



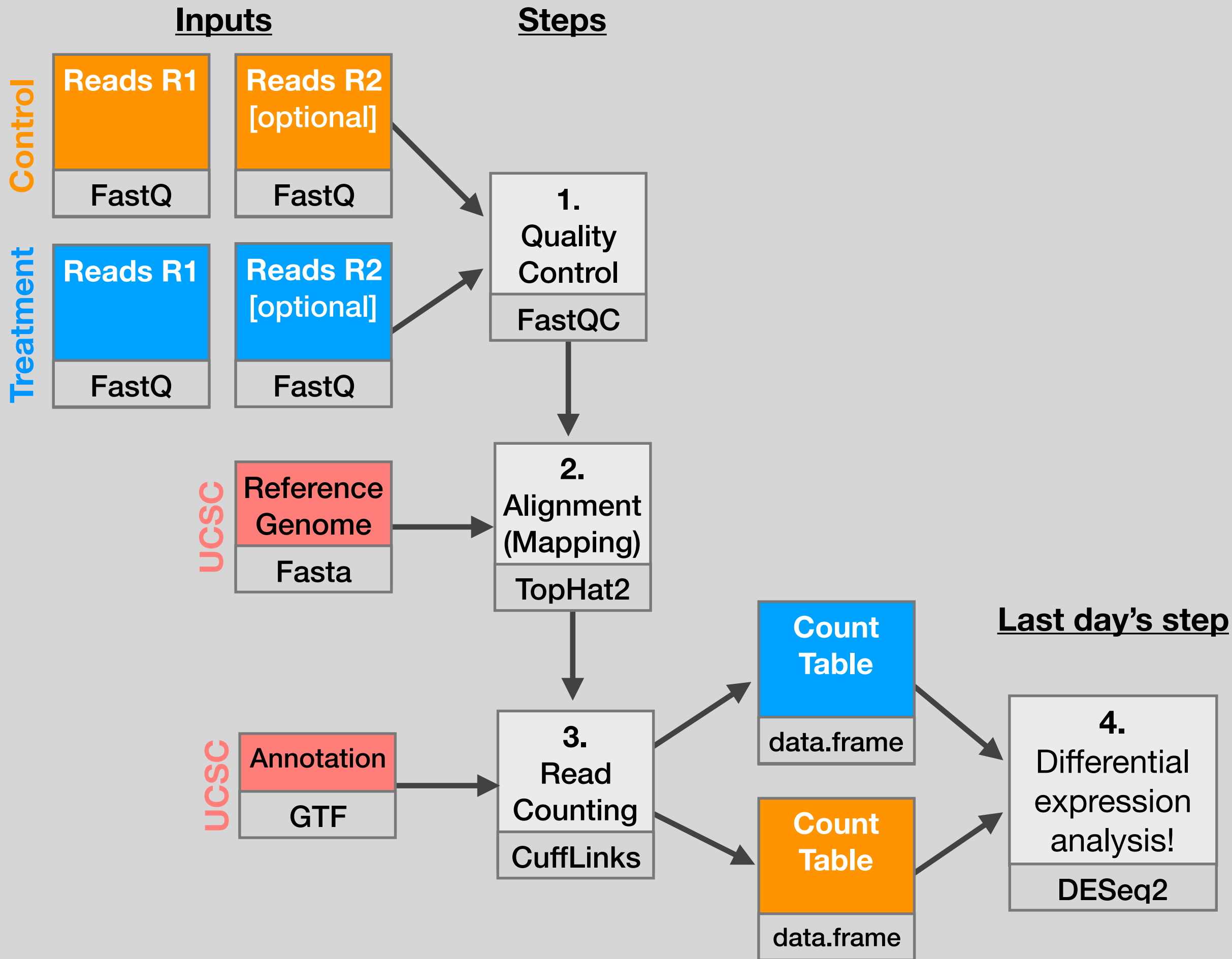
# BGGN 213

## Pathway Analysis and the Interpretation of Gene Lists

Lecture 15

Barry Grant  
UC San Diego

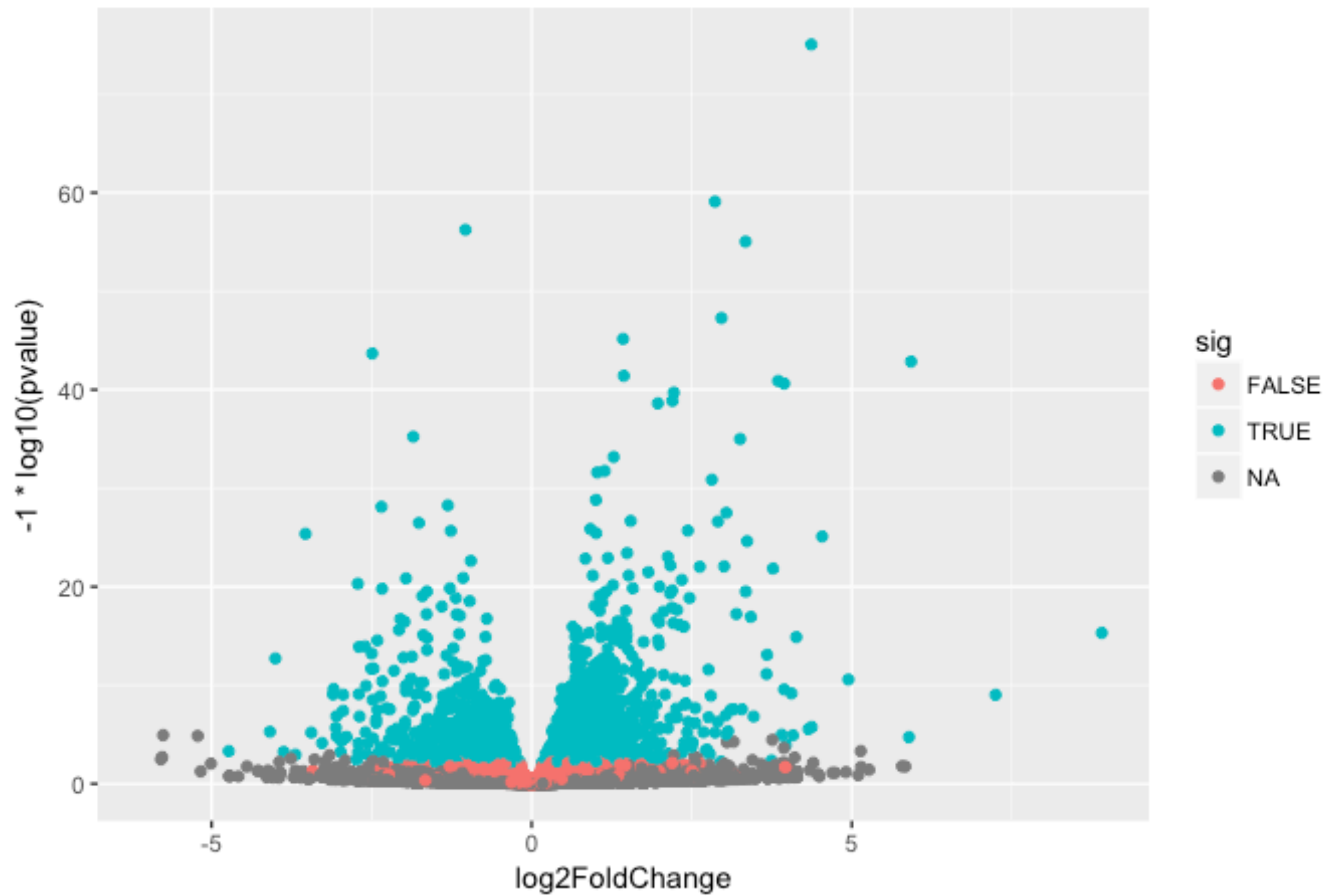
<http://thegrantlab.org/bggn213>





X	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	symbol
ENSG00000152583	954.77093	4.3683590	0.23713648	18.421286	8.867079e-76	1.342919e-71	SPARCL1
ENSG00000179094	743.25269	2.8638885	0.17555825	16.313039	7.972621e-60	6.037267e-56	PER1
ENSG00000116584	2277.91345	-1.0347000	0.06505273	-15.905557	5.798513e-57	2.927283e-53	ARHGEF2
ENSG00000189221	2383.75371	3.3415441	0.21241508	15.731200	9.244206e-56	3.500088e-52	MAOA
ENSG00000120129	3440.70375	2.9652108	0.20370277	14.556557	5.306416e-48	1.607313e-44	DUSP1
ENSG00000148175	13493.92037	1.4271683	0.10036663	14.219550	6.929711e-46	1.749175e-42	STOM
ENSG00000178695	2685.40974	-2.4890689	0.17806407	-13.978501	2.108817e-44	4.562576e-41	KCTD12
ENSG00000109906	439.54152	5.9275950	0.42819442	13.843233	1.397758e-43	2.646131e-40	ZBTB16
ENSG00000134686	2933.64246	1.4394898	0.10582729	13.602255	3.882769e-42	6.533838e-39	PHC2
ENSG00000101347	14134.99177	3.8504143	0.28490701	13.514635	1.281894e-41	1.941428e-38	SAMHD1
ENSG00000096060	2630.23049	3.9450524	0.29291821	13.468102	2.409807e-41	3.317866e-38	FKBP5
ENSG00000166741	7542.25287	2.2195906	0.16673544	13.312050	1.970000e-40	2.486304e-37	NNMT
ENSG00000125148	3695.87946	2.1985636	0.16700546	13.164621	1.402400e-39	1.633797e-36	MT2A
ENSG00000162614	5646.18314	1.9711402	0.15020631	13.122885	2.434854e-39	2.633990e-36	NEXN
ENSG00000106976	989.04683	-1.8501713	0.14778657	-12.519211	5.861471e-36	5.918132e-33	DNM1
ENSG00000187193	199.07694	3.2551424	0.26090711	12.476250	1.006146e-35	9.523804e-33	MT1X
ENSG00000256235	1123.47954	1.2801193	0.10547438	12.136779	6.742862e-34	6.007096e-31	SMIM3
ENSG00000177666	2639.57020	1.1399947	0.09606884	11.866436	1.768422e-32	1.487930e-29	PNPLA2
ENSG00000164125	7257.00808	1.0248523	0.08657600	11.837603	2.494830e-32	1.988642e-29	FAM198B
ENSG00000198624	2020.04495	2.8141014	0.24063429	11.694515	1.359615e-31	1.029569e-28	CCDC69
ENSG00000123562	5008.55294	1.0045453	0.08901501	11.285123	1.554241e-29	1.120904e-26	MORF4L2
ENSG00000144369	1283.77980	-1.3090041	0.11714863	-11.173875	5.473974e-29	3.768333e-26	FAM171B
ENSG00000196517	241.91536	-2.3456877	0.21047366	-11.144804	7.591120e-29	4.998588e-26	SLC6A9
ENSG00000135821	19973.40000	3.0413943	0.27601796	11.018828	3.100706e-28	1.956675e-25	GLUL

Volcano plot



My high-throughput  
experiment generated a  
long list of genes/proteins...

