



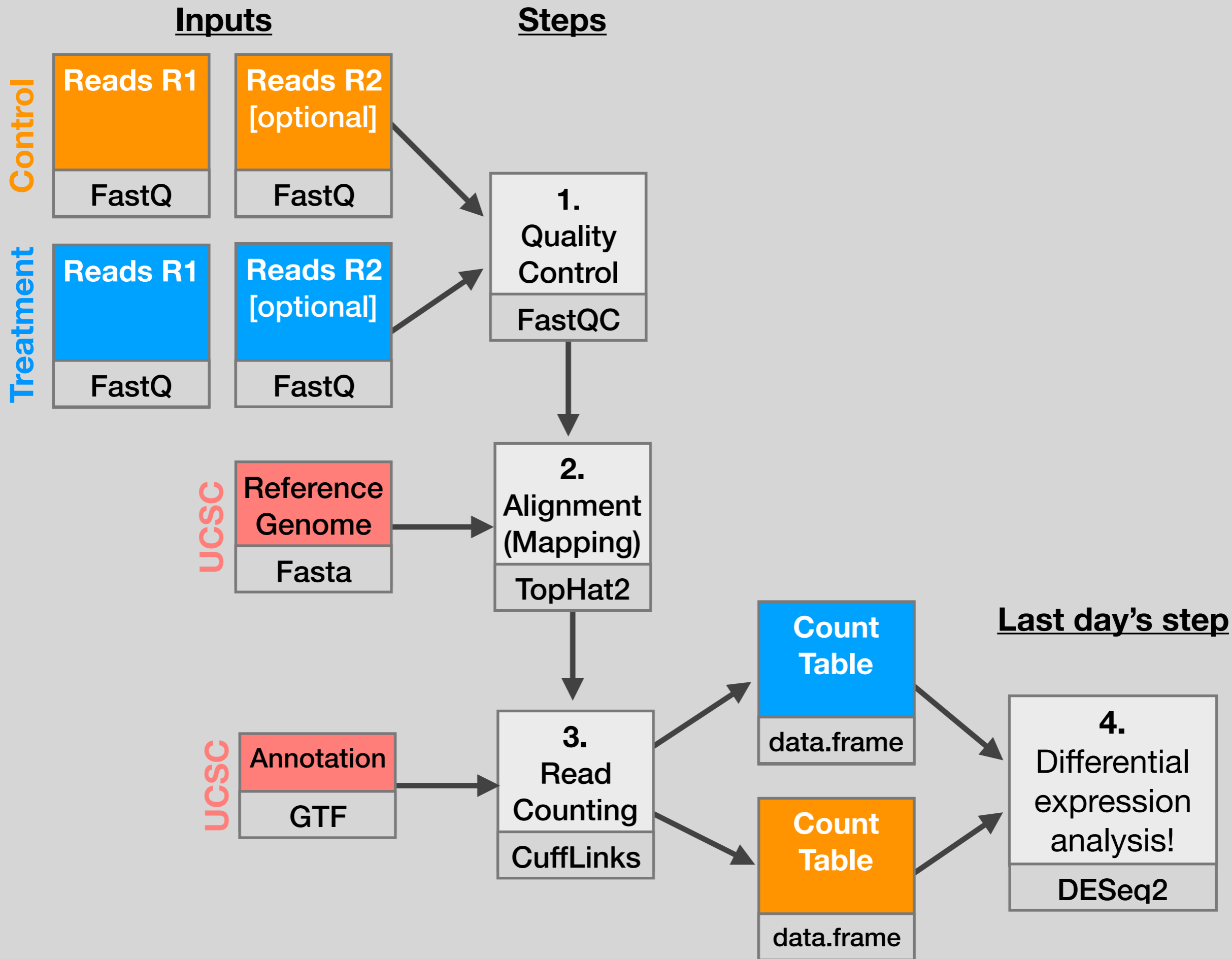
BGGN 213

Pathway Analysis and the Interpretation of Gene Lists

Lecture 15

Barry Grant
UC San Diego

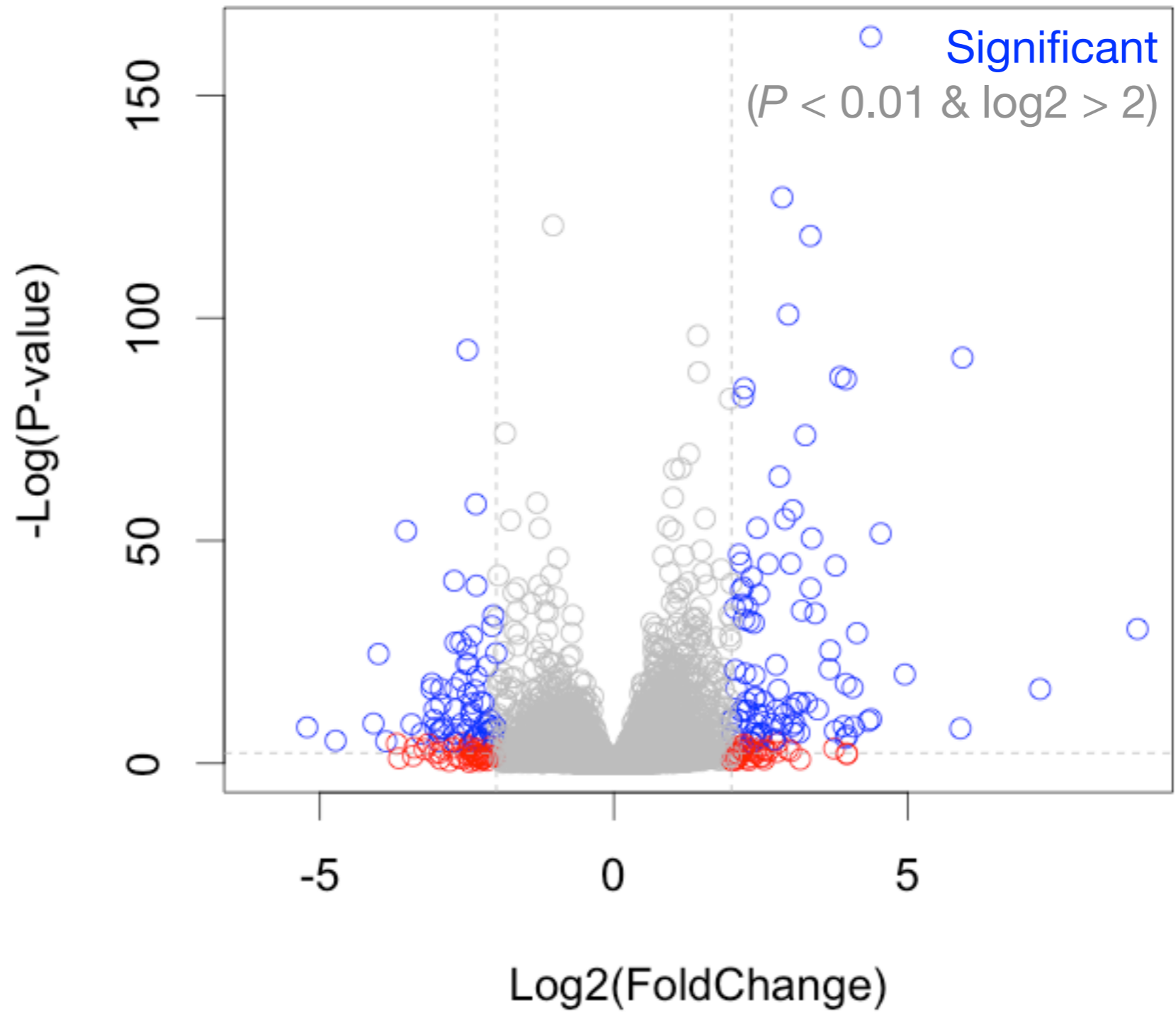
<http://thegrantlab.org/bggn213>



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
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ENSG00000256235	1123.47954	1.2801193	0.10547438	12.136779	6.742862e-34	6.007096e-31	SMIM3
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ENSG00000123562	5008.55294	1.0045453	0.08901501	11.285123	1.554241e-29	1.120904e-26	MORF4L2
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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

