bioinformatics.ca

Canadian Bioinformatics Workshops

www.bioinformatics.ca

Creative Commons

This page is available in the following languages:
Afrikaans български Català Dansk Deutsch Ελληνικά English English (CA) English (GB) English (US) Esperanto Castellano Castellano (AR) Español (CL) Castellano (CO) Español (Ecuador) Castellano (MX) Castellano (PE) Euskara Suomeksi français français (CA) Galego עברית hrvatski Magyar Italiano 日本語 한국어 Macedonian Melayu Nederlands Norsk Sesotho sa Leboa polski Português română slovenski jezik српски srpski (latinica) Sotho svenska 中文 華語 (台灣) isiZulu

creative commons

Attribution-Share Alike 2.5 Canada

You are free:

to Share — to copy, distribute and transmit the work

to Remix — to adapt the work

Free Cultural Works APPROVED FOR

Under the following conditions:

Attribution. You must attribute the work in the manner specified by the author or licensor (but not in any way that suggests that they endorse you or your use of the work).

Share Alike. If you alter, transform, or build upon this work, you may distribute the resulting work only under the same or similar licence to this one.

- For any reuse or distribution, you must make clear to others the licence terms of this work.
- Any of the above conditions can be waived if you get permission from the copyright holder.
- The author's moral rights are retained in this licence.

Disclaimer

Your fair dealing and other rights are in no way affected by the above.
This is a human-readable summary of the Legal Code (the full licence) available in the following languages:
English French