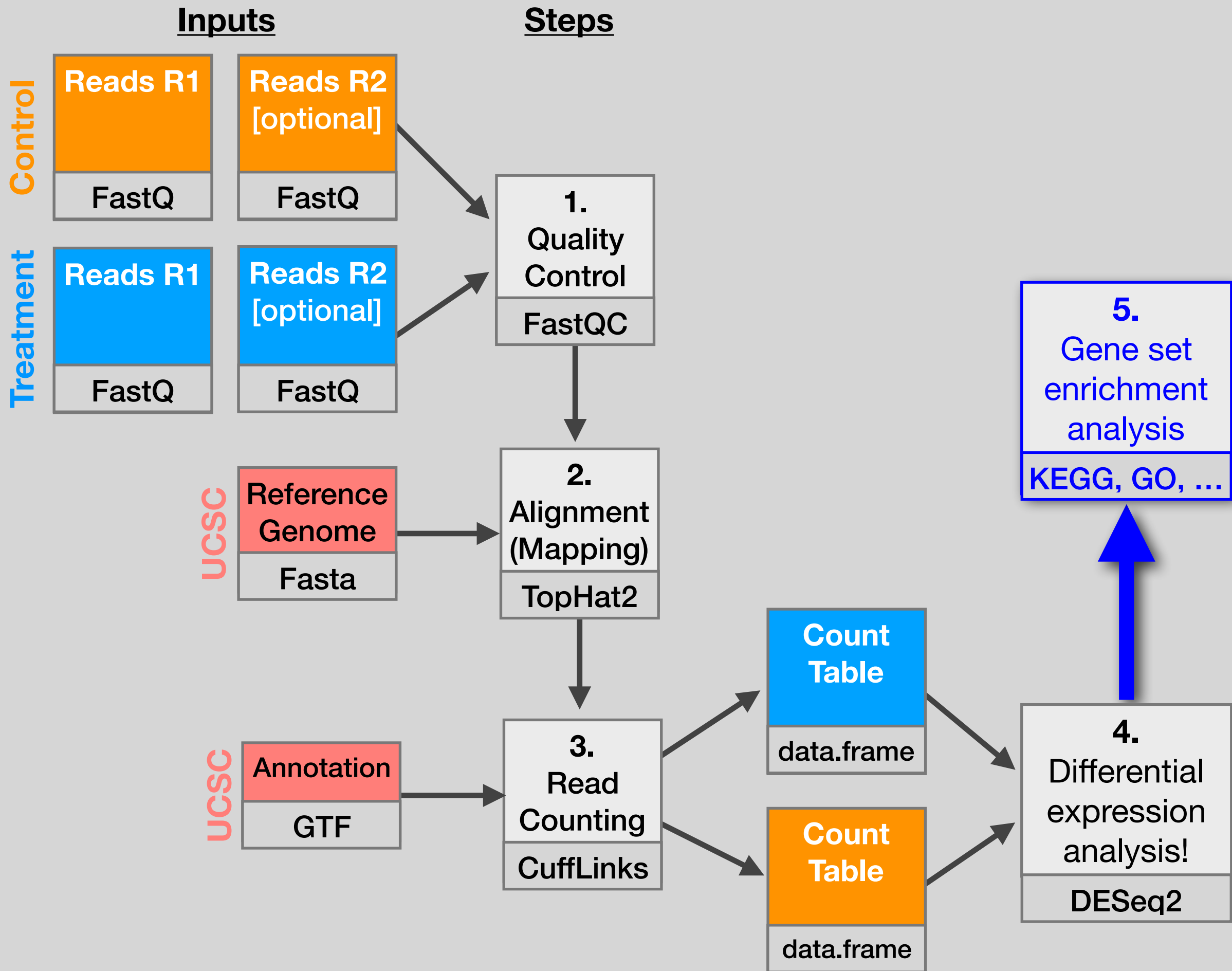
What do I do now?



# Pathway analysis!

(a.k.a. geneset enrichment)

Use bioinformatics methods to help extract biological meaning from such lists...

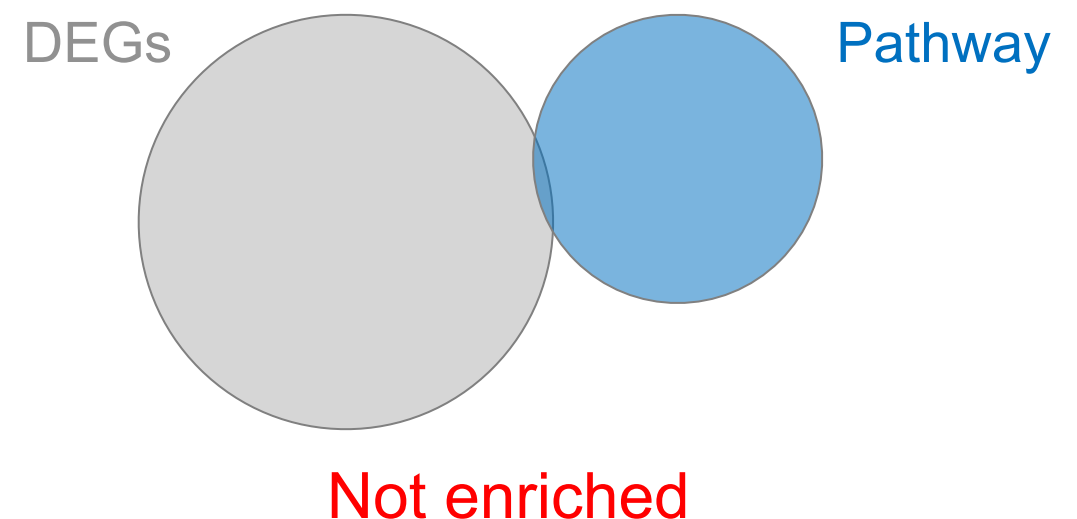
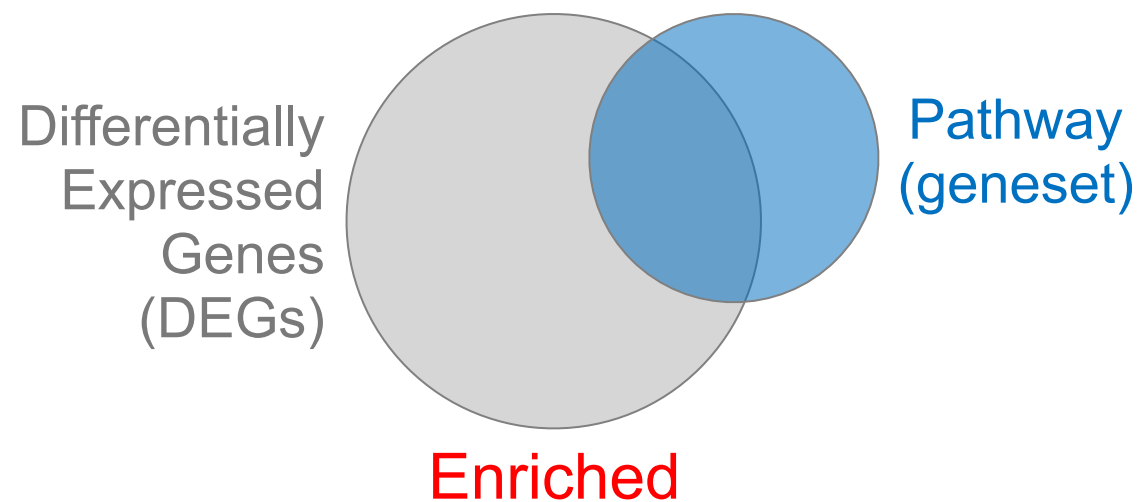




# Pathway analysis (a.k.a. geneset enrichment)

## Principle

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- 
- Variations of the math: overlap, ranking, networks... ➤ *Not critical, different algorithms show similar performances*
  - DEGs come from your experiment ➤ *Critical, needs to be as clean as possible*
  - Pathway genes ("geneset") come from annotations ➤ *Important, but typically not a competitive advantage*



# Pathway analysis (a.k.a. geneset enrichment)

## Limitations

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- **Geneset annotation bias:** can only discover what is already known
- **Post-transcriptional regulation** is neglected
- **Tissue-specific** variations of pathways are not annotated
  - e.g. NF- $\kappa$ B regulates metabolism, not inflammation, in adipocytes
- **Size bias:** stats are influenced by the size of the pathway
- **Non-model organisms:** no high-quality genesets available
- Many pathways/receptors **converge** to few regulators
  - e.g. Tens of innate immune receptors activate four TFs:  
NF- $\kappa$ B, AP-1, IRF3/7, NFAT

# Starting point for pathway analysis:

## Your gene list

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- You have a list of genes/proteins of interest
- You have quantitative data for each gene/protein
  - Fold change
  - p-value
  - Spectral counts
  - Presence/absence

The image shows a stack of overlapping yellow sticky notes. Each note contains a list of gene identifiers and numerical values. The identifiers include ENSG (e.g., ENSG00000090339), NP (e.g., NP\_000192), and C20orf58. The numerical values are integers ranging from 3383 to 124540. The notes are arranged in a way that some are partially obscured by others, creating a layered effect.

