Cytoscape workshop, Tel Aviv University, 25/4/18 -- hands-on examples

\*apps to install: yfiles styles, String + string enrichment, ClueGO

1. String App:
   1. Choose string at the network tab
   2. Paste the list from “cvas\_symbols.txt”
   3. Make sure that the organism is “Homo sapiens”
   4. Search with default parmeters
   5. Change confidence to 0.9, re-layout to “yfiles organic” to see what is left of the largest connected component
   6. Perform functional enrichment with the string enrichment app (from the apps menu)
   7. At the string enrichment tab at the table panel, choose “oxidative phosphorylation” and see the selected nodes
   8. Start a new session (File, new, session)
   9. Repeat network generation with the list of “spinalcord\_list” (uniprot ids of spinal cord related genes)
   10. Go the select tab, and see how many nodes are selected with values of 5 for “tissue: bone” vs “tissue: nervous system”. Try additional tissues. High expression level at the nervous system is expected.

* If you have time, try to retrieve interaction from one of the imex-curated databases using PSICQUIC, and then select just the nodes on the list (“spinalcord\_list” file). Compare number of interactions with respect to default STRING parameters

1. Analyze given network:
   1. Import the network “subnetwork\_pkd\_unfiltered.SIF” (File, Import, Network, from file – or Ctrl+L)
   2. Select the largest connected component by selecting an arbitrary node and expanding selection by “Ctrl+6”
   3. Make new network (look for the button at the tool bar)
   4. Remove self-loops (Edit, Remove self-loops), check the network name and remove all self-loops
   5. Topological analysis: (Tools, network analyzer, network analysis, analyze network) choose “treat as undirected”
   6. Find the degree column at the Table panel. Sort by degree. What is the highest degree?
   7. Color the nodes by the degree (from 1 to 7); do this by opening the color sub menu, choose the degree column and “continuous mapping”; note coloring for COLA1 and PLG
   8. Now color the nodes by the BetweenessCentrality (from 0 to 0.42); note coloring for MMP3, LTBP1, FBN1
   9. Enter the style panel and open “size” sub-menu
   10. Choose the degree column, and choose mapping type to be continuous
   11. Enter “current mapping”, adjust min and max to be 1 and 7 respectively
   12. Set the size for the left handle (min, little square at the left side) to be 30 and the size for the right handle (max) to be 70
   13. Add expression data: (File, Import, Table, from file)
   14. Choose the file “pkd”
   15. Color by Log2FC, set min and max to -8.7 to 6.1
   16. Try some layouts, choose your favorite and export an image (File, export as image)
2. ClueGO:
   1. Open the ClueGO app from the Apps menu
   2. Make sure that the organism is Homo Sapiens, and the Id type is SymbolID
   3. Load markers list: either copy and paste, or upload the file “cvas\_symbols.txt” (genes linked to cardiovascular diseases)
   4. On the ontologies/pathways, check Wikipathways
   5. Check “show only pathways with pV<0.05”
   6. Start
   7. Go over the enriched annotations. Is it related to cardiovascular diseases?
   8. In the visual style, color by significance. Darker nodes are more statistically significant
   9. Uncheck Wikipathways, check “KEGG”
   10. At the Cluepedia panel (tables panel), add participating genes