Learn how to distribute your work using this licence

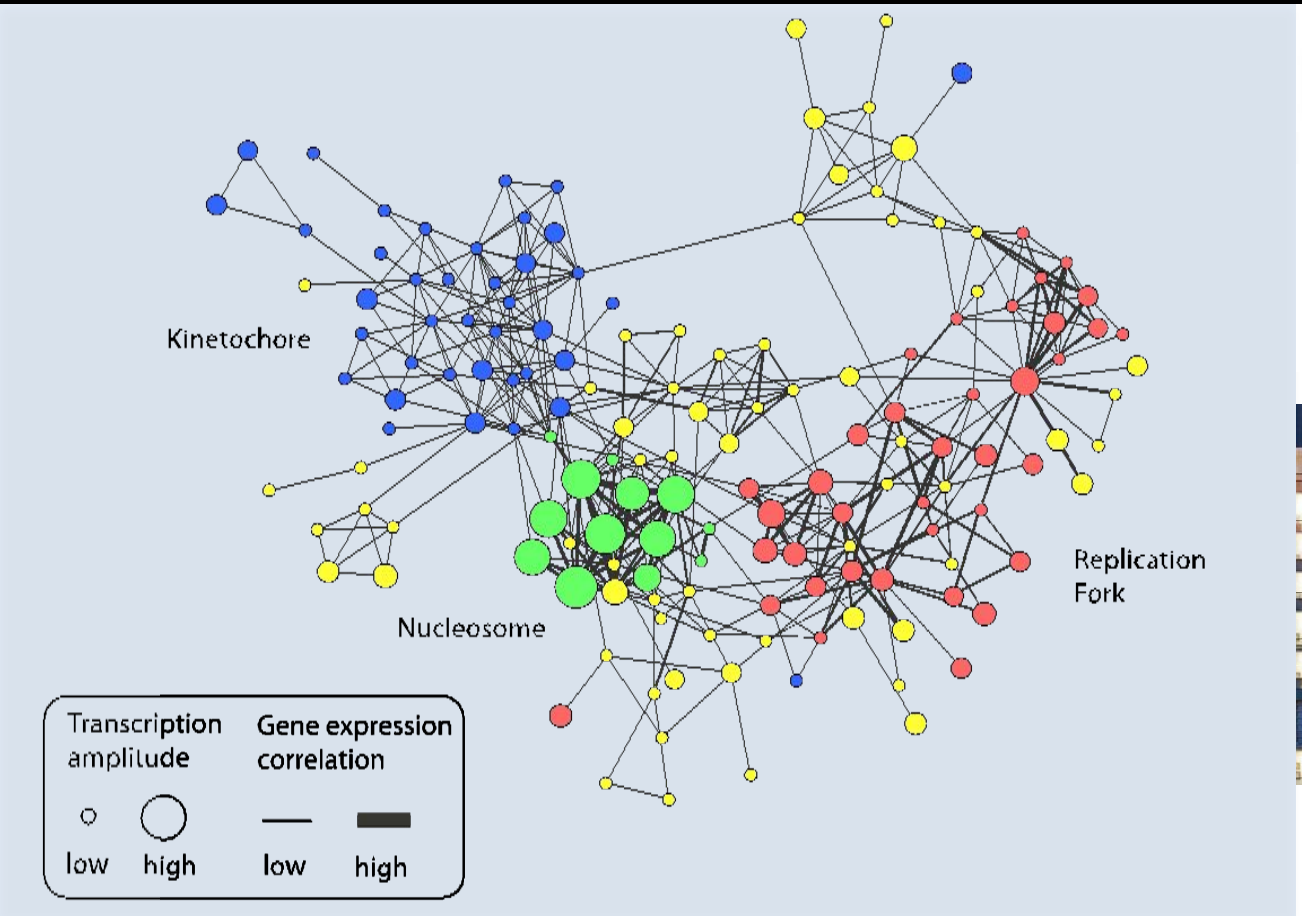
FINAL SLIDES

Veronique Voisin

Pathway and Network Analysis of –omic Data

June 26-28, 2016

bioinformatics.ca

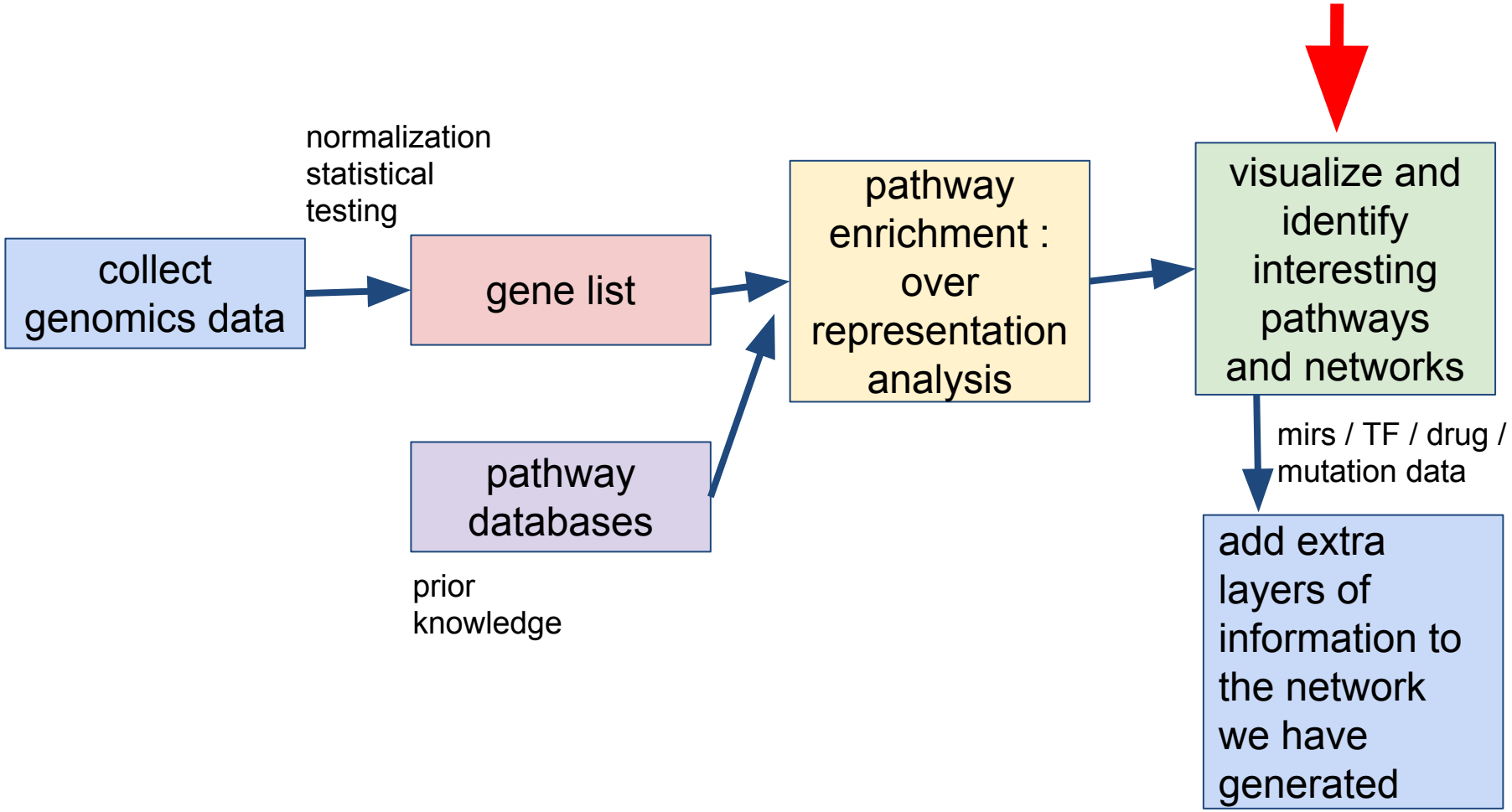


Donnelly Centre for Cellular + Biomolecular Research

UNIVERSITY OF TORONTO

http://baderlab.org

Where are we in the workflow?



Creating Networks

gene list

network

large (100- 2000 genes)

medium (100 genes)

small (1-50 genes)

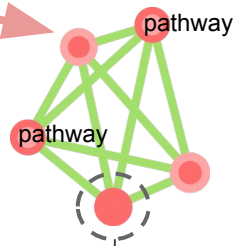
summarize by pathways

expand the list; use function prediction

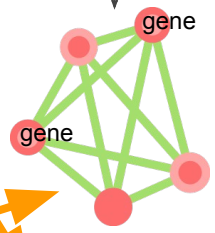
- represent as a network of pathways

- represent as a network of genes (gene products)

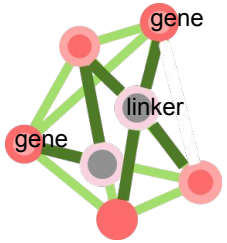
- represent as a network of gene (gene products) and add gene linkers