Fold change vs P-value



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

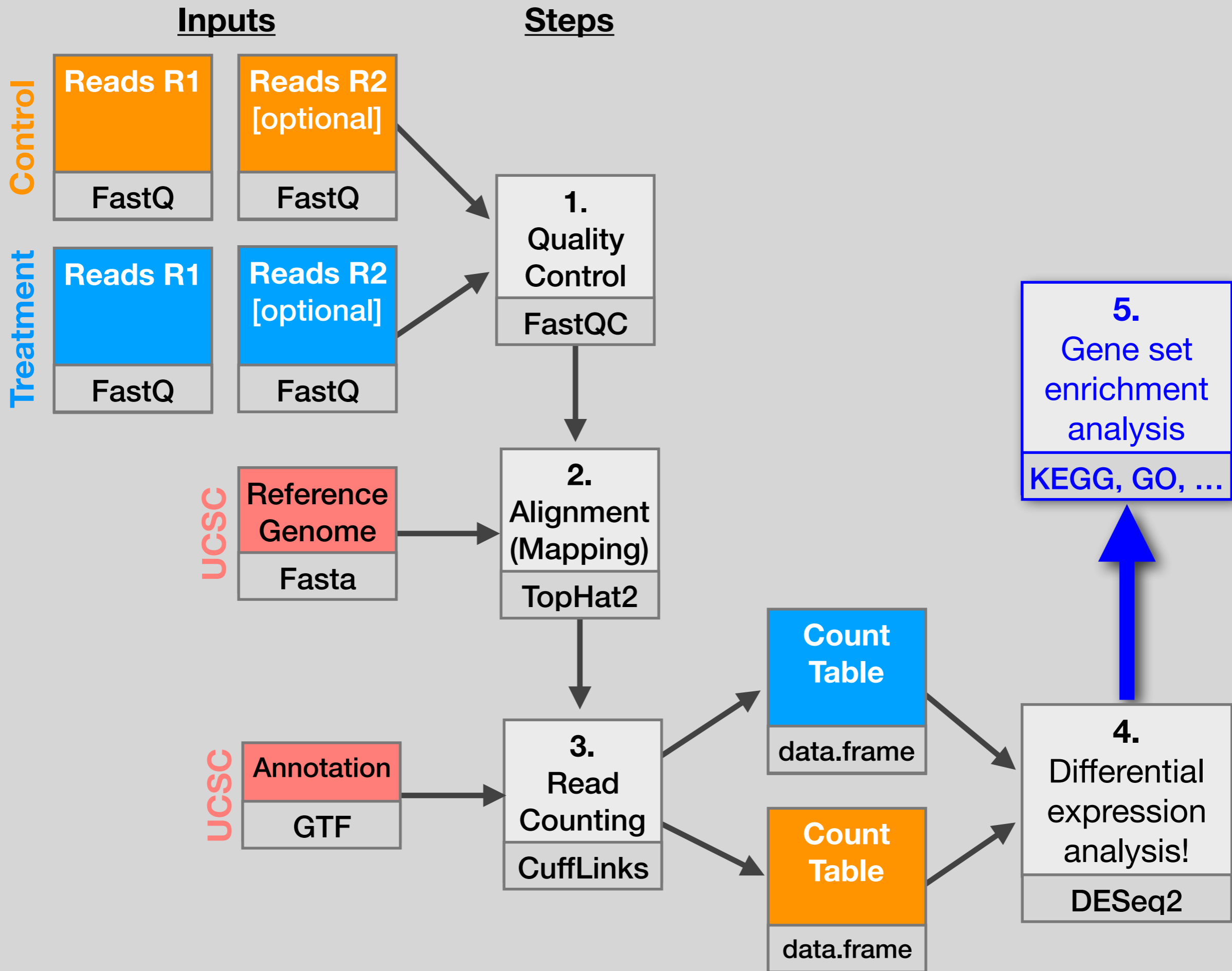
What do I do now?



Pathway analysis!

(a.k.a. geneset enrichment)

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



Basic idea

Differentially Expressed Genes (DEGs)

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Gene-sets (Pathways, annotations, etc...)

Annotate... ←



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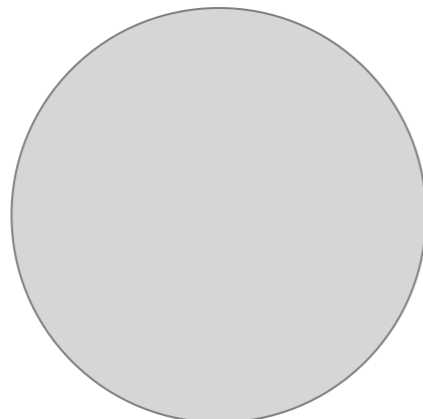
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Annotate...