Gene Identifier	Value
228018_at	
226 ENSG00000090339	
207 ENSG00000010030	
225 ENSG00000013383	3383
221 ENSG000000251513	51513
1553 ENSG00000013613	3613
2184 ENSG00000017124	7124
2049 ENSG0000001757	757
2026 ENSG00000092370	92370
23095 ENSG00000079646	79646
22801 ENSG00000056892	56892
15540 ENSG000000124540	124540
203120 ENSG000000253982	253982
225182 ENSG000000140688	140688
225079 ENSG00000010457	10457
243010 ENSG0000009518	9518
230668 ENSG0000002013	2013
218541 ENSG0000004050	4050
224225 ENSG000000033666	
207339 ENSG000000002332	
202637_s_at	
W03F8.6	
NP_000192	
NP_057219	
NP_055029	
NP_000585	
NP_006125	
NP_589495	
NP_01032249	
NP_78870	
NP_4515	
NP_3839	
NP_412	
NP_069	
NP_83	
NP_01	
NP_05340	
NP_5	
NP_5	
C20orf58	
C20orf58	
C8orf4	
ETV7	
LTB	
ICAM1	

# Translating between identifiers

---

- Many different identifiers exist for genes and proteins, e.g. UniProt, Entrez, etc.
- Sometimes you have to translate one set of ids into another
  - A program might only accept certain types of ids
  - You might have a list of genes with one type of id and info for genes with another type of id

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- **Various web sites translate ids -> *best for small lists***
  - **UniProt < [www.uniprot.org](http://www.uniprot.org)>; IDConverter < [idconverter.bioinfo.cnio.es](http://idconverter.bioinfo.cnio.es) >**



# Translating between identifiers: UniProt < [www.uniprot.org](http://www.uniprot.org) >

UniProt Downloads · Contact · Documentation/Help

Search in **Protein Knowledgebase (UniProtKB)**    [Fields »](#)

WELCOME NEWS 

**Identifiers**

**From**

**To**

or  no file selected

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---

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- **VLOOKUP in Excel - *good if you are an excel whizz - I am not!***
  - **Download flat file from Entrez, Uniprot, etc; Open in Excel; Find columns that correspond to the 2 IDs you want to convert between; Sort by ID; Use vlookup to translate your list**

# Translating between identifiers: Excel VLOOKUP

VLOOKUP(lookup\_value, table\_array, col\_index\_num)

The screenshot shows an Excel spreadsheet with the following structure:

- Formula Bar:** Cell B3 contains the formula `=VLOOKUP(A3,SG$3:$OS$30490,2,FALSE)`.
- Data Table (Columns A-K):**

	A	B	C	D	E	F	G	H	I	J	K
1	Data Table						Annotation Table				
2	RefSeq	Symbol	Exp1	Exp2	Exp3		RefSeq	Symbol	Entrez ID	Unigene	RefSeq
3	NM_153103	Kif1c	2.31975457	1.24558927	2.78816871		NM_001001	Zfp85-rs1	22746	Mm.288396	NM_001
4	NM_146017	Gabrp	4.15029735	3.08055836	1.18919962		NM_001001	Scap	235623	Mm.288741	NM_001
5	NM_018883	Camkk1	3.83282512	0.0522951	0.64684259		NM_001001	Scap	235623	Mm.288741	NM_001
6	NM_145936	Tspyl2	0.45449369	1.62761318	7.59770627		NM_001001	Fbxo41	330369	Mm.38777	NM_001
7	NM_026599	Cgnl1	4.84541871	2.84751796	1.61595768		NM_001001	Taf9b	407786	Mm.19440	NM_001
8	NM_013926	Cbx8	1.22903318	0.2863077	0.02952665		NM_001001	Taf9b	407786	Mm.19440	NM_001
9	NR_015566	A330023F24	1.44695053	0.98809479	1.59330144		NM_001001	BC051142	407788	Mm.73205	NM_001
10	NM_008623	Mpz	0.50749263	0.94350028	6.10581569		NM_001001	BC051142	407788	Mm.73205	NM_001
11	NM_183127	Fate1	2.45672795	4.87960794	3.60759511		NM_001001	BC048546	232400	Mm.259234	NM_001
12	NM_008943		4.78701069	4.15302647	0.85432314		NM_001001	Zfp941	407812	Mm.359154	NM_001
13	NM_025382		0.66397344	1.40664187	3.09539802		NM_001001	BC031181	407819	Mm.29866	NM_001
14	NM_182841		1.25528938	0.20505996	2.76879488		NM_001001	Baz2b	407823	Mm.486364	NM_001
15	NM_030061		0.17670108	2.75415469	2.98900691		NM_001001	Tmem204	407831	Mm.34379	NM_001
16	NM_133216		6.572343	0.59671282	3.84650536		NM_001001	Ccdc111	408022	Mm.217385	NM_001
17	NM_030063		7.05132762	0.65043627	1.68111836		NM_001001	BC048507	408058	Mm.177840	NM_001

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---

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- Use the **merge()** or **mapIDs()** functions in **R** - fast, versatile & reproducible!
  - Also **clusterProfiler::bitr()** function and many others... [[Link to clusterProfiler vignette](#)]



## bitr: Biological Id Translator

clusterProfiler provides `bitr` and `bitr_kegg` for converting ID types. Both `bitr` and `bitr_kegg` support many species including model and many non-model organisms.

```
x <- c("GPX3", "GLRX", "LBP", "CRYAB", "DEFB1", "HCLS1", "SOD2", "HSPA2",
      "ORM1", "IGFBP1", "PTHLH", "GPC3", "IGFBP3", "TOB1", "MITF", "NDRG1",
      "NR1H4", "FGFR3", "PVR", "IL6", "PTPRM", "ERBB2", "NID2", "LAMB1",
      "COMP", "PLS3", "MCAM", "SPP1", "LAMC1", "COL4A2", "COL4A1", "MYOC",
      "ANXA4", "TFPI2", "CST6", "SLPI", "TIMP2", "CPM", "GGT1", "NNMT",
      "MAL", "EEF1A2", "HGD", "TCN2", "CDA", "PCCA", "CRYM", "PDXK",
      "STC1", "WARS", "HMOX1", "FXVD2", "RBP4", "SLC6A12", "KDEL3", "ITM2B")
eg = bitr(x, fromType="SYMBOL", toType="ENTREZID", OrgDb="org.Hs.eg.db")
head(eg)
```



```
## SYMBOL ENTREZID
## 1 GPX3 2878
## 2 GLRX 2745
## 3 LBP 3929
## 4 CRYAB 1410
## 5 DEFB1 1672
## 6 HCLS1 3059
```

See package vignette:

<https://bioconductor.org/packages/release/bioc/html/clusterProfiler.html>

# What functional set databases do you want?

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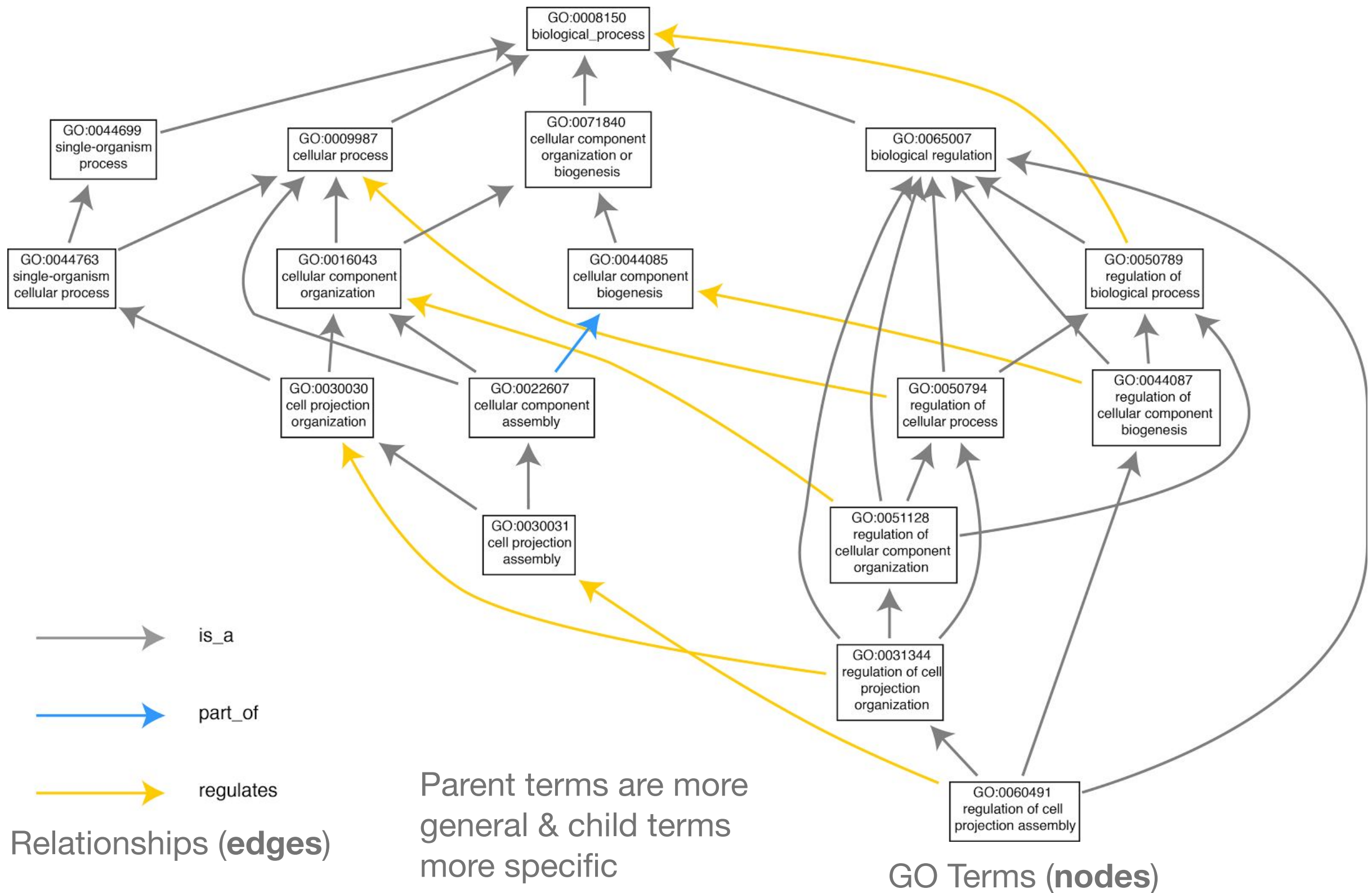
- Commonly used
  - **Gene Ontology (GO)**
  - **KEGG Pathways** (mostly metabolic)
  - **GeneGO MetaBase** 
  - **Ingenuity Pathway Analysis (IPA)** 
  - **MSigDB** (Molecular Signatures Database: gene sets based on chromosomal position, cis-regulatory motifs, GO terms, etc)
- Many others...
  - **Enzyme Classification, PFAM, Reactome, Disease Ontology, Chemical Entities of Biological Interest, Network of Cancer Genes** etc...
  - See: Open Biomedical Ontologies ( [www.obofoundry.org](http://www.obofoundry.org) )

# GO database < [www.geneontology.org](http://www.geneontology.org) >

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- **What function does HSF1 perform?**
  - *response to heat; sequence-specific DNA binding; transcription; etc*
- **Ontology** => a structured and controlled vocabulary that allows us to annotate gene products consistently, interpret the relationships among annotations, and can easily be *handled by a computer*
- GO database consists of 3 ontologies that describe gene products in terms of their associated **biological processes**, **cellular components** and **molecular functions**

# GO is structured as a “directed graph”





# GO Annotations

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- GO is not a database of genes/proteins or sequences
- Gene products get annotated with GO terms by organism specific databases, such as Flybase, Wormbase, MGI, ZFIN, UniProt, etc
- Annotations are available through AmiGO < [amigo.geneontology.org](http://amigo.geneontology.org) >

The screenshot shows the AmiGO web interface. At the top, there is a navigation bar with the text "the Gene Ontology" and "AmiGO". Below this is a search bar with the text "Search the Gene Ontology database" and a search input field. There are three radio buttons for search criteria: "GO terms", "genes or proteins" (which is selected), and "exact match". A "Submit" button is located below the search criteria. In the bottom right corner, there is a vertical label "AmiGO 2 Beta". At the bottom of the page, there is a footer with the text "AmiGO version: 1.8", "Try AmiGO Labs", "GO database release 2013-10-05", "Cite this data", "Terms of use", "GO helpdesk", and "Copyright: © 1999-2010 the Gene Ontology".

