Canadian Bioinformatics Workshops

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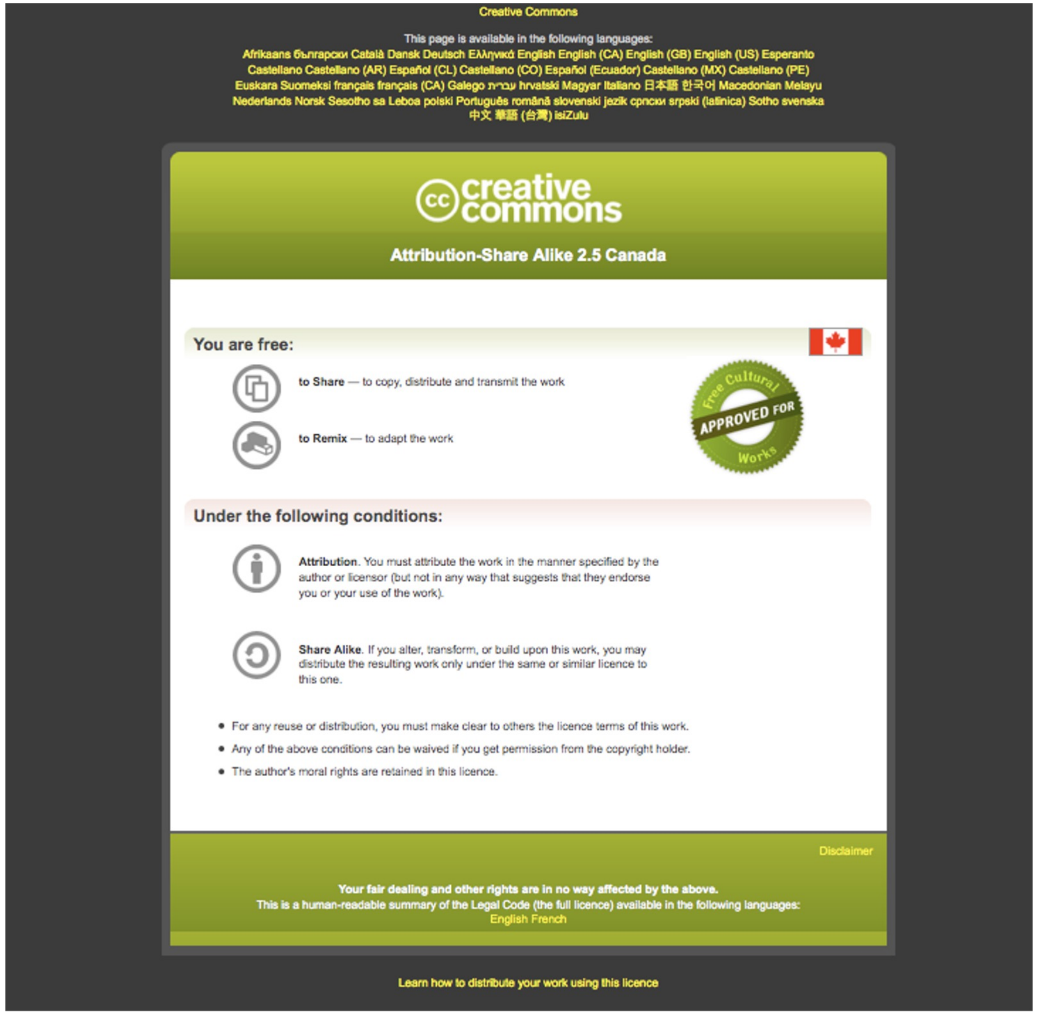

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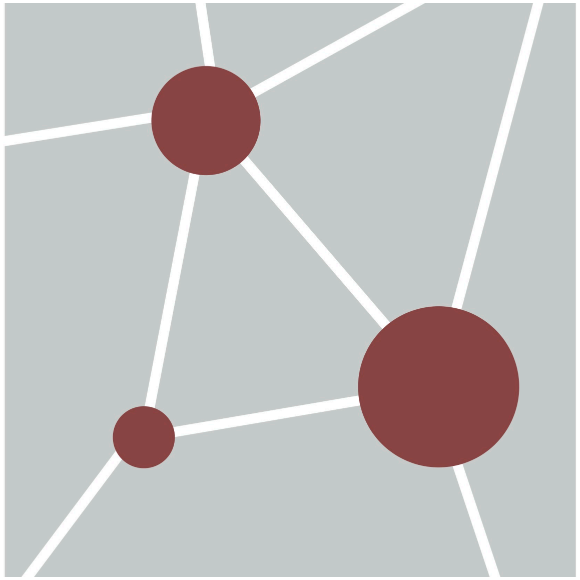
Network Visualization and Analysis: practical lab