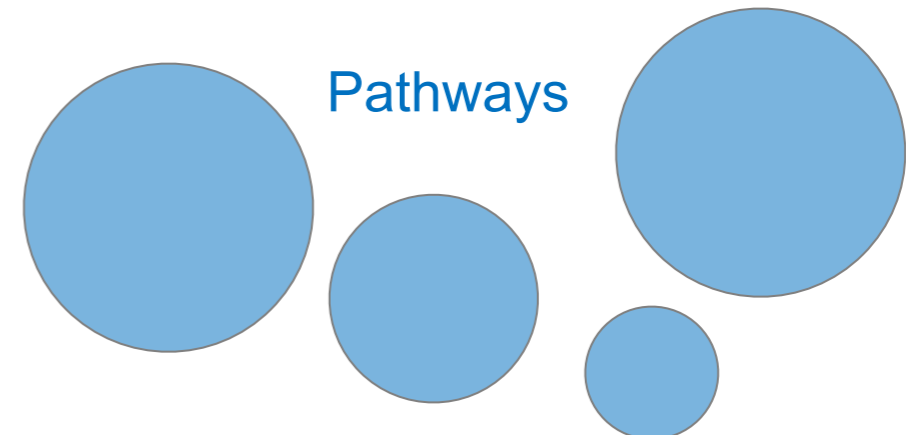


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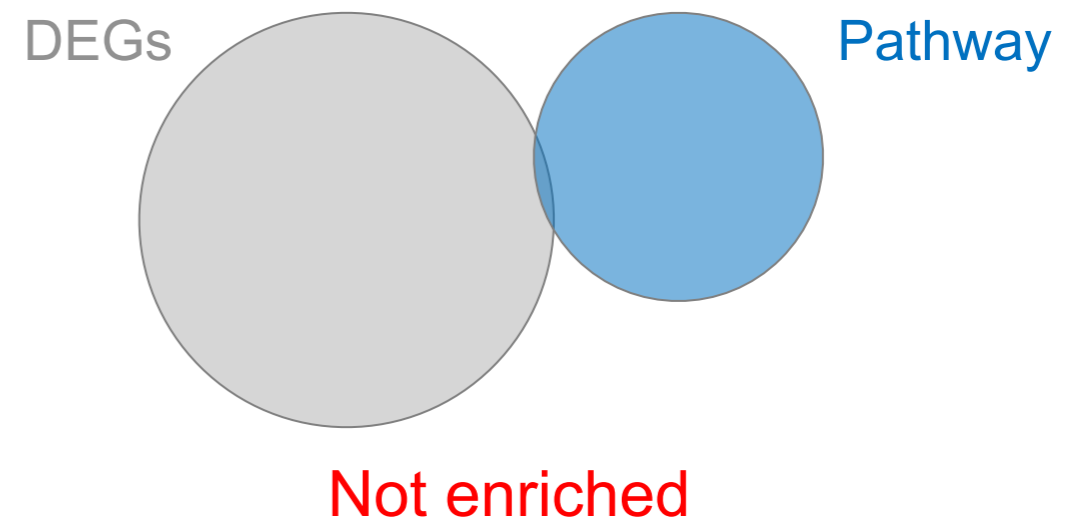
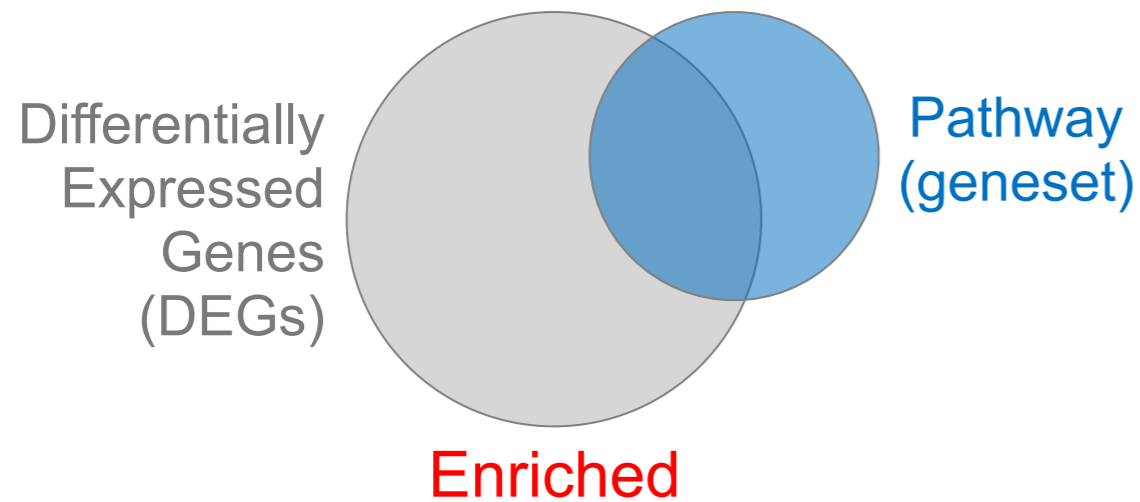
Overlap...

Pathway analysis (geneset enrichment)



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

Principle



-
- 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*
 - Variations of the math: overlap, ranking, networks...
 - *Not critical, different algorithms show similar performances*

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

Limitations

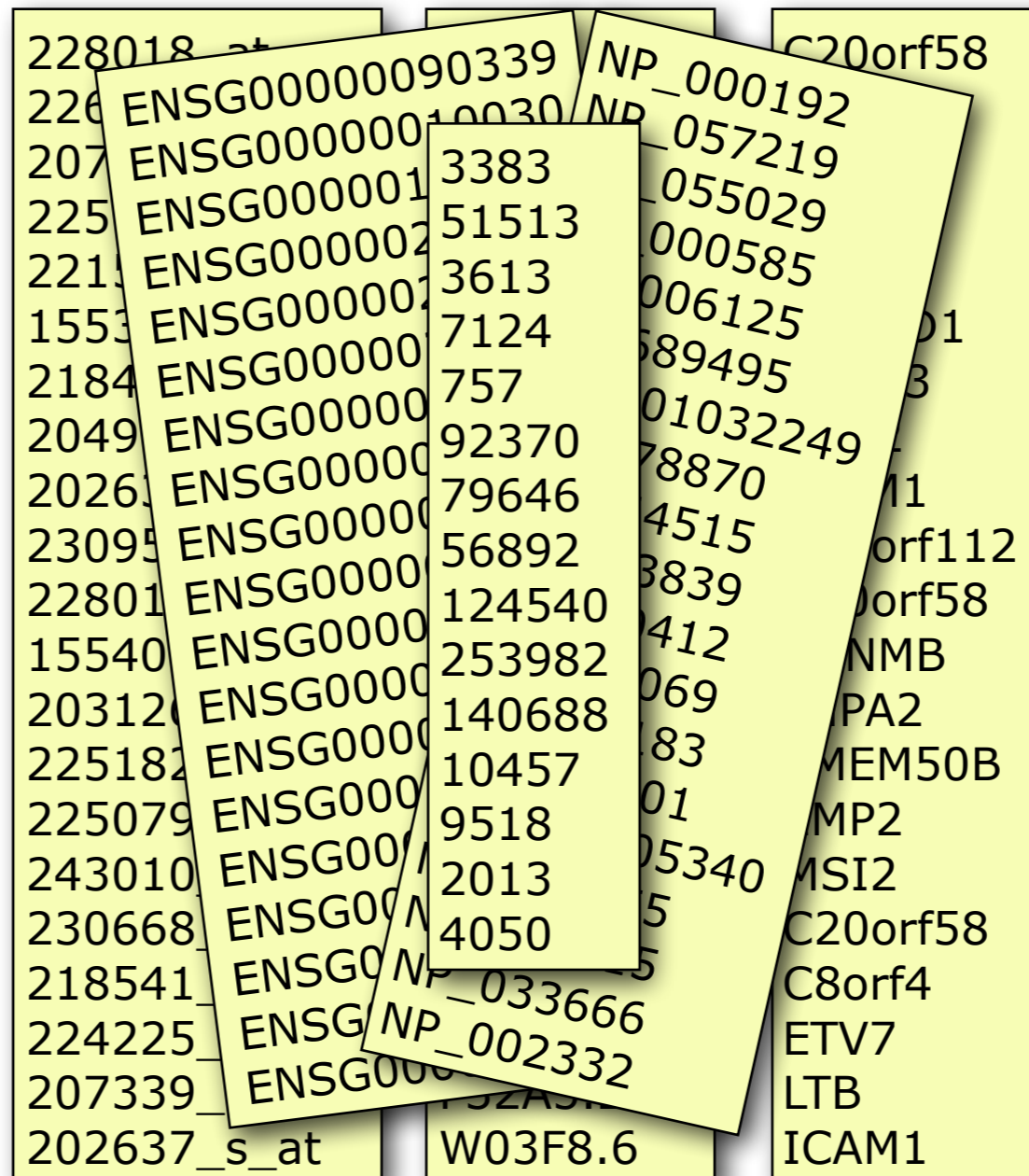
- **Geneset annotation bias:** can only discover what is already known
- **Non-model organisms:** no high-quality genesets available
- **Post-transcriptional regulation** is neglected
- **Tissue-specific** variations of pathways are not annotated
 - e.g. NF- κ B regulates metabolism, not inflammation,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

Starting point for pathway analysis:

Your gene list

- 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 (such as ENSG00000090339, NP_000192, C20orf58) and numerical values (such as 3383, 51513, 055029, 000585, 006125, 589495, 01032249, 78870, 4515, 3839, 412, 069, 83, 01, 05340, 5, 5, 033666, 002332, 5275, W03F8.6). The notes are arranged in a way that they appear to be layered on top of each other, with some text visible through the gaps and overlaps.

