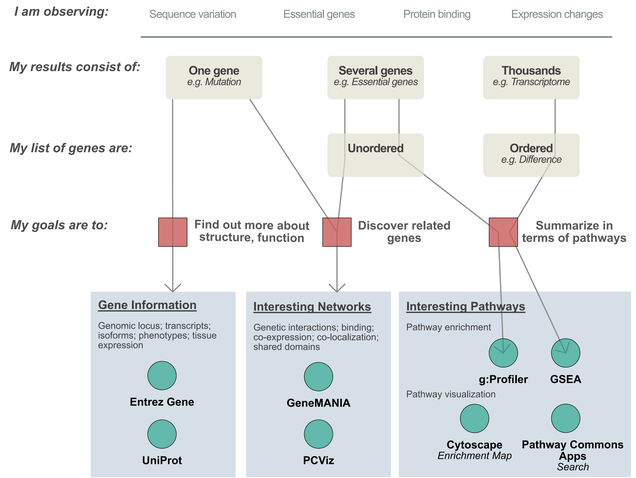
How can you interpret gene lists from -omics experiments?

Jeffrey V Wong[1], Augustin Luna[2,3], Emek Demir[4], Igor Rodchenkov[1], Özgün Babur[4], Chris Sander[2,3] and Gary Bader[1]
[1]University of Toronto, [2]Dana-Farber Cancer Institute, [3]Harvard Medical School, [4]Oregon Health & Sciences University

pathwaycommons.org

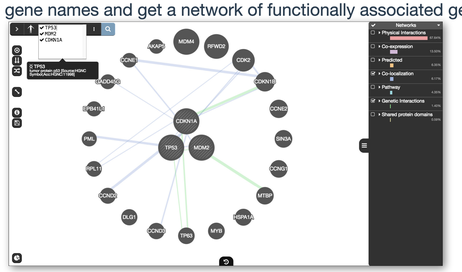
It depends on the number of genes and goals...



Discover related genes

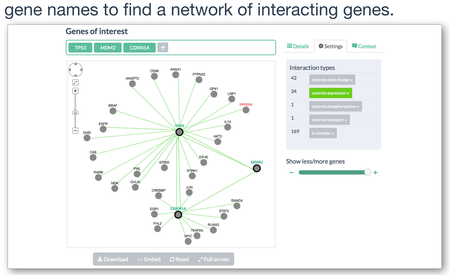
GeneMANIA - genemania.org/

Input gene names and get a network of functionally associated genes.



PCViz - pathwaycommons.org/pcviz/

Input gene names to find a network of interacting genes.



Summarize in terms of pathways

Several genes: Use g:Profiler

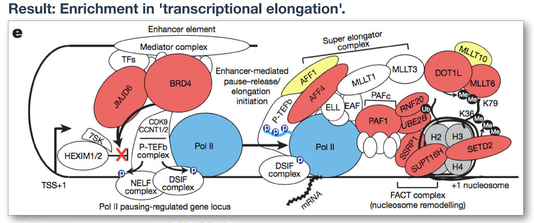
g:Profiler - biit.cs.ut.ee/gprofiler/

Input gene names and get multiple sources of functional evidence, including Gene Ontology terms and biological pathways.

Case Study: RNAi screen reveals 60 genes essential for glioblastoma growth *in vivo*. What pathways are represented?

(Cytoscape Enrichment Map)

Result: Enrichment in 'transcriptional elongation'.



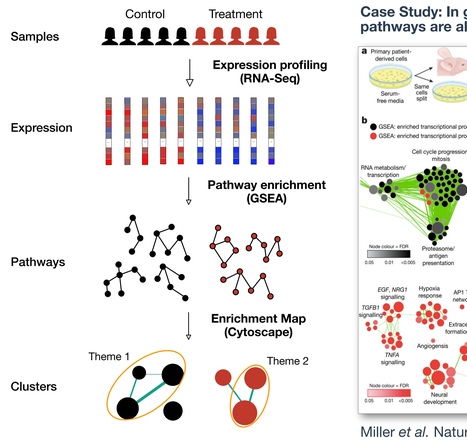
Miller *et al.* Nature vol. 547 (2017)

Many genes: Use GSEA & Enrichment Map

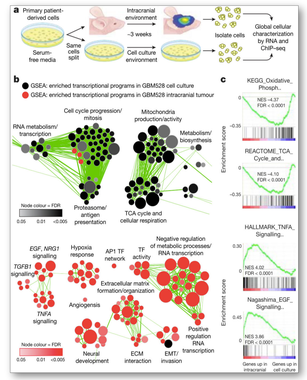
Guide - pathwaycommons.org/guide/

The Pathway Commons 'Guide' is an online textbook for pathway understanding.