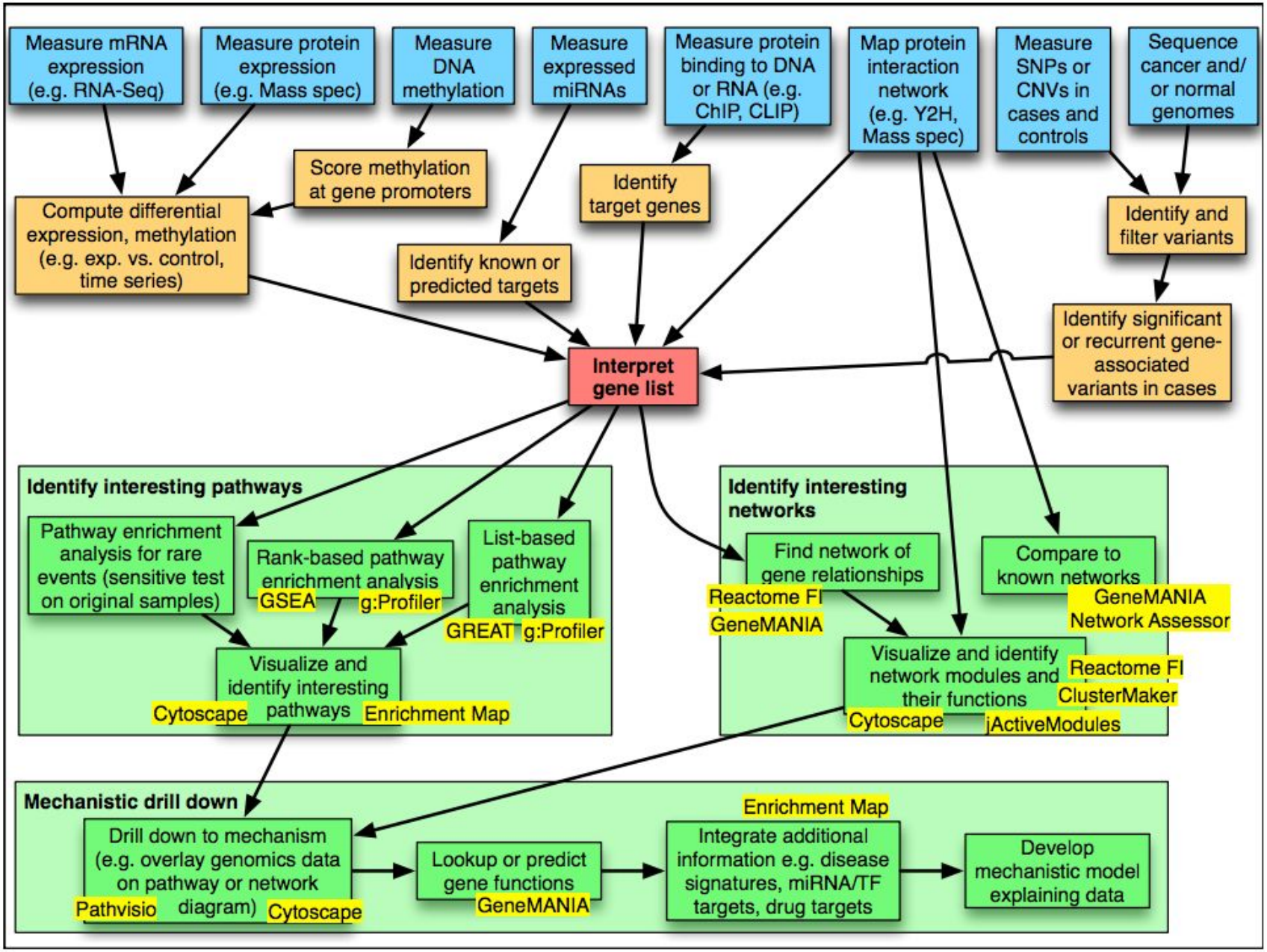
Enrichment Map



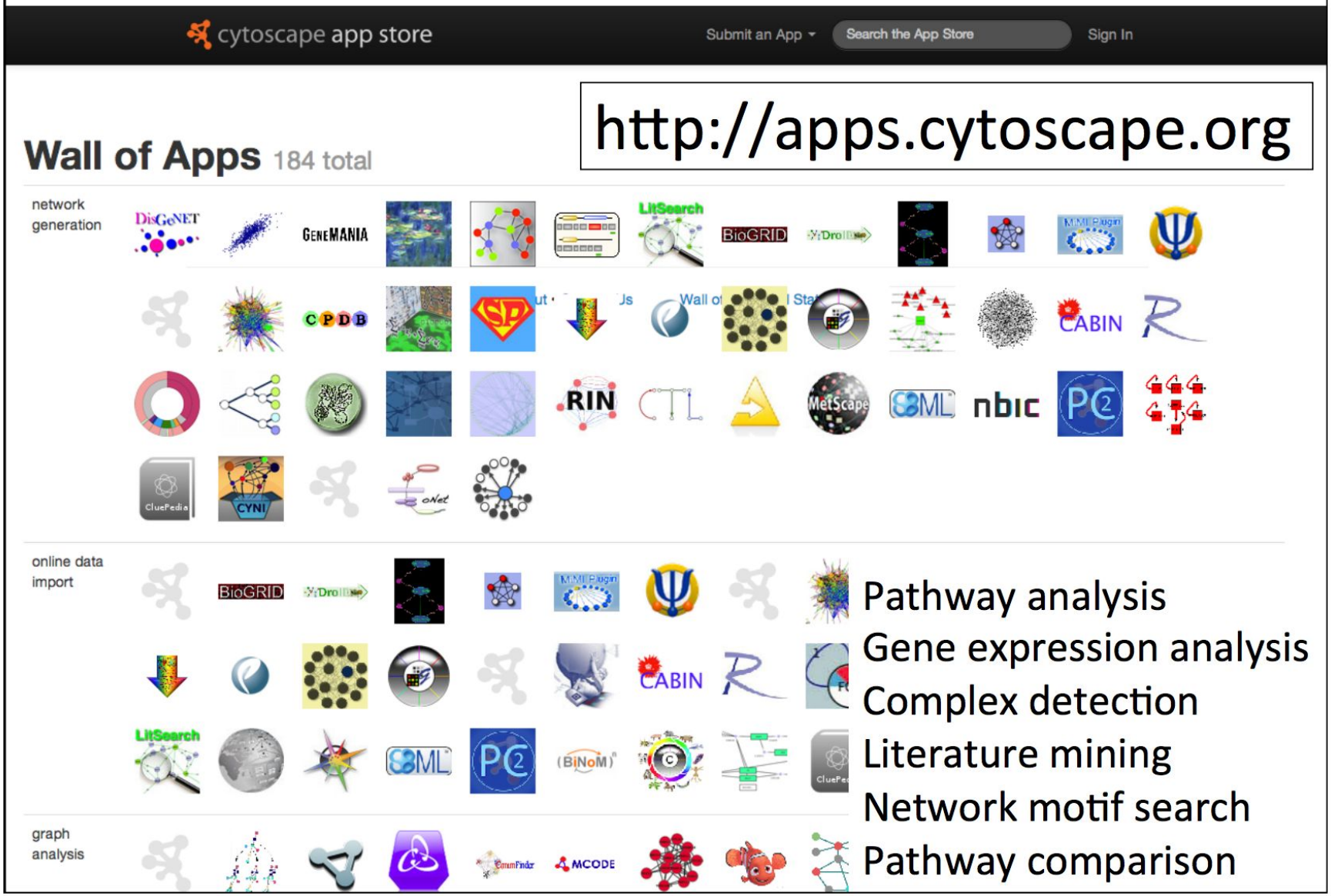
ReactomeFI



ReactomeFI with linkers or geneMANIA


Measure mRNA expression (e.g. RNA-Seq)
Measure protein expression (e.g. Mass spec)
Measure DNA methylation
Measure expressed miRNAs
Measure protein binding to DNA or RNA (e.g. ChIP, CLIP)
Map protein interaction network (e.g. Y2H, Mass spec)
Measure SNPs or CNVs in cases and controls
Sequence cancer and/ or normal genomes
Score methylation at gene promoters
Identify target genes
Identify and filter variants
Compute differential expression, methylation (e.g. exp. vs. control, time series)
Identify known or predicted targets
Identify significant or recurrent gene-associated variants in cases
Interpret gene list
Identify interesting pathways
Pathway enrichment analysis for rare events (sensitive test on original samples)
Rank-based pathway enrichment analysis
GSEA
g:Profiler
List-based pathway enrichment analysis
GREAT
g:Profiler
Visualize and identify interesting pathways
Cytoscape
Enrichment Map
Identify interesting networks
Find network of gene relationships
Reactome FI
GeneMANIA
Compare to known networks
GeneMANIA
Network Assessor
Visualize and identify network modules and their functions
Cytoscape
Reactome FI
ClusterMaker
jActiveModules
Mechanistic drill down
Drill down to mechanism (e.g. overlay genomics data on pathway or network diagram)
Pathvisio
Cytoscape
Lookup or predict gene functions
GeneMANIA
Enrichment Map
Integrate additional information e.g. disease signatures, miRNA/TF targets, drug targets
Develop mechanistic model explaining data

The Cytoscape App Store



CONGRATULATIONS!