Translating between identifiers

- Many different identifiers exist for genes and proteins, e.g. UniProt, Entrez, etc.
- Often you will have to translate one set of ids into another
 - A program might only accept certain types of ids
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 - **UniProt < www.uniprot.org>; IDConverter < idconverter.bioinfo.cnio.es >**

Translating between identifiers: UniProt < www.uniprot.org >

The image shows the UniProt website interface. At the top, the UniProt logo is on the left, and navigation links for "Downloads", "Contact", and "Documentation/Help" are on the right. Below the header is a search bar with a dropdown menu set to "Protein Knowledgebase (UniProtKB)", a "Query" input field, and buttons for "Search", "Clear", and "Fields »". Below the search bar are buttons for "Search", "Blast", "Align", "Retrieve", and "ID Mapping", with the "ID Mapping" button highlighted by a red rectangle. Below the search bar, there are sections for "WELCOME" and "NEWS" with a feed icon. The main content area is titled "Identifiers" and contains a large empty text box on the left. To the right of the text box are two dropdown menus: "From" set to "EMBL/GenBank/DDBJ" and "To" set to "UniProtKB AC". Below these are three buttons: "Map", "Swap", and "Clear". At the bottom of the "Identifiers" section, there is a "Choose File" button and the text "no file selected".

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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 two tables. The 'Data Table' (columns A-F) lists RefSeq IDs and various expression values. The 'Annotation Table' (columns G-K) lists RefSeq IDs, Symbol names, Entrez IDs, and Unigene IDs. The VLOOKUP function is used in cell B3 to find the Symbol for the RefSeq ID 'NM_153103' in the Data Table.

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

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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](#)]

Reminder

2. class-material (bash)

Using the merge() function

> anno <- read.csv("data/annotables_grch38.csv")

This is an annotation file

> merge(mygenes, anno, by.x="row.names", by.y="ensgene")

This is our differential expressed genes

Using the merge() function

> anno <- read.csv("data/annotables_grch38.csv")

> merge(mygenes, anno, by.x="row.names", by.y="ensgene")

Using mapIDs() function from bioconductor

> library("AnnotationDbi")

> library("org.Hs.eg.db")

Load the required Bioconductor packages

> mygenes\$symbol <- mapIDs(org.Hs.eg.db,
column="SYMBOL",
keys=row.names(mygenes),
keytype="ENSEMBL")

Annotation we want to add

Our vector of gene names & their format

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?

- **Most commonly used:**

- **Gene Ontology (GO)**
- **KEGG Pathways** (mostly metabolic)

- **GeneGO MetaBase**



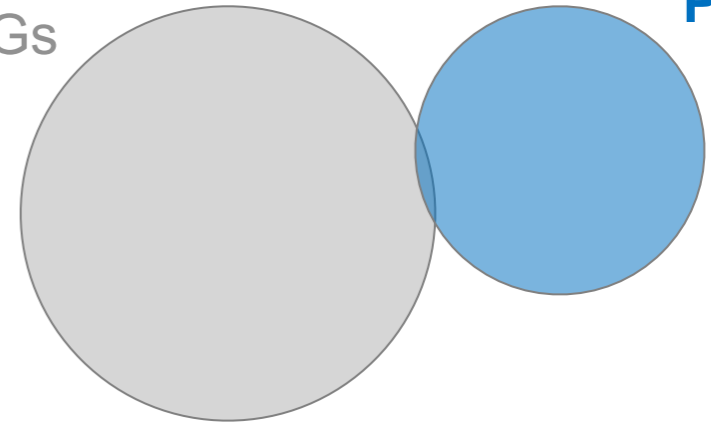
- **Ingenuity Pathway Analysis (IPA)**



- Many others...

- **Enzyme Classification, PFAM, Reactome,**
- Disease Ontology, MSigDB, Chemical Entities of Biological Interest, Network of Cancer Genes etc...
- See: Open Biomedical Ontologies (www.obofoundry.org)

DEGs



Pathway

GO
KEGG
IPA
etc....

GO < www.geneontology.org >

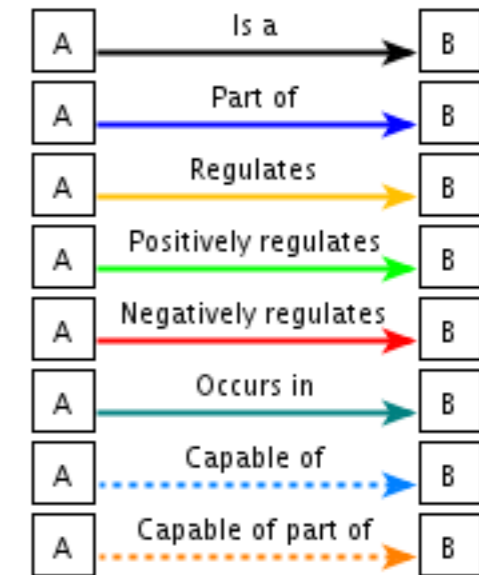
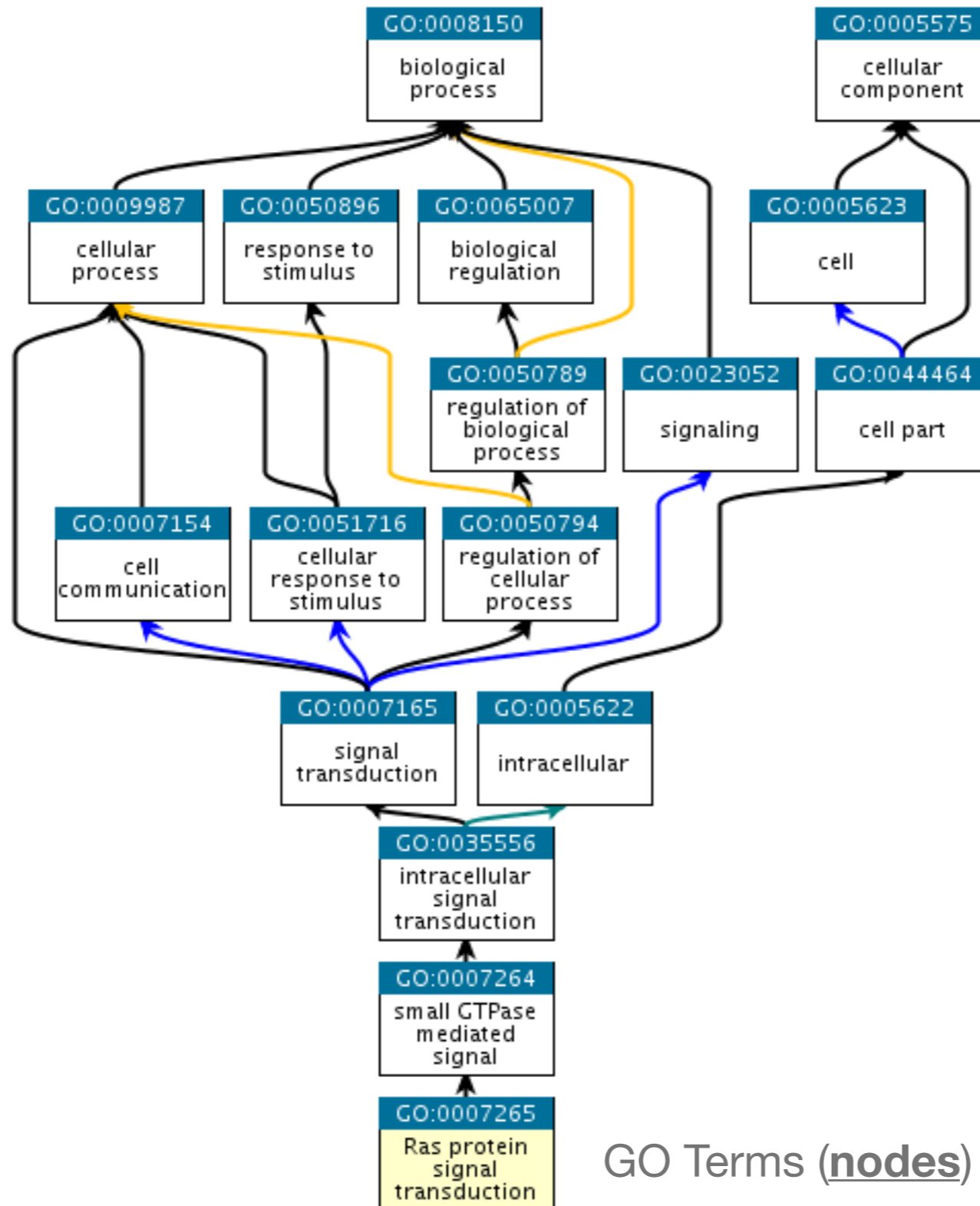
- **What function does HSF1 perform?**
 - *response to heat; sequence-specific DNA binding; transcription; etc*
- **Ontology** => a structured and controlled vocabulary that allows us to annotate gene products consistently, interpret the relationships among annotations, and can easily be *handled by 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 Annotations