See our **pathway enrichment analysis workflows** for step-by-step instructions on how to convert transcriptomic differences into a corresponding set of pathways using Gene Set Enrichment Analysis (GSEA); use Cytoscape Enrichment Map to visually group pathways by shared themes. Also available as an R Notebook.



Case Study: In glioblastoma, which pathways are altered *in vivo (in vitro)*?



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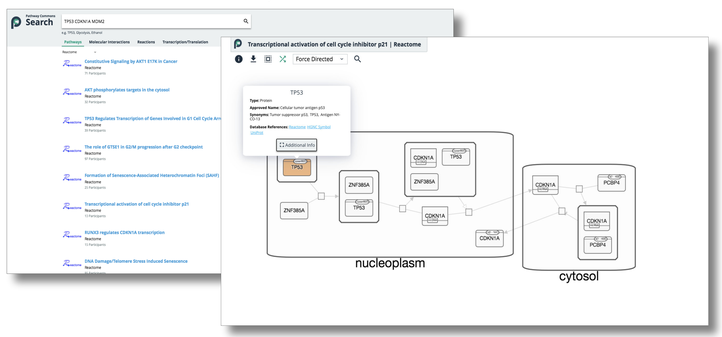
Visualize a pathway: Pathway Commons Apps

Search - pathwaycommons.org/pathways/

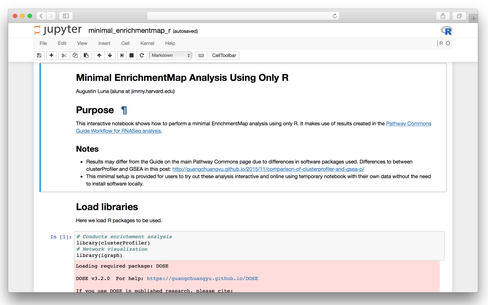
Input keywords or gene names and get relevant pathways from public pathway and interaction databases in Pathway Commons.



Coming soon: More apps

Pathway analysis & visualization

Interactive Jupyter and R Notebooks that couple pathway enrichment analysis with visualization of results.



Pathway Commons: A pathway resource

Pathway Commons - pathwaycommons.org/

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Public databases

BIND • BioGRID • CORUM • CTD • DIP • DrugBank • HPRD • HumanCyc • IntAct (Complex) • INOH • KEGG • miRTarBase • MSigDB • NCI - PID • NetPath • PANTHER Pathway • PhosphoSitePlus • Reactome • Recon X • SMPD • WikiPathways

ID Mapping
Validation
Integration

Pathway Commons

Over **4 000** pathways & **1.3 million** interactions:

Metabolic Pathways
Molecular Interactions
Signalling Pathways
Regulatory Networks
Genetic Interactions

For programmers: Get the data

Downloads - pathwaycommons.org/downloads/

Perform enrichment analyses with gene set database (GMT) files which list genes in each pathway; View and analyze pathways using Simple Interaction Format (SIF) files which list interacting gene pairs; Get rich, machine-readable descriptions in the Biological Pathway Exchange (BioPAX) format.

Web services - pathwaycommons.org/pc2/

Perform a full-text Search over the entire database; Get a specific pathway or interaction in the database in a variety of output formats (BioPAX, SIF, SBGN-ML, GMT); Use Traverse and Graph services to access and navigate over pathways and interactions in the database.

Tools

Search and view pathways in **Cytoscape** with the **CyPath2 app.** Export and validate BioPAX using the **Paxtools** software library; Use **R** to interact with pathway data in BioPAX using the **paxtoolsr package**; Visually interact with pathways using **Chisio BioPAX Editor (ChiBE)**.

Contact and links

Help email - pathway-commons-help@googlegroups.com
Github - github.com/pathwaycommons/
Twitter - @pathwaycommons
Cytoscape - www.cytoscape.org/

- Cerami E. *et al. Pathway Commons, a web resource for biological pathway data*. Nucleic Acids Research, 39: D685-90, 2011.
- Reimand J. *et al. g:Profiler - a web server for functional interpretation of gene lists.* Nucleic Acids Research, 44(W1): W83-89, 2016.
- Warde-Farley *et al. The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function*. Nucleic Acids Research, 38: W214–W220, 2010.