

# Canadian Bioinformatics Workshops

[www.bioinformatics.ca](http://www.bioinformatics.ca)

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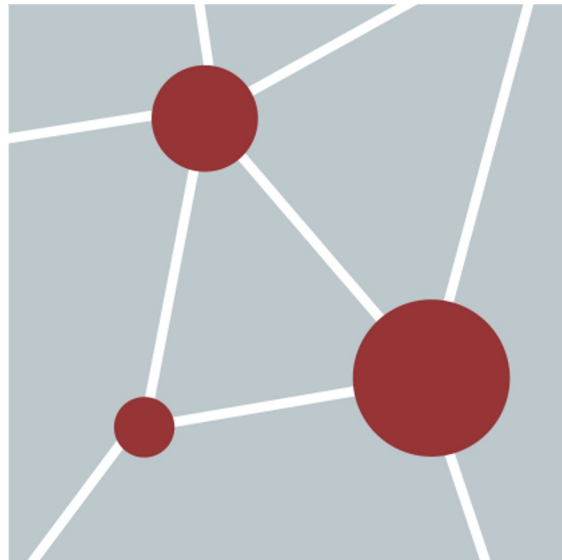
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# Module 3: Network Visualization and Analysis: Enrichment Map lab



# Learning Objectives of Module

- By the end of this lab, you will:
  - 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:

g:Profiler



**Create Enrichment Map**

Data Set List:

- gProfiler\_hsapiens\_lab2\_results\_GEM\_termm3\_max10000.gem
- gProfiler\_hsapiens\_lab2\_results\_GEM\_termm3\_max250.gem

\* Name: gProfiler\_hsapiens\_lab2\_results\_GEM\_termm3\_max10000.gem

\* Analysis Type: Generic/gProfiler/Enrichr

\* Enrichments: /Users/risserlin/Bader Lab Dropbox/Ruth Isserlin/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

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Network Name:  Use Default gProfiler\_hsapiens\_lab2\_results\_GEM\_termm3\_max10000.gem

Layout: yFiles Organic Layout

Number of Nodes (gene-set filtering)

Filter genes by expressions:

FDR q-value cutoff:

Number of Edges (gene-set similarity filtering)

Data Set Edges: Automatic

sparse  dense

Scientific Notation  Show Advanced Options





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](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](https://risserlin.github.io/CBW_pathways_workshop_R_notebooks/setup.html)



# Part 2:





Time to start practical part:



- 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-gsea-results.html](https://risserlin.github.io/CBW_pathways_workshop_R_notebooks/create-enrichment-map-from-r-with-gsea-results.html)
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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://github.com/BaderLab/Cytoscape_workflows/tree/master/EnrichmentMapPipeline)

[https://baderlab.github.io/Cytoscape\\_workflows/EnrichmentMapPipeline/index.html](https://baderlab.github.io/Cytoscape_workflows/EnrichmentMapPipeline/index.html)

# We are on a Coffee Break & Networking Session

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