# GO evidence codes

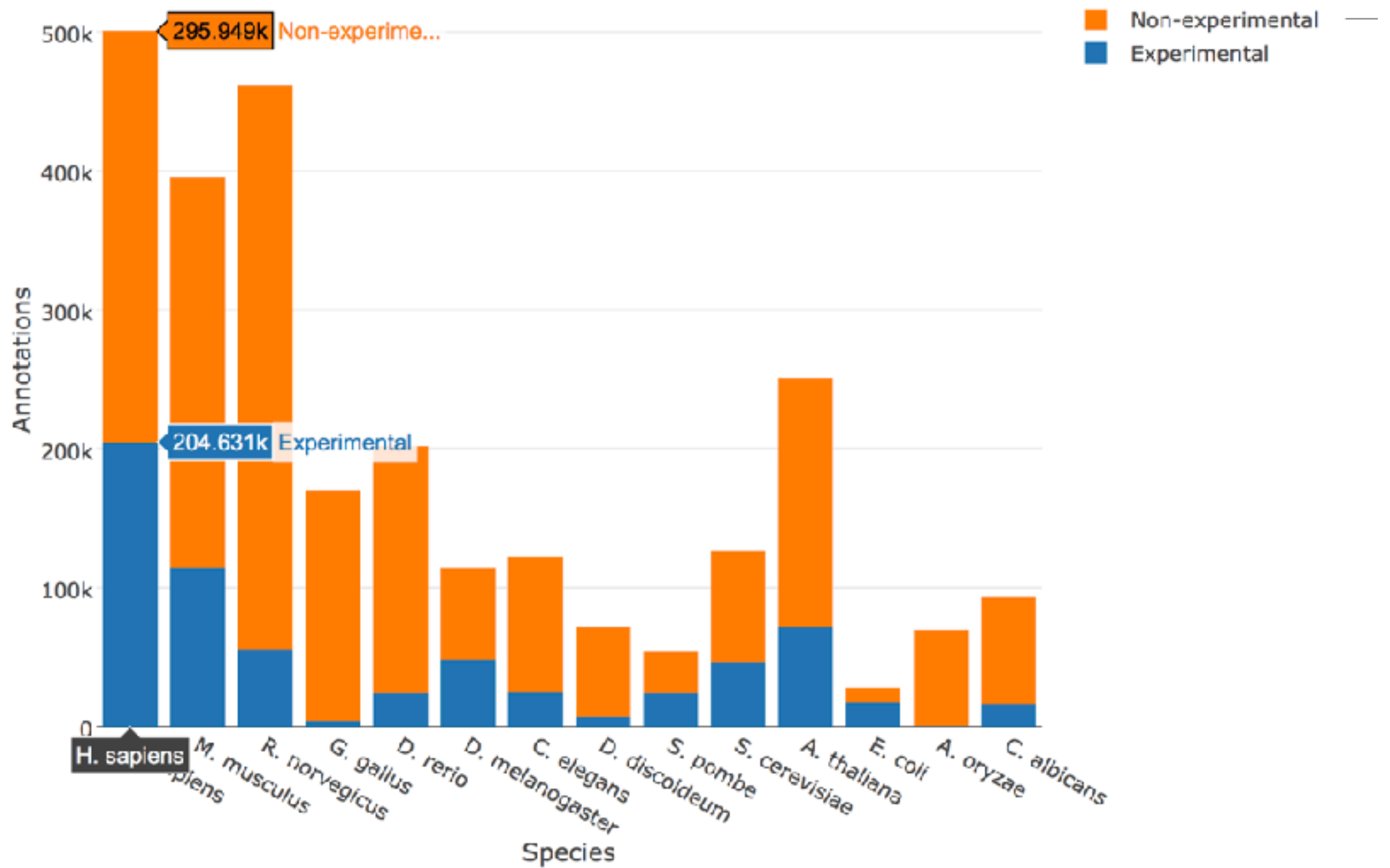
Evidence code	Evidence code description	Source of evidence	Manually checked	Current number of annotations*
IDA	Inferred from direct assay	Experimental	Yes	71,050
IEP	Inferred from expression pattern	Experimental	Yes	4,598
IGI	Inferred from genetic interaction	Experimental	Yes	8,311
IMP	Inferred from mutant phenotype	Experimental	Yes	61,549
IPI	Inferred from physical interaction	Experimental	Yes	17,043
ISS	Inferred from sequence or structural similarity	Computational	Yes	196,643
RCA	Inferred from reviewed computational analysis	Computational	Yes	103,792
IGC	Inferred from genomic context	Computational	Yes	4
IEA	Inferred from electronic annotation	Computational	No	15,687,382
IC	Inferred by curator	Indirectly derived from experimental or computational evidence made by a curator	Yes	5,167
TAS	Traceable author statement	Indirectly derived from experimental or computational evidence made by the author of the published article	Yes	44,564
NAS	Non-traceable author statement	No 'source of evidence' statement given	Yes	25,656
ND	No biological data available	No information available	Yes	132,192
NR	Not recorded	Unknown	Yes	1,185

\*October 2007 release

## Use and misuse of the gene ontology annotations

Seung Yon Rhee, Valerie Wood, Kara Dolinski & Sorin Draghici  
*Nature Reviews Genetics* 9, 509-515 (2008)

### Experimental annotations by species




- See AmiGO for details: [http://amigo.geneontology.org/amigo/base\\_statistics](http://amigo.geneontology.org/amigo/base_statistics)

# Can now do gene list analysis with GeneGO

The screenshot shows the PANTHER Classification System web interface. The browser address bar displays `pantherdb.org/wabservices/go/overrep.jsp`. The page header includes the GeneOntology logo and the PANTHER Classification System logo. A navigation menu contains links for Home, About, PANTHER Data, PANTHER Tools, Workspace, Downloads, and Help/Tutorial. A secondary menu includes LOGIN, REGISTER, and CONTACT US. A banner at the top left announces "New! PANTHER13.1 released." The main content area is titled "Gene List Analysis" and features a sub-menu with options for Browse, Sequence Search, cSNP Scoring, and Keyword Search. A message states: "Please refer to our article in [Nature Protocols](#) for detailed instructions on how to use this page." Below this, a red error message reads: "Error parsing request, no input specified". The interface is divided into three numbered steps: 1. Enter IDs and or select file for batch upload. This step includes a text input field for "Enter IDs: Supported IDs" with a note to "separate IDs by a space or comma", a file upload button labeled "Choose File" (with "no file selected" next to it), and a "Select List Type" section with radio buttons for "ID List" (selected), "Previously exported text search results", "Workspace list", "PANTHER Generic Mapping File", and "VCF File". A "Flanking region" dropdown is set to "20 Kb". 2. Select organism. This step shows a list of organisms: Homo sapiens, Mus musculus, Rattus norvegicus, Gallus gallus, and Danio rerio. 3. Select Analysis. This step has radio buttons for "Functional classification viewed in gene list" (selected) and "Functional classification viewed in pie chart". On the left side of the page, there is a "Search" section with a dropdown menu set to "All" and a "Go" button. Below that is a "Quick Links" section with links to "Whole genome function views", "Genome statistics", "Data Version", and "How to cite PANTHER". A "News" section mentions "PANTHER13.1 Released" and provides a link for "additional info.". At the bottom left, there is a "Newsletter subscription" form with an email input field and a "Subscribe" button, along with a "PostgreSQL POWERED" logo.



# DAVID at NIAID < [david.abcc.ncifcrf.gov](http://david.abcc.ncifcrf.gov) >



## Analysis Wizard

DAVID Bioinformatics Resources 2008, NIAID/NIH

[Home](#) [Start Analysis](#) [Shortcut to DAVID Tools](#) [Technical Center](#) [Downloads & APIs](#) [Term of Service](#) [Why DAVID?](#) [About Us](#)

**Upload** **List** **Background**

### Analysis Wizard

[Tell us how you like the tool](#)  
[Contact us for questions](#)

← Step 1. Submit your gene list through left panel.

**new!**Note: Affy Exon IDs and Affy Gene Array IDs are now supported in DAVID, as "affy\_id" type.

An example:

Copy/paste IDs to "box A" -> Select Identifier as "Affy\_ID" -> List Type as "Gene List" -> Click "Submit" button

```
1007_s_at
1053_at
117_at
121_at
1255_g_at
1294_at
1316_at
1320_at
1405_i_at
1431_at
1438_at
1487_at
1494_f_at
1598_g_at
```

**Upload Gene List**

[Demolist 1](#) [Demolist 2](#)  
[Upload Help](#)

**Step 1: Enter Gene List**

A: Paste a list

Or

B:Choose From a File

 no file selected

**Step 2: Select Identifier**

AFFY\_ID

**Step 3: List Type**

Gene List   
Background

**Step 4: Submit List**

# DAVID

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- Notice that you can pick a *Background* (Universe)

The screenshot displays the DAVID Analysis Wizard interface. On the left is the 'Gene List Manager' sidebar, and the main area is the 'Analysis Wizard'.

