fill Color
Column
Interactor Type
Mapping Type
Discrete Mapping
deoxyribonucleic acid
double stranded deoxyribonu...
R:0 G:51 B:204 - #0033CC
gene
R:0 G:255 B:51 - #00FF33
protein
ribonucleic acid
R:255 G:102 B:0 - #FF6600
Height
Image/Chart 1
Label
Column
Human Readable Label
Mapping Type
Passthrough Mapping
Label Color
12
Label Font Size
Column
query genes
Mapping Type
Discrete Mapping
true
55
Label Position
Shape
Column
query genes
Mapping Type
Discrete Mapping
true
Diamond
25.0
Size
Column
query genes
Mapping Type
Discrete Mapping
true
60
200
Transparency
Width
Lock node width and height
Node
Edge
Network


Control Panel
Network
Style
Select
Style1
Properties
Def.
Map.
Byp.
Bend
Color (Unselected)
Label
Label Color
10
Label Font Size
Line Type
None
Source Arrow Shape
Source Arrow Unselected Paint
Stroke Color (Unselected)
Column
Interaction Type
Mapping Type
Discrete Mapping
association
R:255 G:102 B:0 - #FF6600
colocalization
R:162 G:253 B:125 - #A2F...
dephosphorylation reaction
R:30 G:246 B:153 - #1EF6...
direct interaction
R:36 G:150 B:235 - #2496...
lipoprotein cleavage reaction
R:132 G:97 B:220 - #8461...
phosphorylation reaction
R:201 G:0 B:173 - #C900...
physical association
None
Target Arrow Shape
Target Arrow Unselected Paint
60
Transparency
2.0
Width
Edge color to arrows
Node
Edge
Network

I'll show the result of this mappings in the 2nd lecture.

Part 2: Setup Python and Jupyter Notebook

We will use Jupyter Notebook and Python to control Cytoscape in the next lecture. Please make sure you can use them on your machine.

- Read and follow this instruction: https://github.com/idekerlab/tsri-lecture/blob/master/documents/Setup%20Guide.pdf
- Start Cytoscape
- Start Jupyter Notebook
- Create a new Python 3 notebook
- Copy & Paste the following code to the cell and run:

```
from py2cytoscape.data.cyrest_client import CyRestClient
from IPython.display import Image

cy = CyRestClient()
yeast_net = cy.network.create_from('http://
chianti.ucsd.edu/~kono/data/galFiltered.sif')
net_svg = yeast_net.get_png()

Image(net_svg)
```

If you can see the image like the following, you are ready to use Cytoscape via REST API!

jupyter Untitled Last Checkpoint: 10 minutes ago (autosaved)

File Edit View Insert Cell Kernel Help Python 3

Code CellToolbar

In [13]:
```
from py2cytoscape.data.cyrest_client import CyRestClient
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net_svg = yeast_net.get_png()

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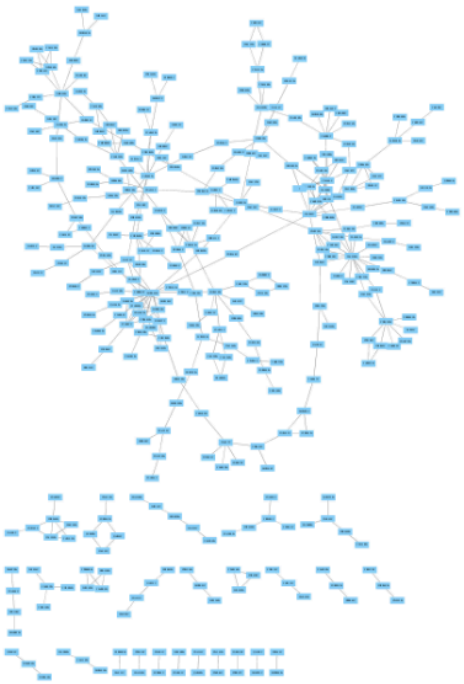
Out[13]: