

Canadian Bioinformatics Workshops

www.bioinformatics.ca
bioinformaticsdotca.github.io



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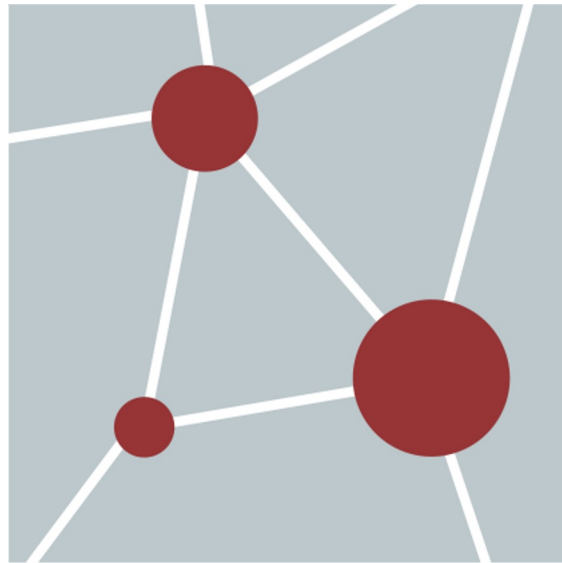
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Module 3: Network Visualization and Analysis: practical lab



Ruth Isserlin
Pathway and Network Analysis
June 26-28, 2024



**BADER
LAB**



UNIVERSITY OF
TORONTO



Donnelly Centre
Cellular & Biomolecular Research
UNIVERSITY OF TORONTO

Learning Objectives

- By the end of this lecture, you will:
 - Understand...
 - Be able to define...
 - Know...

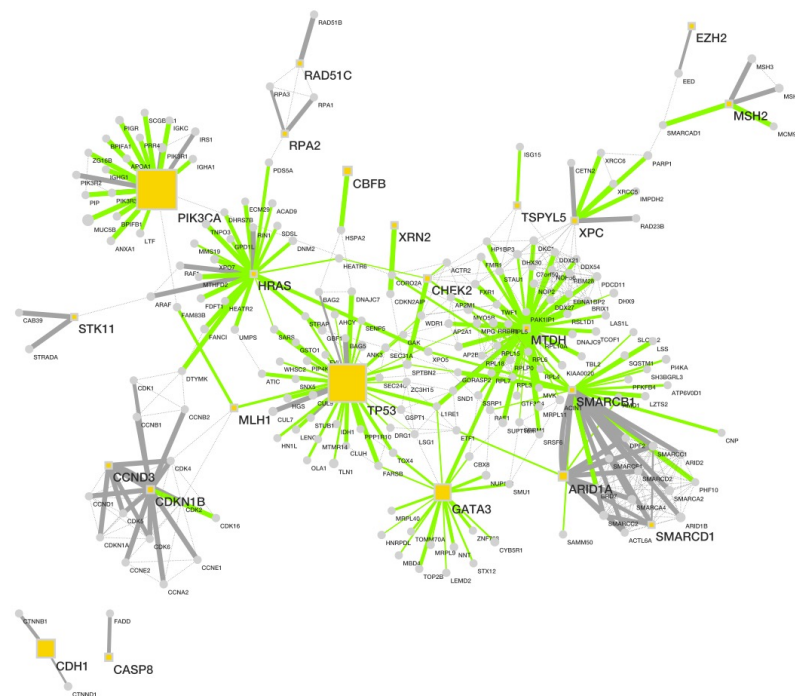
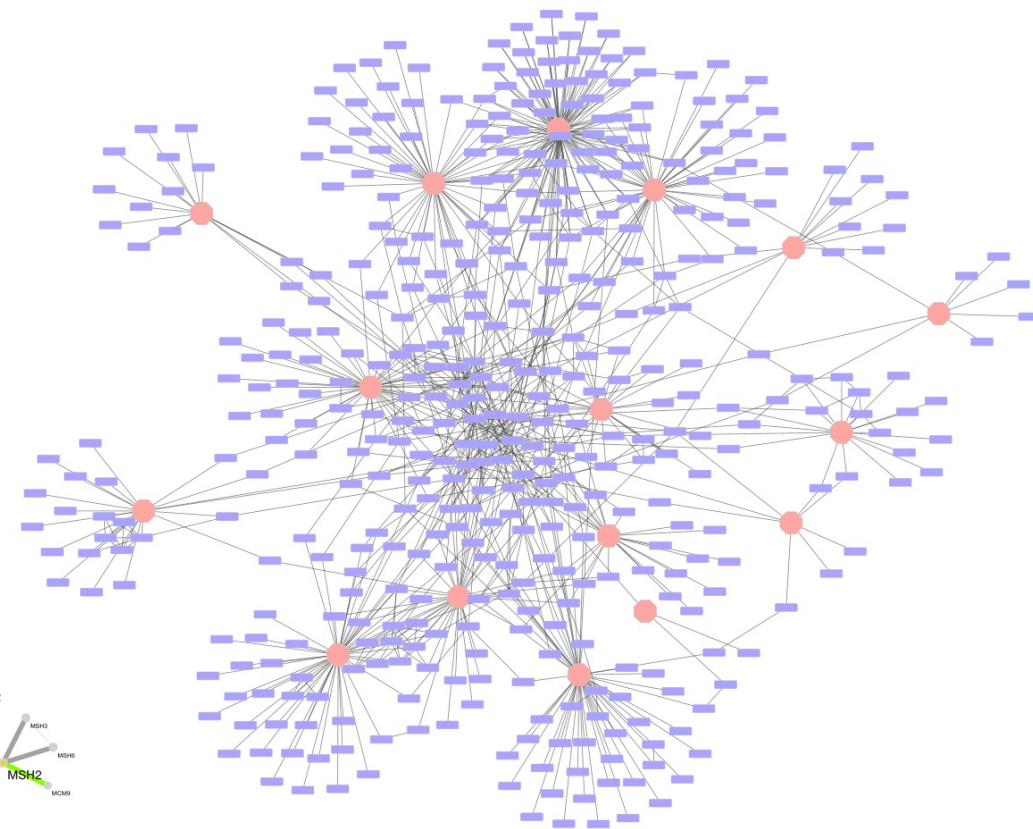
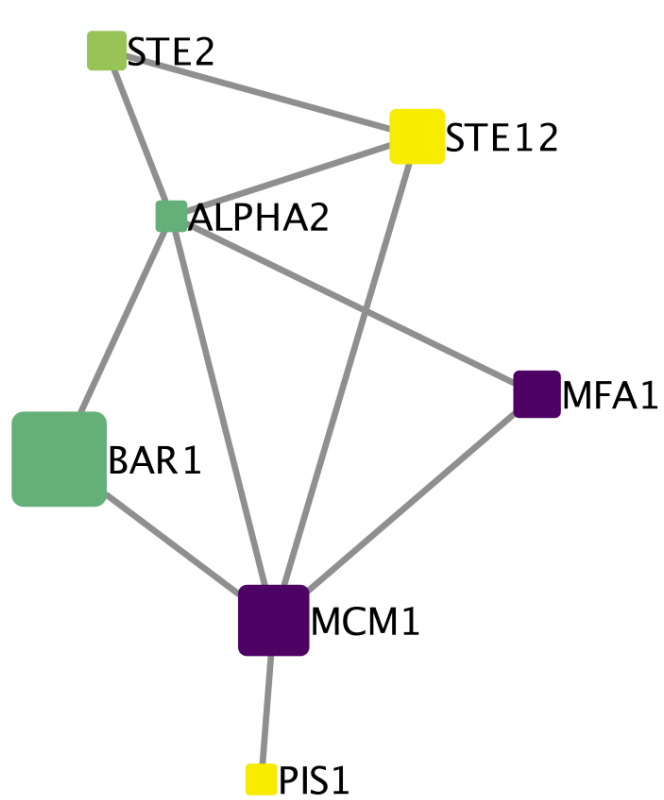
Learning Objectives of Module