**Gene List Manager (Left Sidebar):**

- Upload | **List** | Background
- Gene List Manager
- Select to limit annotations by one or more species [Help](#)
- Dropdown menu: - Use All Species -, HOMO SAPIENS(4402), SYNTHETIC CONSTRUCT(5)
- Select button
- List Manager [Help](#)
- Uploaded List\_2
- Select List to:
- Use, Rename, Remove, Combine buttons
- Show Gene List <sup>new!</sup> button

**Analysis Wizard (Main Area):**

- Analysis Wizard**
- [Tell us how you like the tool](#)
- [Contact us for questions](#)
- Step 1. Successfully submitted gene list**
- Current Gene List: Uploaded List\_2
- Current Background: HOMO SAPIENS
- Step 2. Analyze above gene list with one of DAVID tools**
- 
- [Which DAVID tools to use?](#)
- [Functional Annotation Tool](#)

  - [Functional Annotation Clustering](#)
  - [Functional Annotation Chart](#)
  - [Functional Annotation Table](#)

- [Gene Functional Classification Tool](#)
- [Gene ID Conversion Tool](#)
- [Gene Name Batch Viewer](#)

# DAVID

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- *Functional Annotation Tool*

## Annotation Summary Results

[Help and Tool Manual](#)

**Current Gene List: Uploaded List\_3**      **2320 DAVID IDs**

**Current Background: HOMO SAPIENS**      **Check Defaults**      

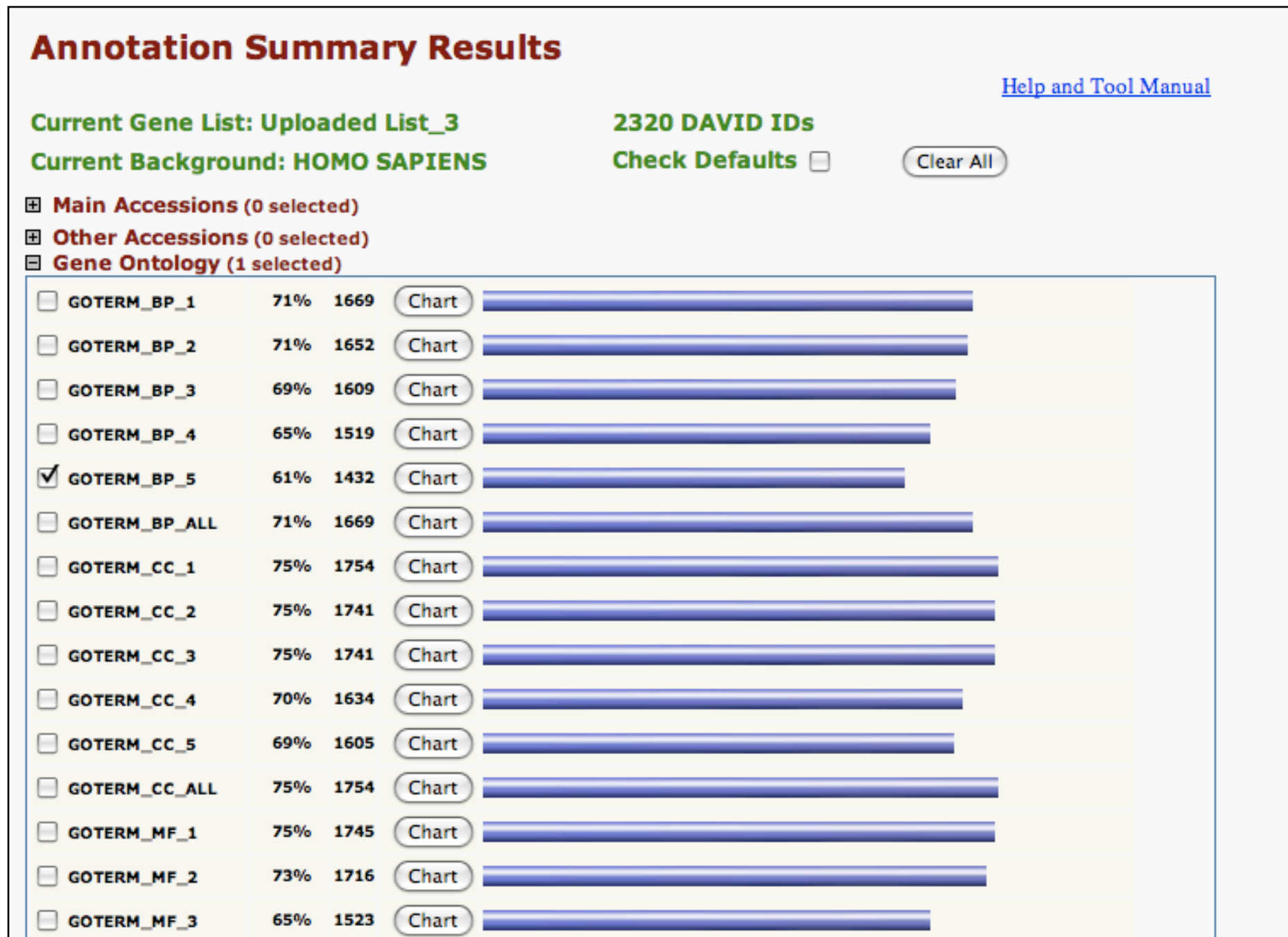
- ⊕ **Main Accessions** (0 selected)
- ⊕ **Other Accessions** (0 selected)
- ⊕ **Gene Ontology** (4 selected)
- ⊕ **Protein Domains** (3 selected)
- ⊕ **Pathways** (3 selected)
- ⊕ **General Annotations** (0 selected)
- ⊕ **Functional Categories** (3 selected)
- ⊕ **Protein Interactions** (0 selected)
- ⊕ **Literature** (0 selected)
- ⊕ **Disease** (1 selected)
- ⊕ **Tissue Expression**

**Combined View for Selected Annotation**

←

# DAVID

- Specify functional sets



# DAVID

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- Let's look at the *Functional Annotation Chart*

## Annotation Summary Results


[Help and Tool Manual](#)

**Current Gene List: Uploaded List\_3**      **2320 DAVID IDs**

**Current Background: HOMO SAPIENS**      **Check Defaults**      

- Main Accessions** (0 selected)
- Other Accessions** (0 selected)
- Gene Ontology** (4 selected)
- Protein Domains** (3 selected)
- Pathways** (3 selected)
- General Annotations** (0 selected)
- Functional Categories** (3 selected)
- Protein Interactions** (0 selected)
- Literature** (0 selected)
- Disease** (1 selected)
- Tissue Expression**

**Combined View for Selected Annotation**





# DAVID

- *Functional Annotation Chart*

**Functional Annotation Chart** [Help and Manual](#)

Current Gene List: **Uploaded List\_1**  
Current Background: **Homo sapiens**  
2316 DAVID IDs

**Options**

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">regulation of progression through cell cycle</a>	RT		98	4.2	3.3E-7	8.6E-4
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">apoptosis</a>	RT		131	5.7	1.6E-6	2.1E-3
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">cell death</a>	RT		136	5.9	3.8E-6	3.3E-3
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">regulation of transcription from RNA polymerase II promoter</a>	RT		83	3.6	3.7E-5	2.4E-2
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">protein kinase cascade</a>	RT		71	3.1	4.7E-5	2.4E-2
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">regulation of kinase activity</a>	RT		48	2.1	5.4E-5	2.3E-2
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">negative regulation of cell proliferation</a>	RT		48	2.1	1.0E-4	3.7E-2
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">regulation of cell size</a>	RT		41	1.8	1.2E-4	3.9E-2
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">monocarboxylic acid metabolic process</a>	RT		48	2.1	1.3E-4	3.6E-2
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	RT		61	2.6	1.5E-4	3.8E-2
<input type="checkbox"/>	GOTERM_BP_5	<a href="#">positive regulation of cellular metabolic process</a>	RT		72	3.1	1.7E-4	3.8E-2

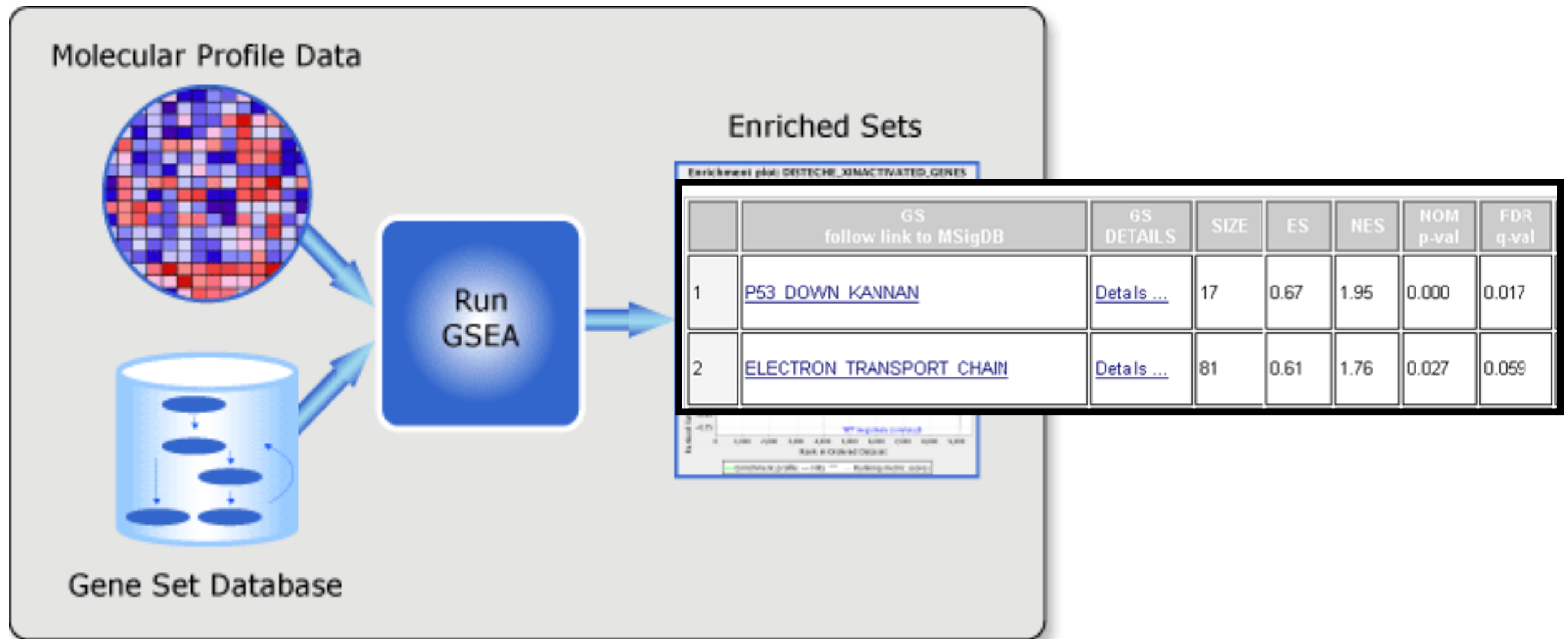
**Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources**

Da Wei Huang, Brad T Sherman & Richard A Lempicki

*Nature Protocols* **4**, 44 - 57 (2009)

# GSEA < [www.broadinstitute.org/gsea](http://www.broadinstitute.org/gsea) >

- Download GSEA desktop application



- Excellent tutorial, user's guide and example datasets to work through

**Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles**

Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, ...