Ruth Isserlin

Pathway and Network Analysis

June 5-7, 2023



Auto Annotate

Word Cloud

BADER LAB

UNIVERSITY OF TORONTO

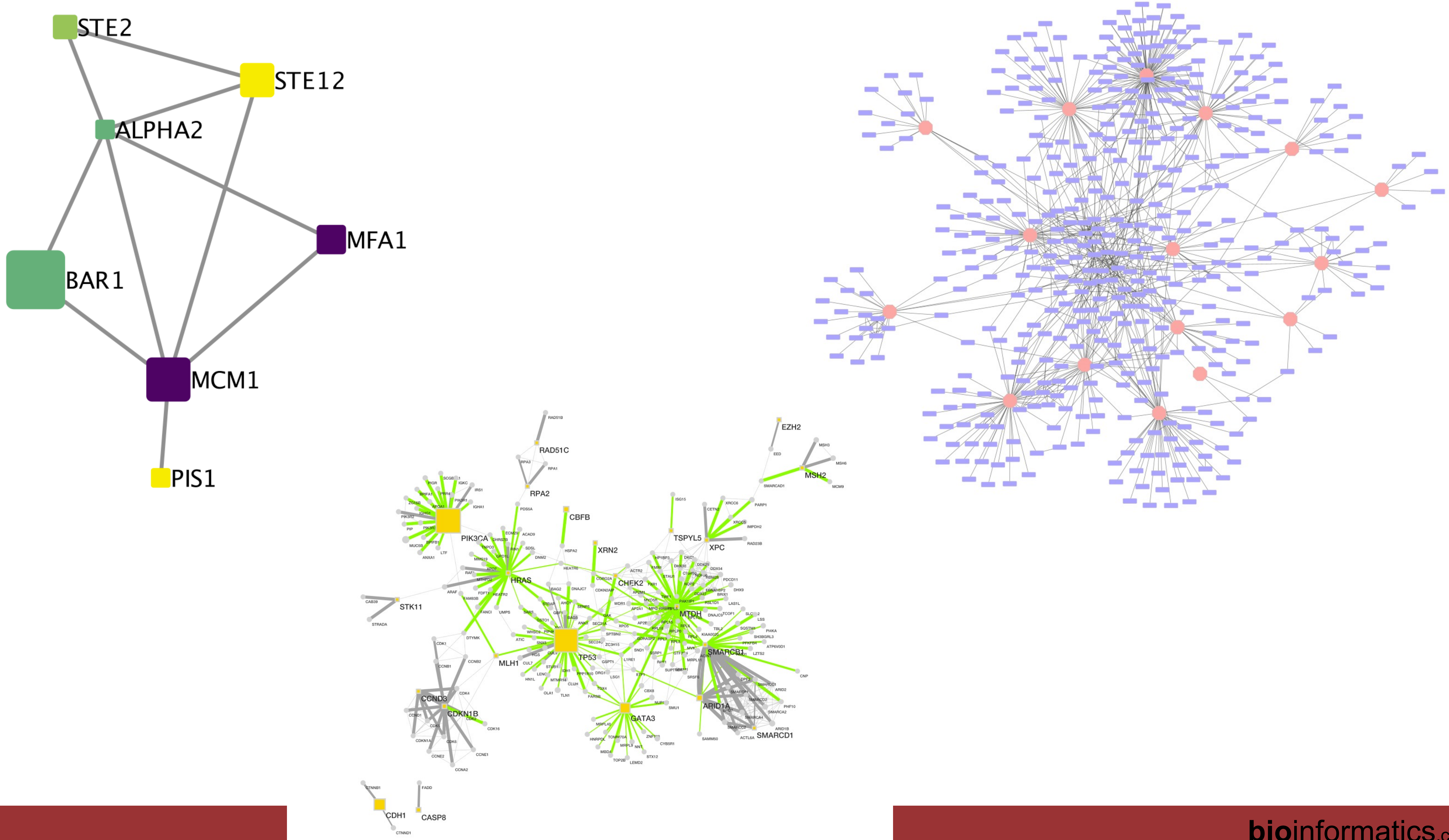
Donnelly Centre
Cellular & Biomolecular Research
UNIVERSITY OF TORONTO

Learning Objectives of Module

- By the end of this lab, you will:
  - Be able to 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


STE2
STE12
ALPHA2
MFA1
BAR1
MCM1
PIS1
RAD51C
EZH2
RPA2
MSH2
CBFB
PIK3CA
XRN2
TSPYL5
XPC
HRAS
CHEK2
STK11
MTDH
TP53
MLH1
SMARCB1
CCND3
CDKN1B
ARID1A
GATA3
SMARCD1
CDH1
CASP8

Time to start practical part:

Cytoscape Primer

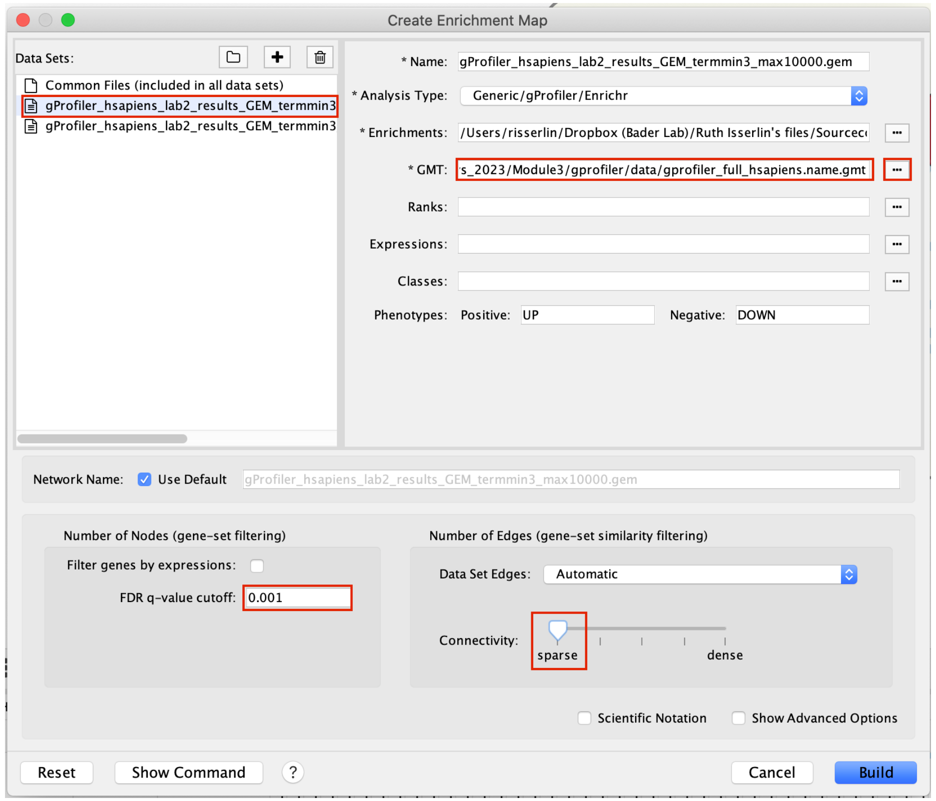
- Go the the CBW course page and go to module 3.
- Open the ‘Lab practical Cytoscape Primer’ document.
- Download required files on your computer.
- Do the exercise at your own pace and ask teaching assistants for help or questions.

Part 2:

g:Profiler

↓

EM



Create Enrichment Map

Data Sets:

- Common Files (included in all data sets)
- gProfiler_hsapiens_lab2_results_GEM_termmin3
- gProfiler_hsapiens_lab2_results_GEM_termmin3

* Name: gProfiler_hsapiens_lab2_results_GEM_termmin3_max10000.gem

* Analysis Type: Generic/gProfiler/Enrichr

* Enrichments: /Users/risserlin/Dropbox (Bader Lab)/Ruth Isserlin's files/Sourcec

* GMT: s_2023/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_termmin3_max10000.gem

Number of Nodes (gene-set filtering)