- By the end of this lab, you will:
 - Be able to create simple networks with **Cytoscape** using different **data types** and make use of basic cytoscape functions to visualize multiple aspects of the data.
 - Be able to run **EnrichmentMap** with both g:profiler and GSEA results data and further analyse the network using additional apps such as autoannotate.

Part 1:



Cytoscape





Time to start practical part:



Cytoscape Primer

- Go to the CBW course page and go to module 3.
- Open the 'Lab practical Cytoscape Primer' document.
- Download required files on your computer.
- Do the exercise at your own pace and ask teaching assistants for help or questions.

Part 2:

g:Profiler



Create Enrichment Map

Data Set List:

+ Add...

gProfiler_hsapiens_lab2_results_GEM_termin3_max10000.gem

gProfiler_hsapiens_lab2_results_GEM_termin3_max250.gem

* Name: gProfiler_hsapiens_lab2_results_GEM_termin3_max10000.gem

* Analysis Type: Generic/gProfiler/Enrichr

* Enrichments: /Users/risserlin/Bader Lab Dropbox/Ruth Isserlin's files/Sourcecode/CBW_Pathways_2024/Module

* GMT: Ruth Isserlin's files/Sourcecode/CBW_Pathways_2024/Module3/gprofiler/data/gprofiler_full_hsapiens.name.gmt

Ranks:

Expressions:

Classes:

Phenotypes: Positive: UP Negative: DOWN

Network Name: ☒ Use Default gProfiler_hsapiens_lab2_results_GEM_termin3_max10000.gem

Layout: yFiles Organic Layout

Number of Nodes (gene-set filtering)

Filter genes by expressions:

FDR q-value cutoff: 0.001

Number of Edges (gene-set similarity filtering)

Data Set Edges: Automatic

sparse

dense

☐ Scientific Notation

☐ Show Advanced Options

Reset

Show Command

?

Cancel

Build





Time to start practical part:

g:Profiler



- Go to the CBW course page.
- Download or open the Module 3 Lab practical documents.
- Download required files on your computer.
- Do the exercise at your own pace and ask teaching assistant for help or questions.



Bonus – Run GSEA programmatically from R

- See example code - https://risserlin.github.io/CBW_pathways_workshop_R_notebooks/create-enrichment-map-from-r-with-gprofiler-results.html
- For instructions on how to set up R so you can run the above notebooks - https://risserlin.github.io/CBW_pathways_workshop_R_notebooks/setup.html

Part 3:





Time to start practical part:



- Go to the CBW course page.
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- Download required files on your computer.
- Do the exercise at your own pace and ask teaching assistant for help or questions.



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Links to more tutorials

Step by Step Protocol: Pathway enrichment analysis of -omics data:

<https://www.nature.com/articles/s41596-018-0103-9>

Notebooks of the protocol:

https://github.com/BaderLab/Cytoscape_workflows/tree/master/EnrichmentMapPipeline

https://baderlab.github.io/Cytoscape_workflows/EnrichmentMapPipeline/index.html

We are on a Coffee Break & Networking Session

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