*PNAS* 102, 15545-15550 (2005)

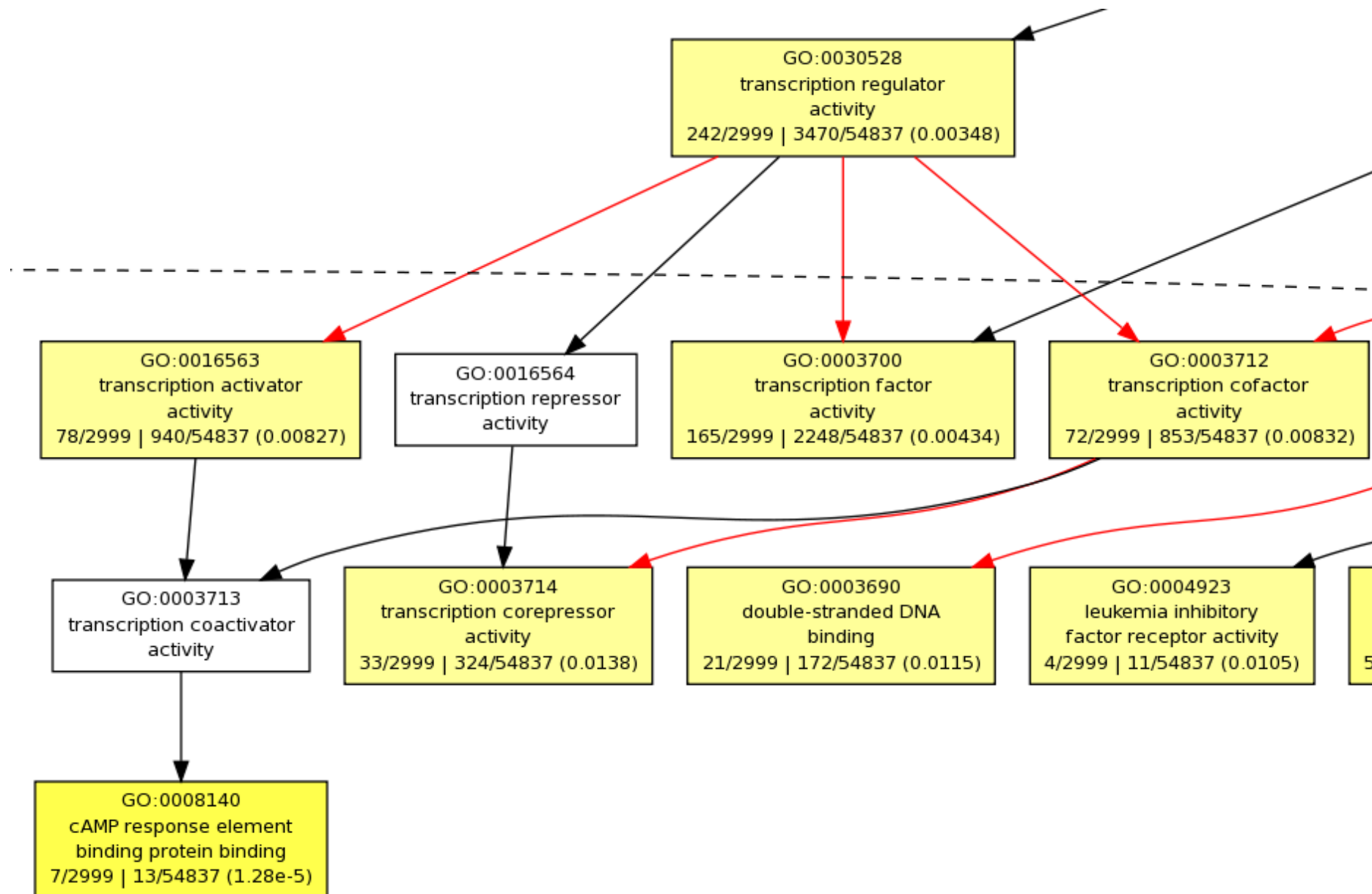
# Overlapping functional sets

---

- Many functional sets overlap, in particular those from databases that are hierarchical in nature (e.g. GO)
- Hierarchy enables:
  - Annotation flexibility (e.g. allow different degrees of annotation completeness based on what is known)
  - Computational methods to “understand” function relationships (e.g. ATPase function is a subset of enzyme function)
- Unfortunately, this also makes functional profiling trickier

# GOEast < [omicslab.genetics.ac.cn/GOEAST](http://omicslab.genetics.ac.cn/GOEAST) >

- Graphical view of enriched GO terms and their relationships



# GO SLIMs

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- Cut-down versions of the GO ontologies containing a subset of the terms in the whole GO
- GO FAT (DAVID):
  - filters out very broad GO terms based on a measured specificity of each term



# DAVID Functional Annotation Clustering

- Based on shared genes between functional sets

**Functional Annotation Clustering** [Help and Manual](#)

Current Gene List: Uploaded List\_3  
2320 DAVID IDs

Options Classification Stringency Medium

Rerun using options Create Sublist [Download File](#)

Annotation Cluster	Enrichment Score	Color	Count	P_Value	Benjamini
<b>Annotation Cluster 1</b>	<b>Enrichment Score: 3.72</b>	<b>G</b>			
<input type="checkbox"/> GOTERM_BP_5	<a href="#">regulation of transcription from RNA polymerase II promoter</a>	RT	83	3.7E-5	2.4E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	RT	61	1.5E-4	3.8E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">positive regulation of cellular metabolic process</a>	RT	72	1.7E-4	3.8E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">positive regulation of transcription</a>	RT	58	3.8E-4	5.0E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">positive regulation of transcription, DNA-dependent</a>	RT	48	7.4E-4	7.6E-2
<b>Annotation Cluster 2</b>	<b>Enrichment Score: 3.54</b>	<b>G</b>			
<input type="checkbox"/> GOTERM_BP_5	<a href="#">regulation of cell size</a>	RT	41	1.2E-4	3.9E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">regulation of cell growth</a>	RT	33	3.7E-4	5.1E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">cell morphogenesis</a>	RT	81	5.2E-4	5.7E-2
<b>Annotation Cluster 3</b>	<b>Enrichment Score: 3.37</b>	<b>G</b>			
<input type="checkbox"/> GOTERM_BP_5	<a href="#">apoptosis</a>	RT	131	1.6E-6	2.1E-3
<input type="checkbox"/> GOTERM_BP_5	<a href="#">cell death</a>	RT	136	3.8E-6	3.3E-3
<input type="checkbox"/> GOTERM_BP_5	<a href="#">regulation of programmed cell death</a>	RT	88	3.2E-4	5.8E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">positive regulation of apoptosis</a>	RT	48	3.3E-4	5.6E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">regulation of apoptosis</a>	RT	87	3.5E-4	5.2E-2
<input type="checkbox"/> GOTERM_BP_5	<a href="#">positive regulation of programmed cell death</a>	RT	48	4.0E-4	5.0E-2

# Want more?

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- **GeneGO** < [portal.genego.com](http://portal.genego.com) >
  - MD/PhD curated annotations, great for certain domains (eg, Cystic Fibrosis)
  - Nice network analysis tools
  - Email us for access
- **Oncomine** < [www.oncomine.org](http://www.oncomine.org) >
  - Extensive cancer related expression datasets
  - Nice concept analysis tools
  - Research edition is free for academics, Premium edition \$\$\$
- **Lots and lots other R/Bioconductor packages in this area!!!**

Do it Yourself!

# Hands-on time!

[https://bioboot.github.io/bgggn213\\_S18/lectures/#15](https://bioboot.github.io/bgggn213_S18/lectures/#15)

Also: **R Quiz Online**

# Data structure: counts + metadata

## countData

gene	ctrl_1	ctrl_2	exp_1	exp_2
geneA	10	11	56	45
geneB	0	0	128	54
geneC	42	41	59	41
geneD	103	122	1	23
geneE	10	23	14	56
geneF	0	1	2	0
...	...	...	...	...

**countData** is the count matrix  
(number of reads coming from  
each gene for each sample)

## colData

id	treatment	sex	...
ctrl_1	control	male	...
ctrl_2	control	female	...
exp_1	treatment	male	...
exp_2	treatment	female	...

Sample names:

ctrl\_1, ctrl\_2, exp\_1, exp\_2

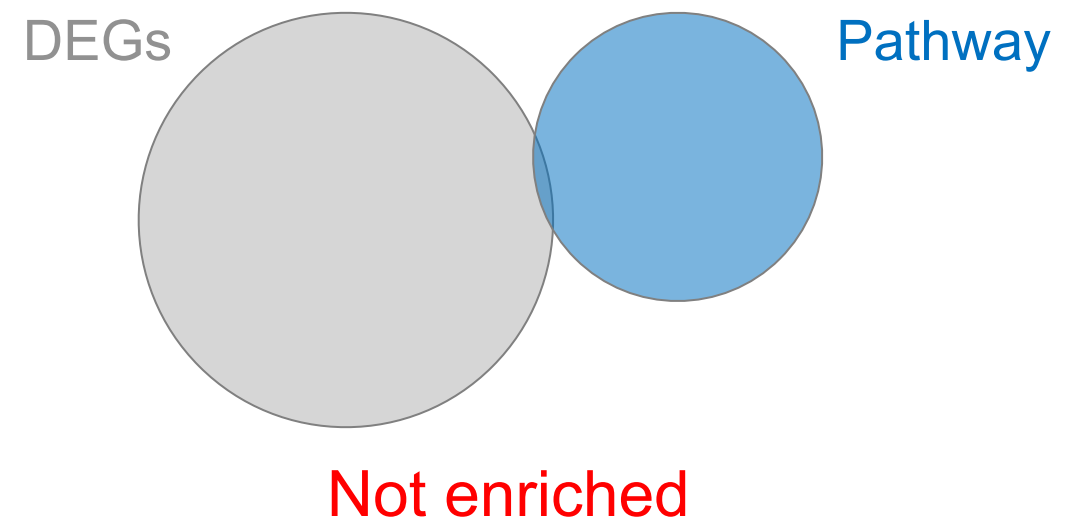
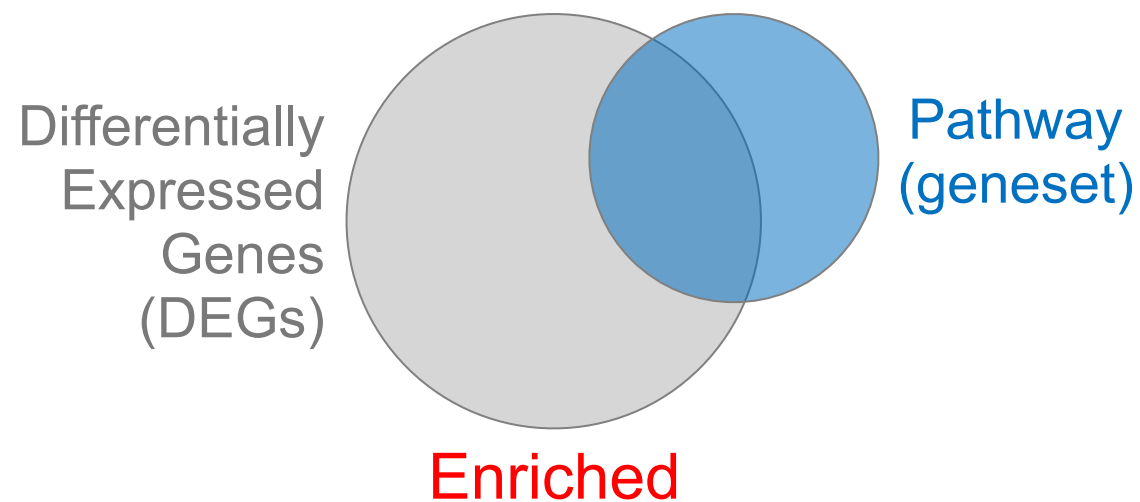
**colData** describes metadata  
about the *columns* of countData