- GO is not a stand-alone database of genes/proteins or sequences
- Rather gene products get annotated with **GO terms** by UniProt and other organism specific databases, such as Flybase, Wormbase, MGI, ZFIN, etc.
- Annotations are available through AmiGO < 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 bar. On the right side, there is a vertical label "Beta AmiGO 2". At the bottom, 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 is structured as a “directed graph”



Relationships (edges)

Parent terms are more general & child terms more specific

GO Terms (nodes)

GO evidence codes

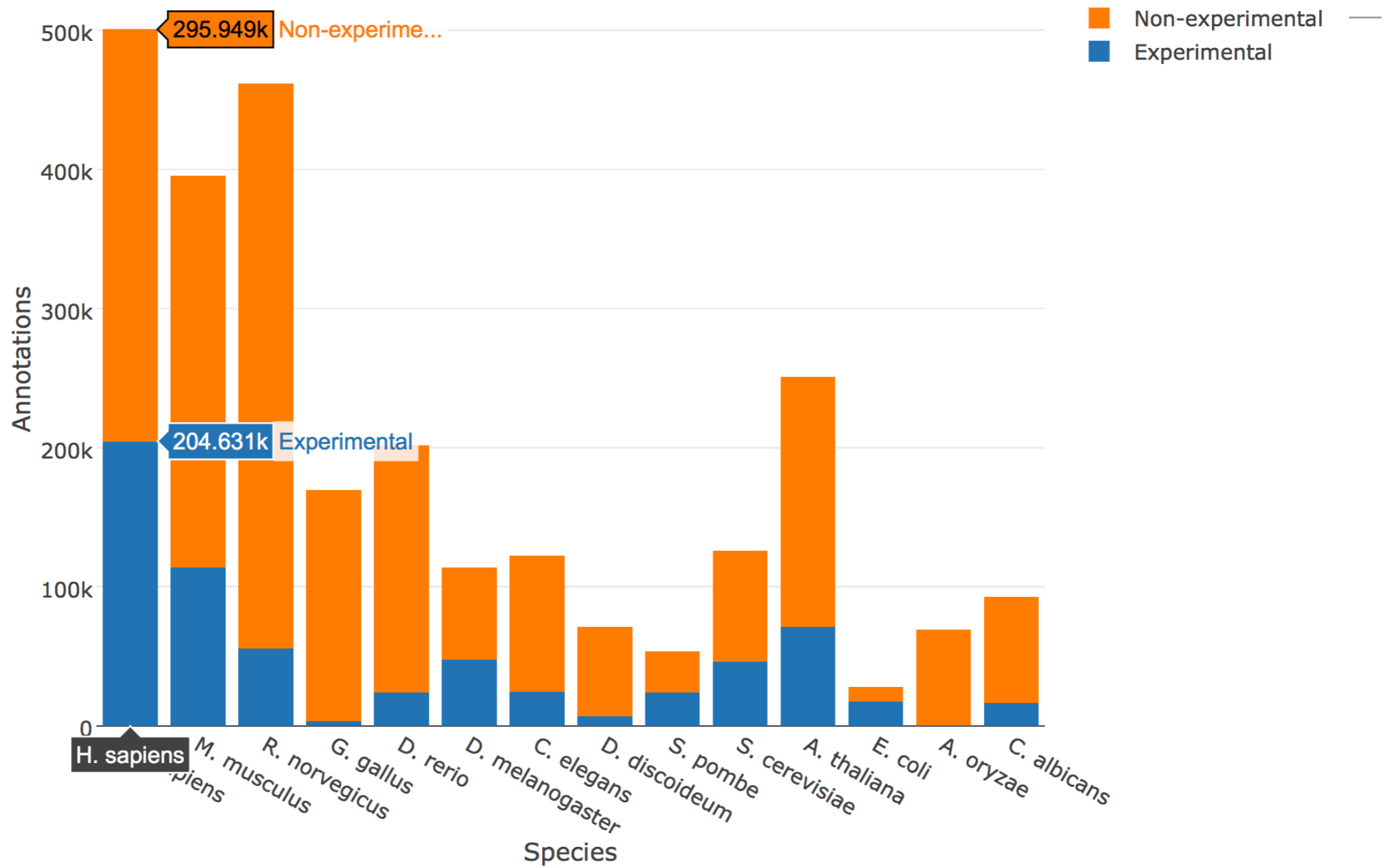
Evidence code	Evidence code description	Source of evidence	Manually checked	Current number of annotations*
IDA	Inferred from direct assay	Experimental	Yes	71,050
IEP	Inferred from expression pattern	Experimental	Yes	4,598
IGI	Inferred from genetic interaction	Experimental	Yes	8,311
IMP	Inferred from 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

Can now do gene list analysis with GeneGO online!

The screenshot shows a web browser window with the URL `pantherdb.org/webservices/go/overrep.jsp`. The page header includes the GeneOntology logo (Unifying Biology) and the PANTHER Classification System logo. Navigation links include Home, About, PANTHER Data, PANTHER Tools, Workspace, Downloads, and Help/Tutorial. A notification banner states "New! PANTHER13.1 released." The main content area is titled "Gene List Analysis" and contains a message: "Please refer to our article in [Nature Protocols](#) for detailed instructions on how to use this page." Below this is a red error message: "Error parsing request, no input specified". The interface is divided into three main sections:

- 1. Enter ids and or select file for batch upload. Else enter ids or select file or list from workspace for comparing to a reference list.**
 - Enter IDs:** A text input field with the label "Supported IDs" and a note "separate IDs by a space or comma".
 - Upload IDs:** A "Choose File" button with the text "no file selected".
 - Select List Type:** Radio buttons for "ID List" (selected), "Previously exported text search results", "Workspace list", "PANTHER Generic Mapping File", and "VCF File". A "Flanking region" dropdown menu is set to "20 Kb".
- 2. Select organism.**
 - A list of organisms: Homo sapiens, Mus musculus, Rattus norvegicus, Gallus gallus, and Danio rerio.
- 3. Select Analysis.**
 - Radio buttons for "Functional classification viewed in gene list" (selected) and "Functional classification viewed in pie chart".

The left sidebar contains a search box, quick links (Whole genome function views, Genome statistics, Data Version, How to cite PANTHER), news (PANTHER13.1 Released), and a newsletter subscription form. A PostgreSQL logo is visible at the bottom left.