Filter genes by expressions: ☐

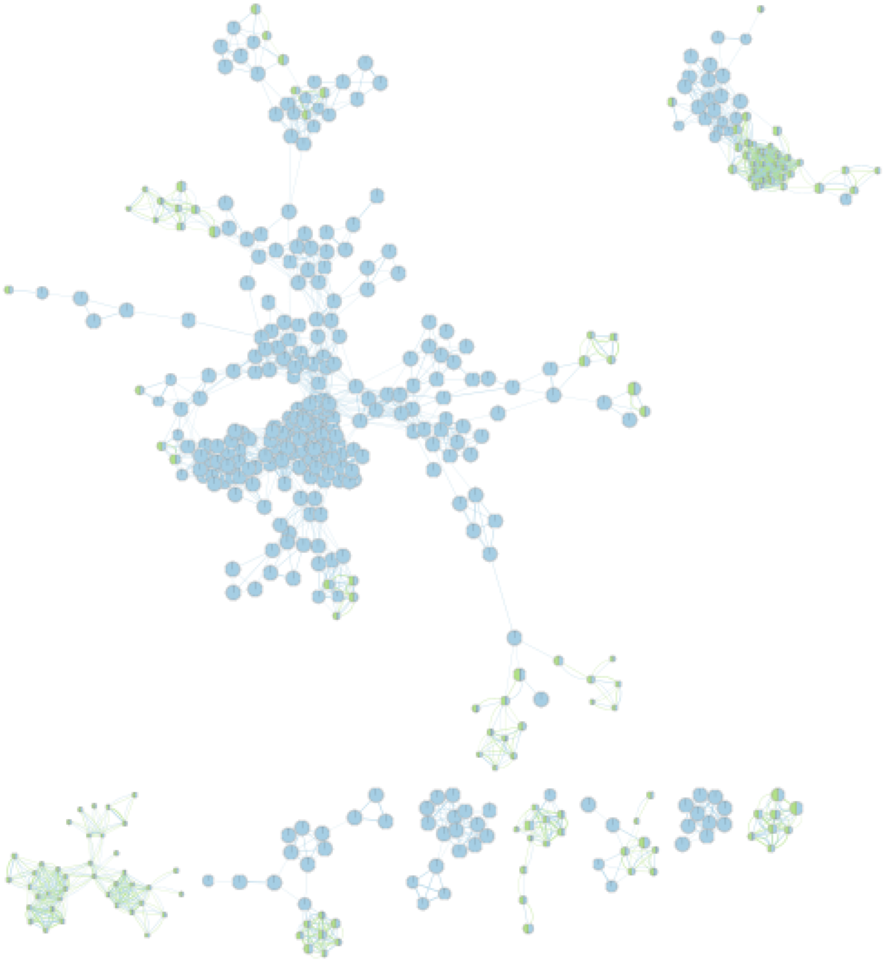
FDR q-value cutoff: 0.001

Number of Edges (gene-set similarity filtering)

Data Set Edges: Automatic

Connectivity: sparse dense

☐ Scientific Notation ☐ Show Advanced Options



Time to start practical part:

g:Profiler

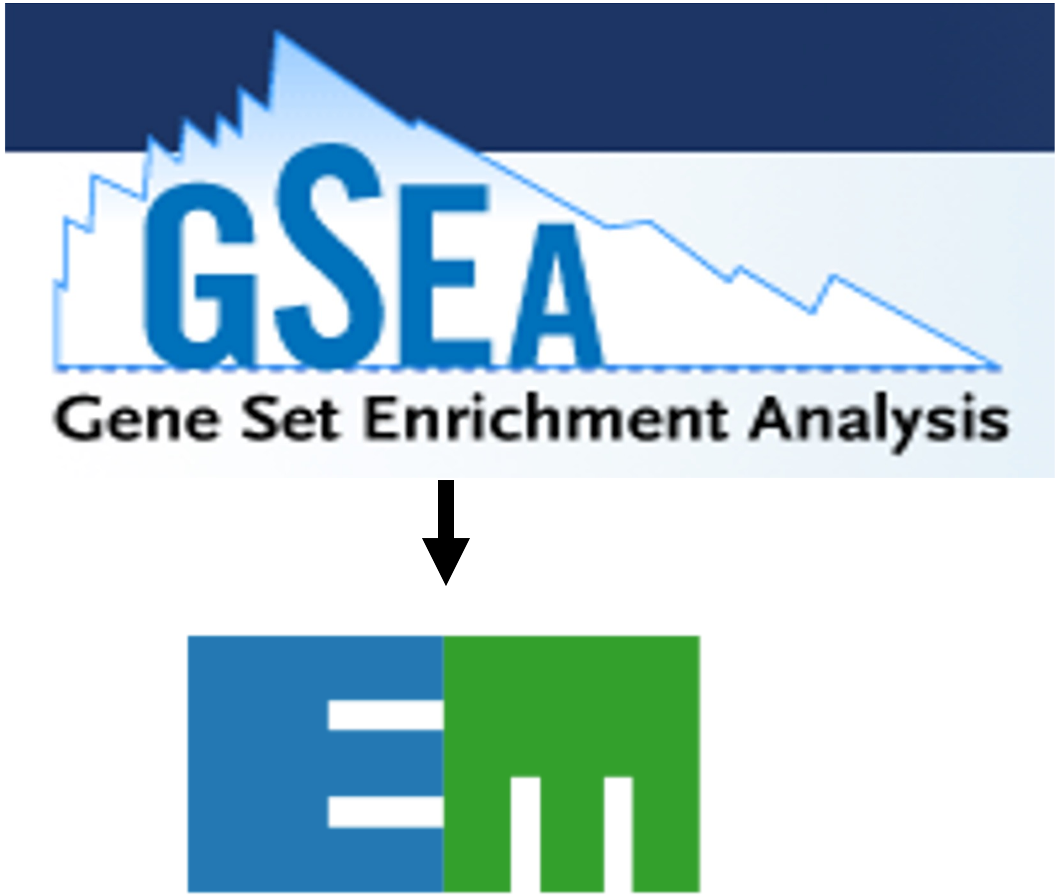
- Go the the CBW course page.
- Download or open the Module 3 Lab practical documents.
- Download required files on your computer.
- Do the exercise at your own pace and ask teaching assistant for help or questions.

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:

GSEA
Gene Set Enrichment Analysis

- Go the 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-gsea-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

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

Workshop Sponsors:

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