First column of **colData** must match column names of **countData** (-1st)

# Pathway analysis (a.k.a. geneset enrichment)

## Principle

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- 
- Variations of the math: overlap, ranking, networks... ➤ *Not critical, different algorithms show similar performances*
  - DEGs come from your experiment ➤ *Critical, needs to be as clean as possible*
  - Pathway genes ("geneset") come from annotations ➤ *Important, but typically not a competitive advantage*

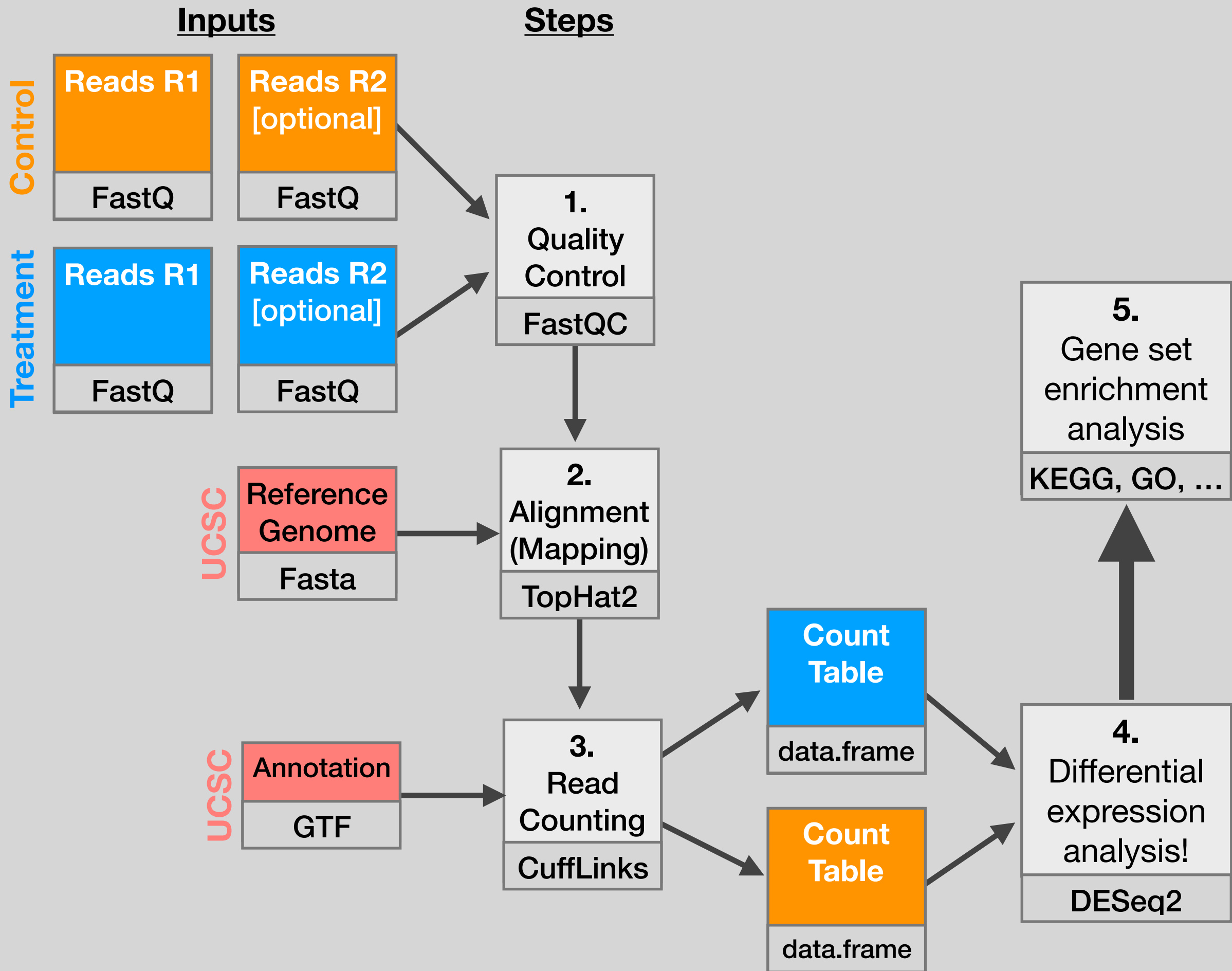


# Pathway analysis (a.k.a. geneset enrichment)

## Limitations

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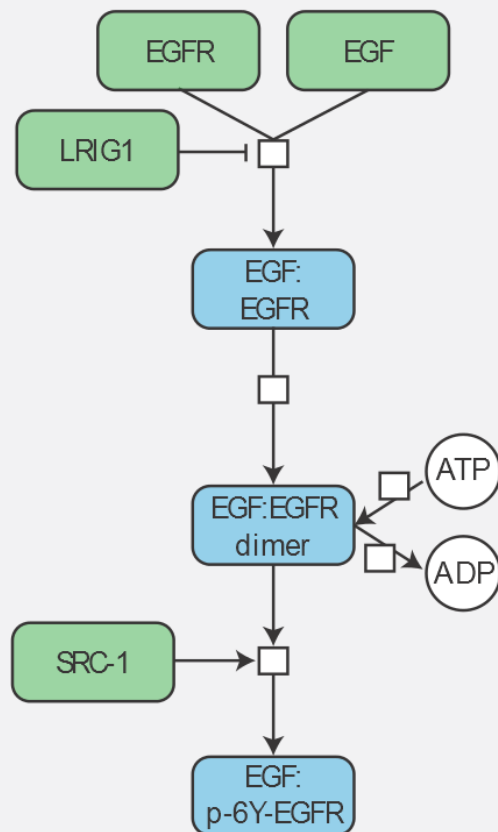
- **Geneset annotation bias:** can only discover what is already known
- **Post-transcriptional regulation** is neglected
- **Tissue-specific** variations of pathways are not annotated
  - e.g. NF- $\kappa$ B regulates metabolism, not inflammation, in adipocytes
- **Size bias:** stats are influenced by the size of the pathway
- **Non-model organisms:** no high-quality genesets available
- Many pathways/receptors **converge** to few regulators
  - e.g. Tens of innate immune receptors activate four TFs:  
NF- $\kappa$ B, AP-1, IRF3/7, NFAT



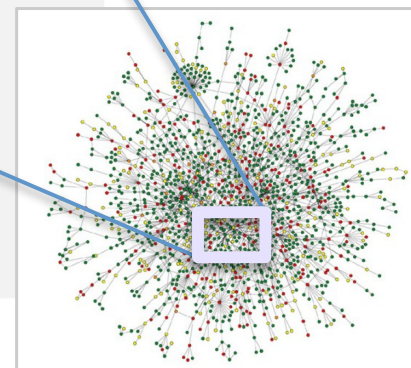
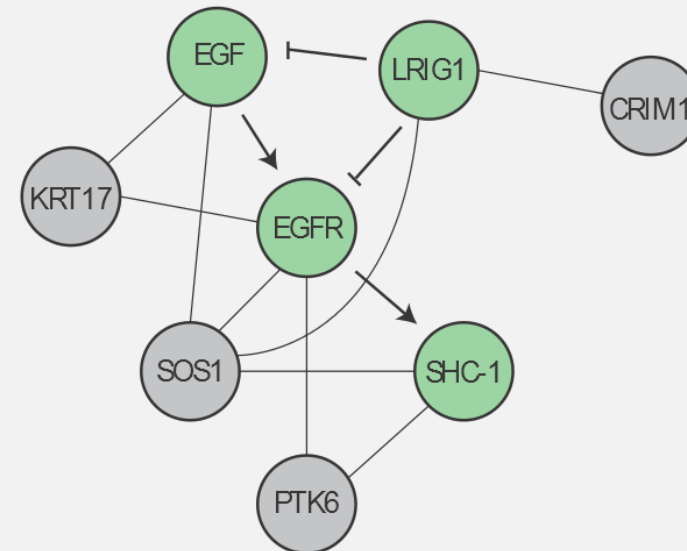
# Pathways vs Networks

Next Class

EGFR-centered  
Pathway



EGFR-centered  
Network



- Detailed, high-confidence consensus
- Biochemical reactions
- Small-scale, fewer genes
- Concentrated from decades of literature

- Simplified cellular logic, noisy
- Abstractions: directed, undirected
- Large-scale, genome-wide
- Constructed from *omics* data integration

## Goal

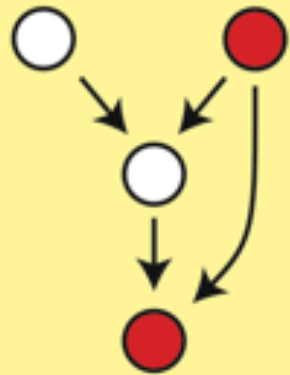
### 1 Enrichment of fixed gene sets

Identification of pre-built pathways or networks that are enriched in a set of mutated or differentially expressed genes