Another popular online tool:

DAVID at NIAID < 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

Analysis Wizard

[Upload](#) **List** Background

Upload Gene List

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

Step 1: Enter Gene List
A: Paste a list

Clear

Or
B: Choose From a File

Choose File no file selected

Step 2: Select Identifier

AFFY_ID

Step 3: List Type

Gene List
Background

Step 4: Submit List

Submit List

[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

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

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**
 - Clustering of functional sets can be helpful in these cases

DAVID

- DAVID now offers functional annotation clustering:

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 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

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

Want more?

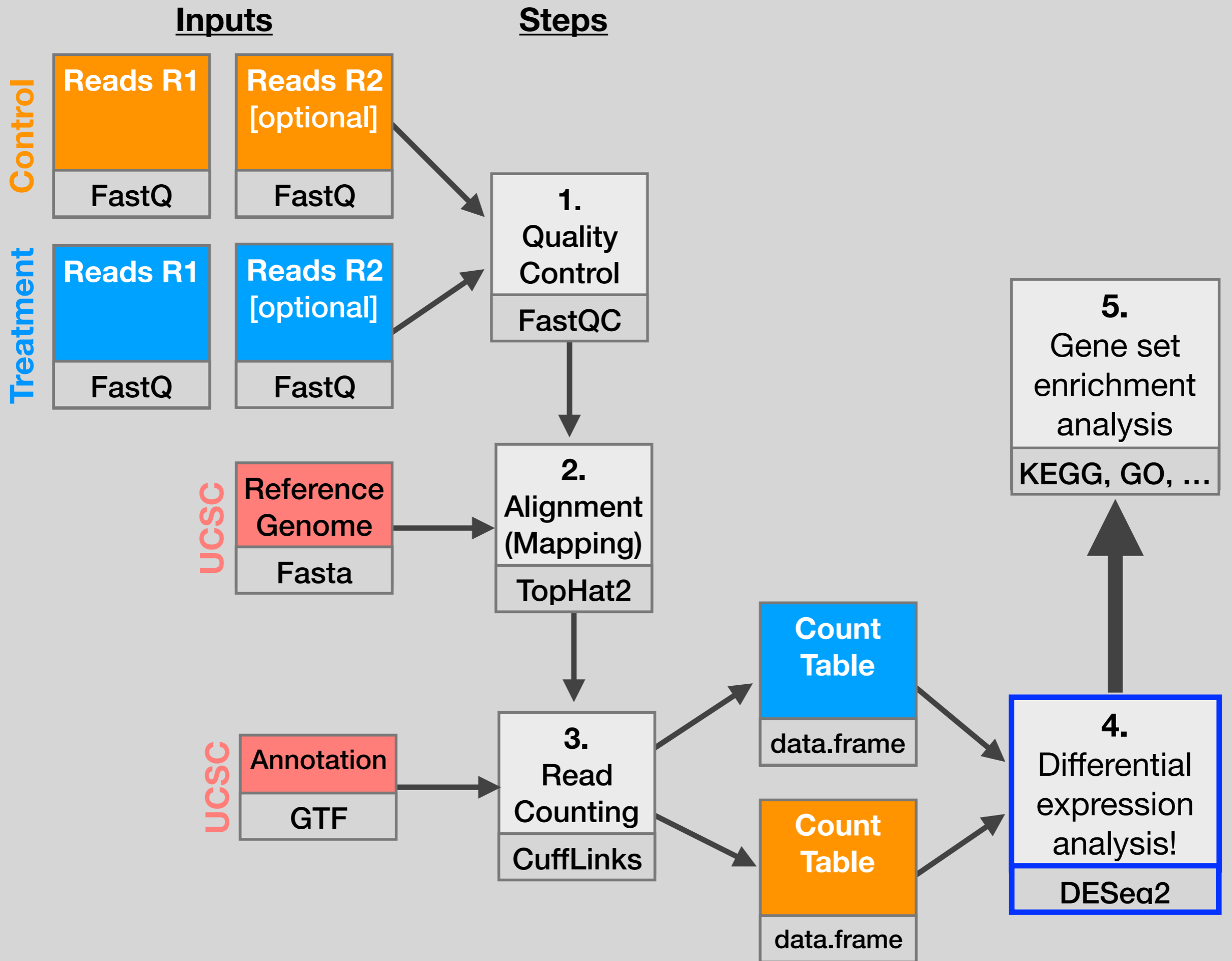


- **GeneGO** < portal.genego.com >
 - MD/PhD curated annotations, great for certain domains (eg, Cystic Fibrosis)
 - Nice network analysis tools
 - Email us for access
- **Oncomine** < www.oncomine.org >
 - Extensive cancer related expression datasets
 - Nice concept analysis tools
 - Research edition 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_S19/lectures/#15



counts + metadata

1

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
...

2

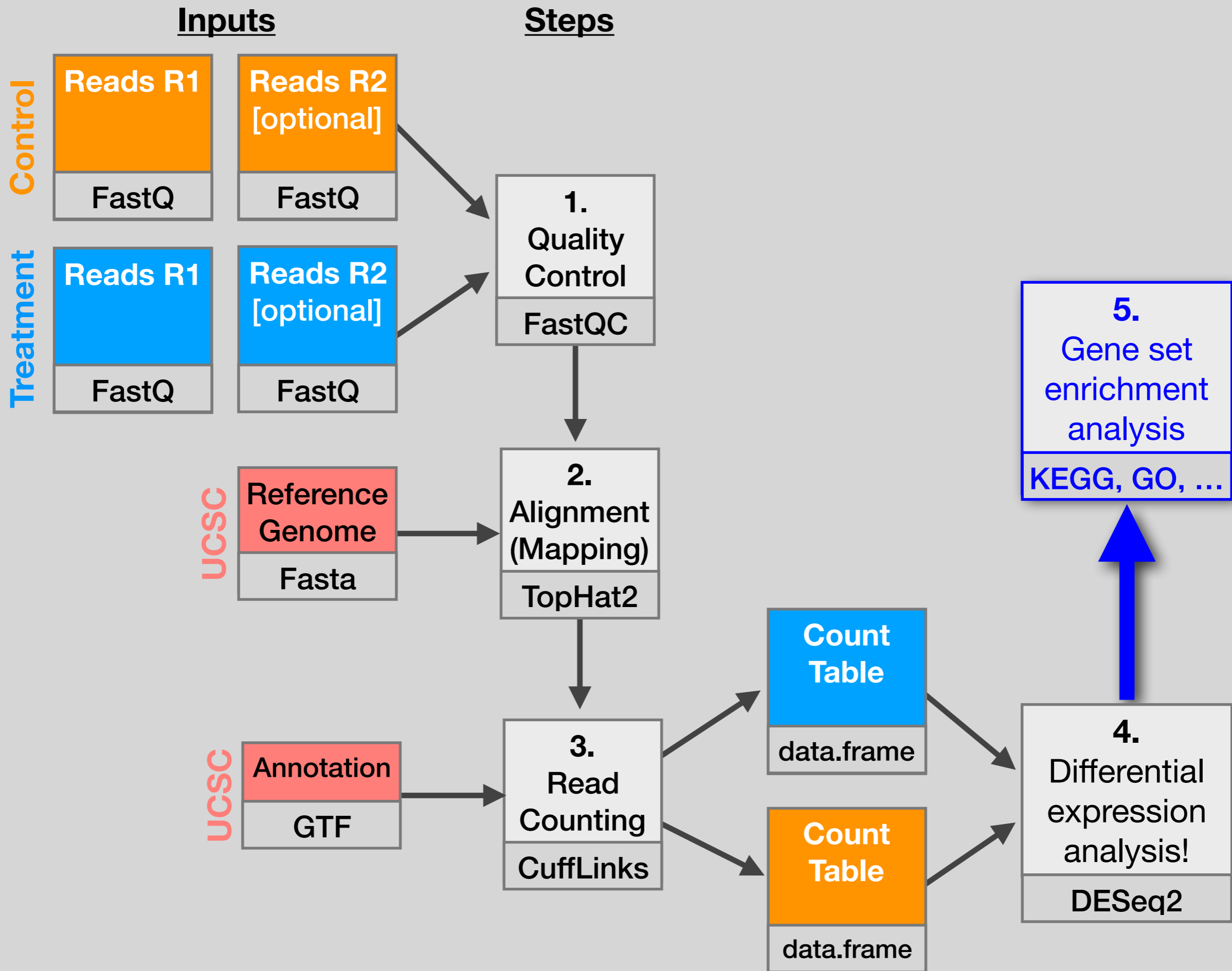
colData

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

colData describes metadata about the *columns* of countData

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

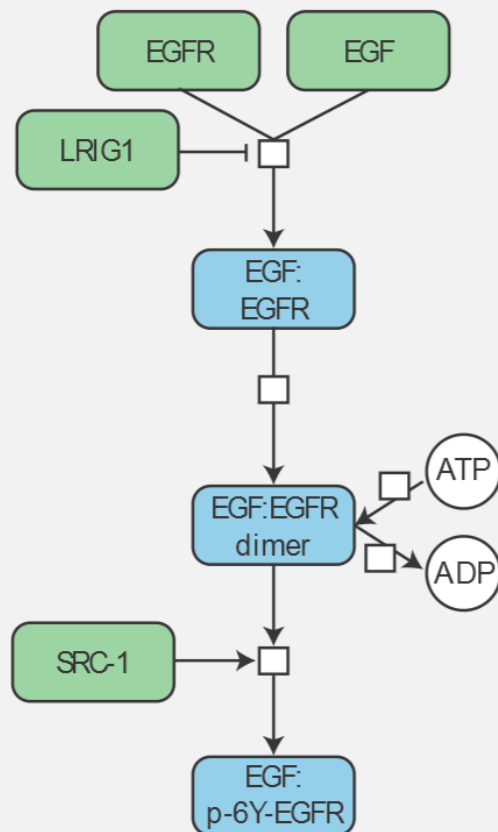
N.B. First column of colData must match column names (i.e. **sample names**) of countData (-1st)



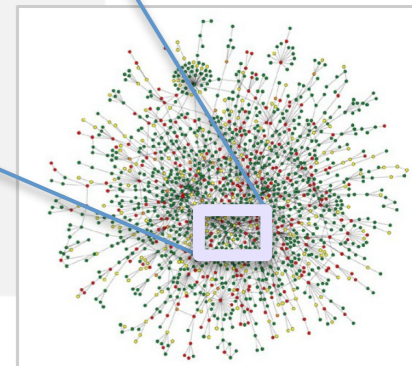
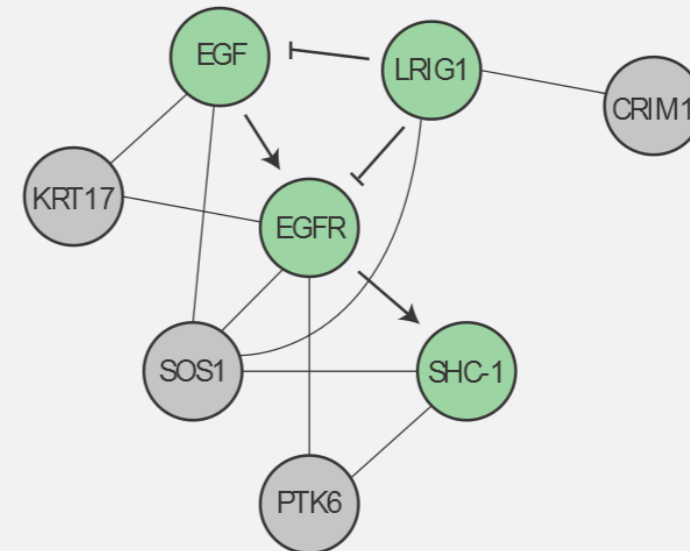
Pathways vs Networks

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

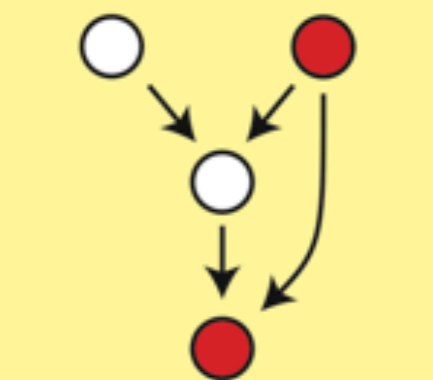
1 Enrichment of fixed gene sets

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

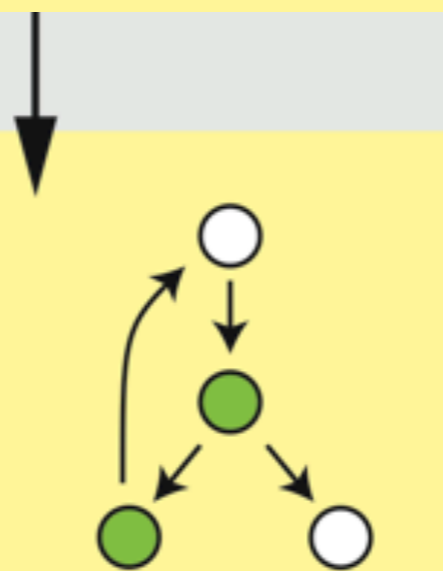
2 De novo sub-network construction and clustering