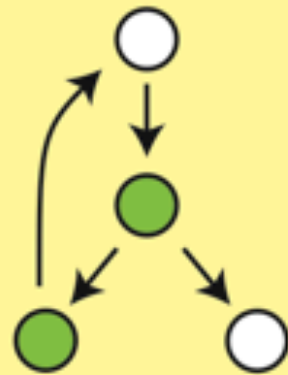
### 2 De novo sub-network construction and clustering

Construction of specific sub-networks from the set of mutated or differentially expressed genes to identify an extended list of putative cancer genes

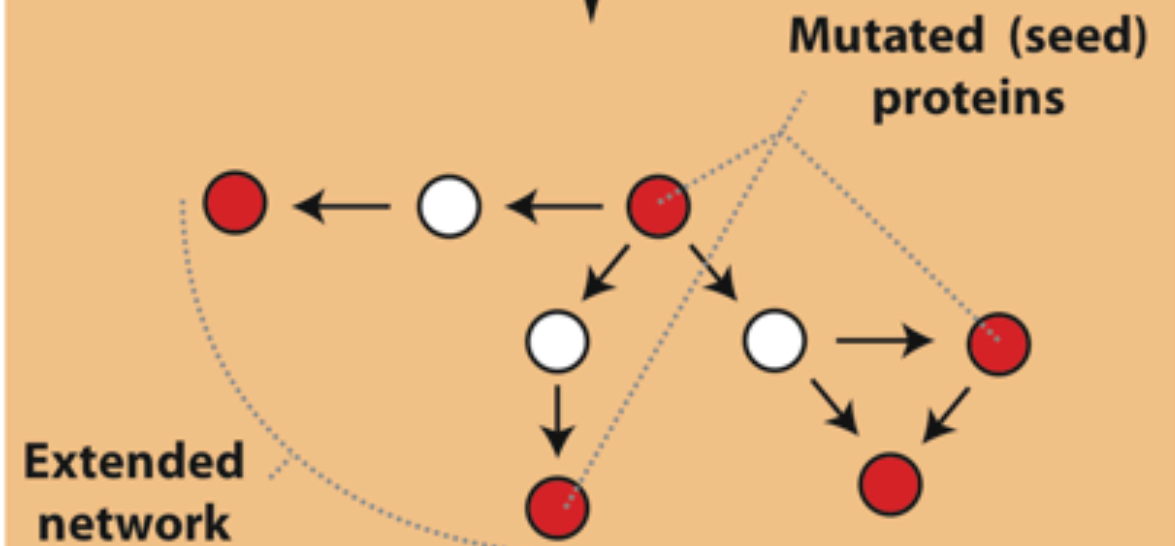
## Output



Enriched network



Depleted network



## Goal

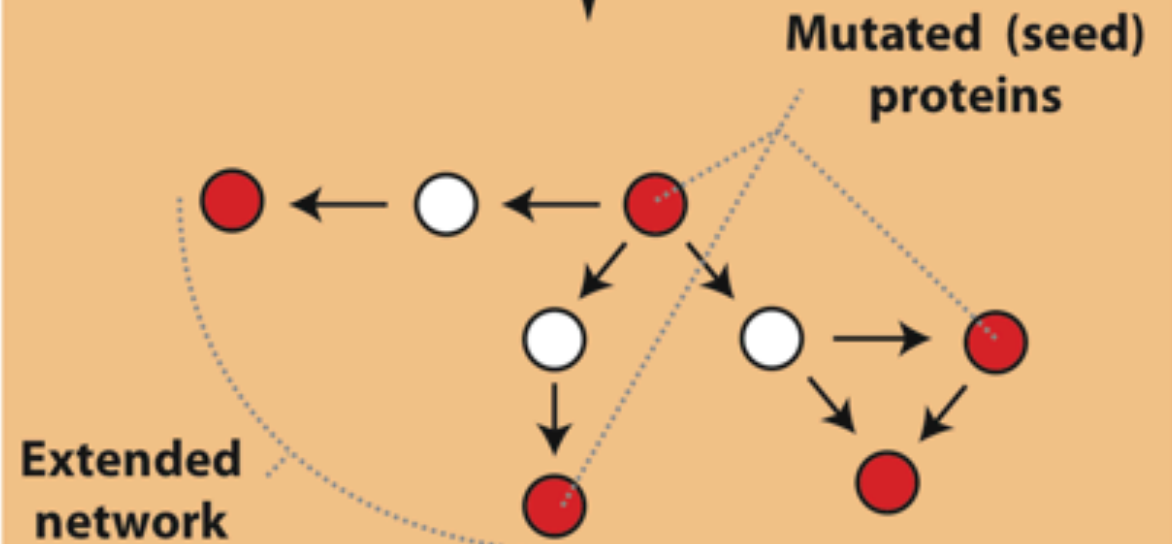
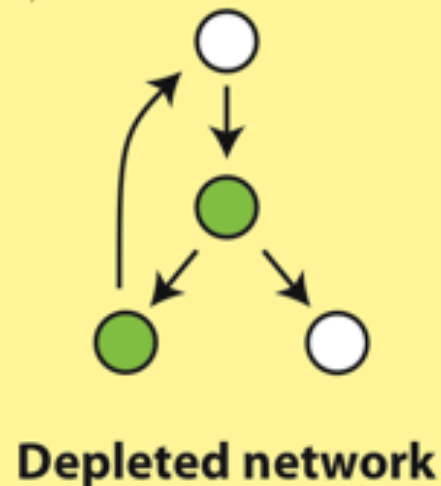
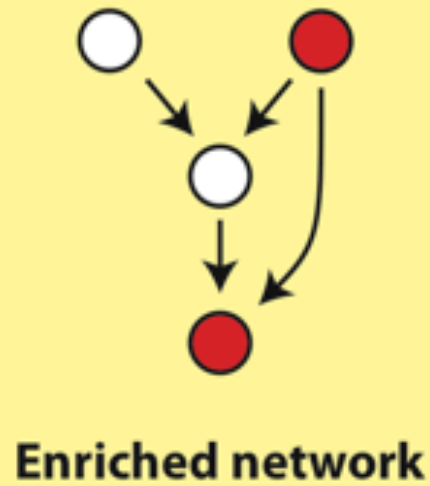
### 1 Enrichment of fixed gene sets

Identification of pre-built pathways or networks that are enriched in a set of mutated or differentially expressed genes

### 2 De novo sub-network construction and clustering

Construction of specific sub-networks from the set of mutated or differentially expressed genes to identify an extended list of putative cancer genes

## Output

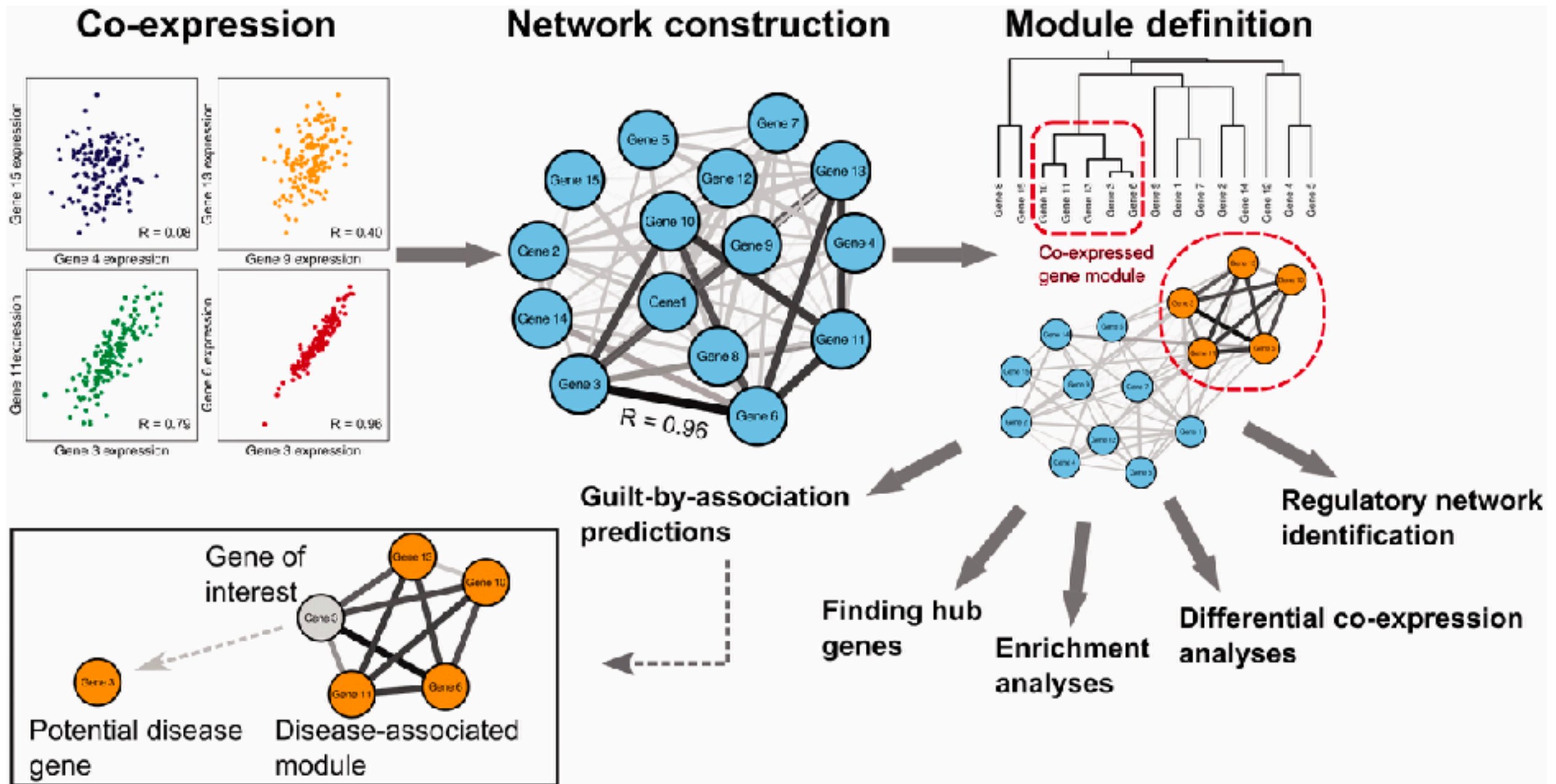


What biological process is altered in this cancer?

Are NEW pathways altered in this cancer? Are there clinically relevant tumor subtypes?



# Network analysis approaches



Do it Yourself!

# R Quiz time!

[https://bioboot.github.io/bgggn213\\_S18/lectures/#15](https://bioboot.github.io/bgggn213_S18/lectures/#15)

Also: **R Quiz Online**