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

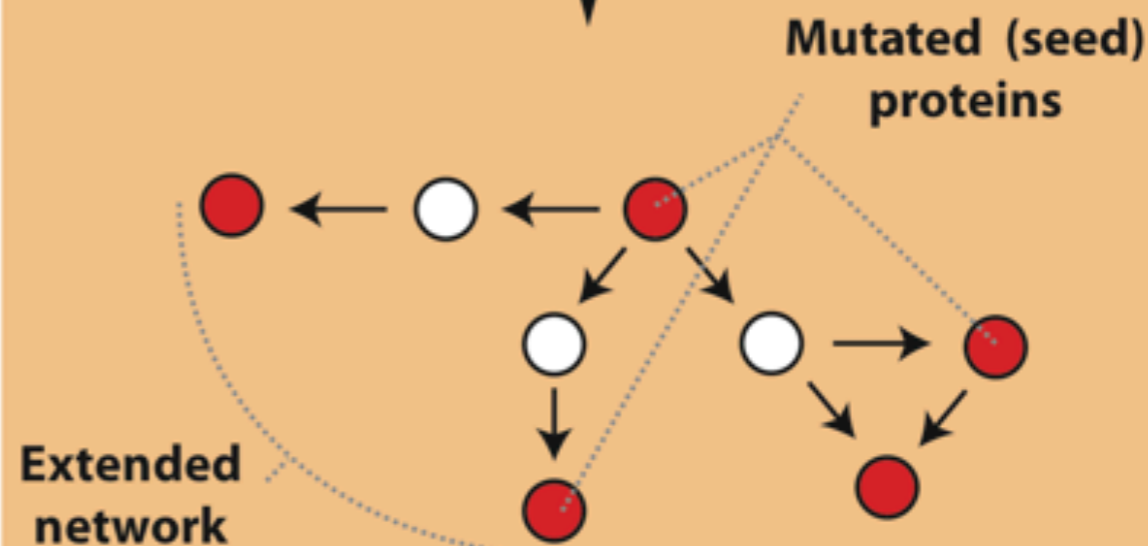
Output



Enriched network



Depleted network



Extended network

Goal

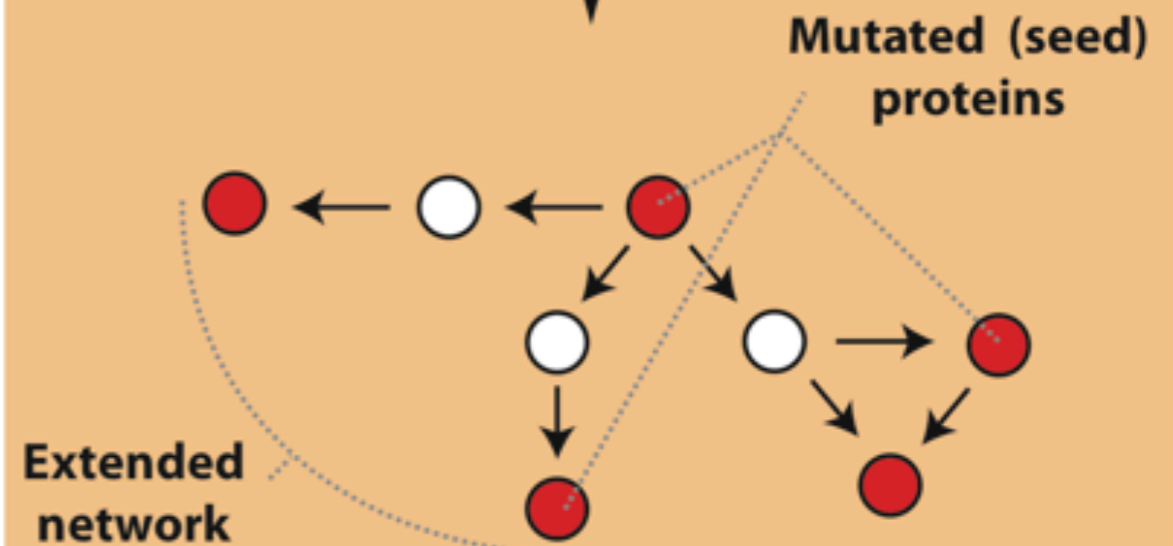
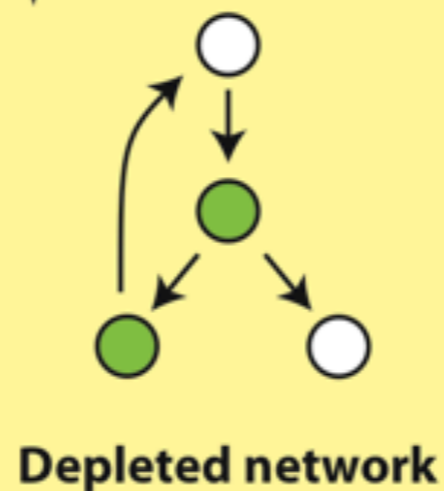
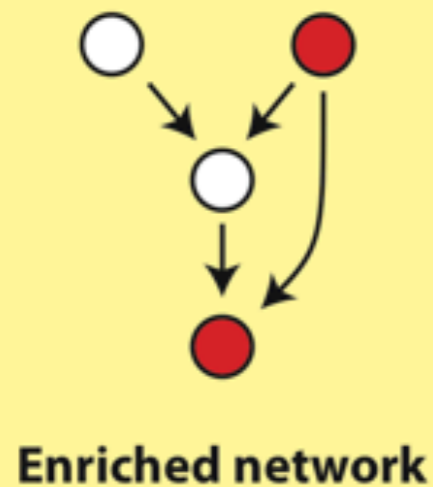
1 Enrichment of fixed gene sets

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?

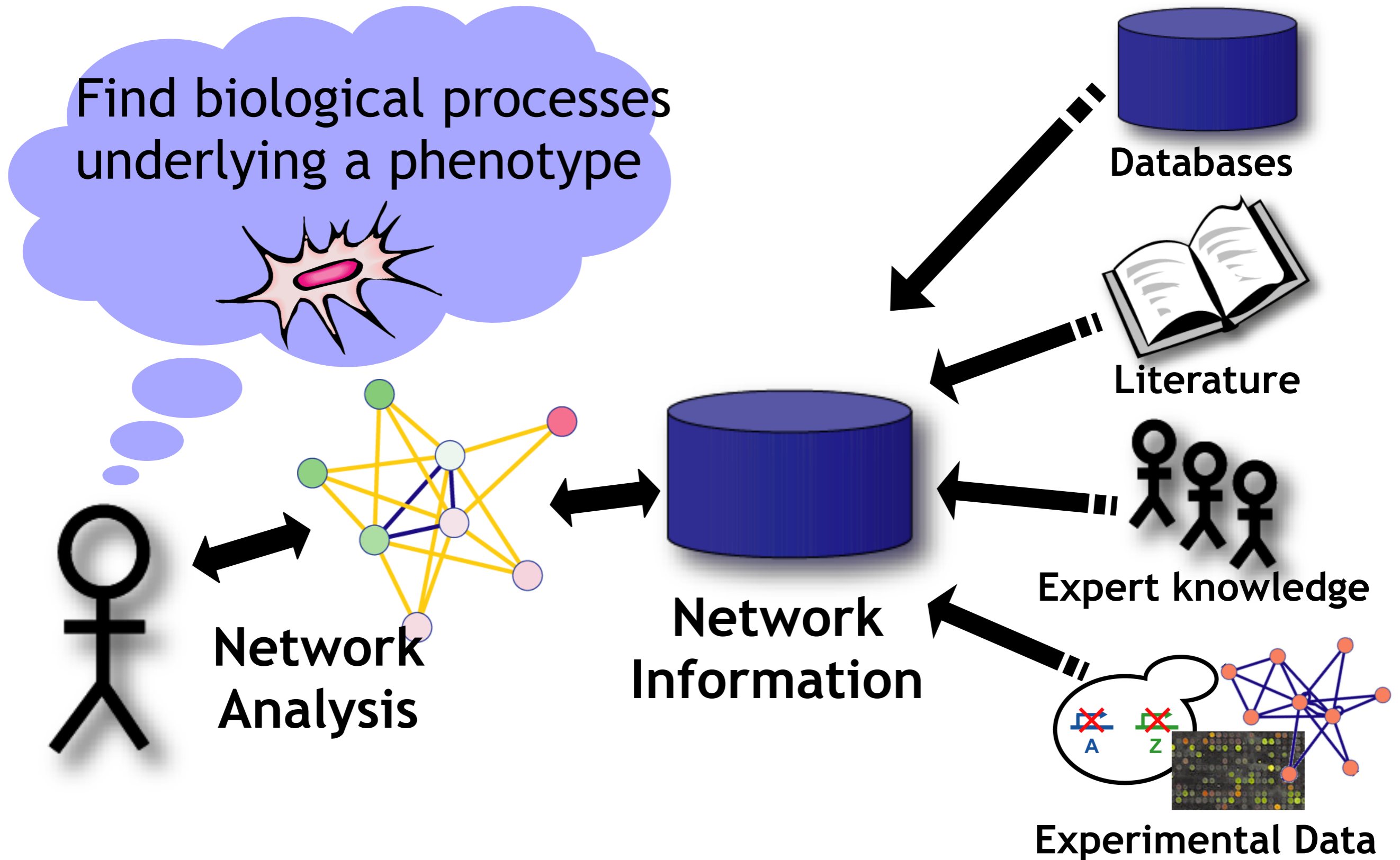
Are NEW pathways altered in this cancer? Are there clinically relevant tumor subtypes?

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

Limitations

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

Pathway & Network Analysis Overview



Do it Yourself!

R Knowledge Check For BGGN-213 Quiz

This will be marked but not graded
(*i.e.* will not factor into your course grade)

Time Limit: 40 mins

