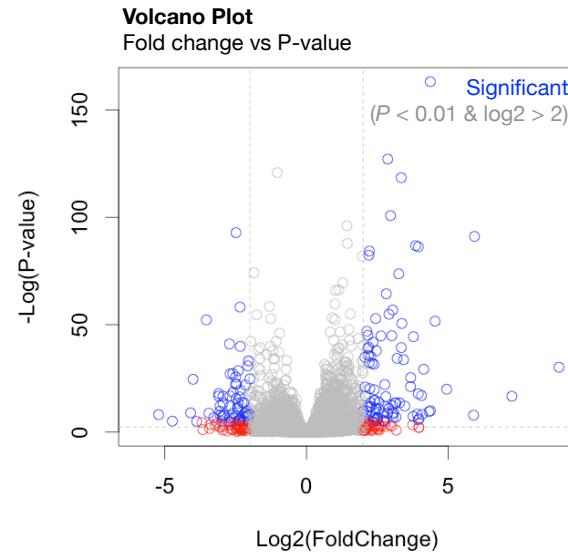


X	baseMean	log2FoldChange	IfSE	stat	pvalue	padj	symbol
ENSG00000152583	954.77093	4.3683590	0.23713648	18.421286	8.867079e-76	1.342919e-71	SPARC1
ENSG00000179094	743.25269	2.8638885	0.17555825	16.313039	7.972621e-60	6.037267e-56	PER1
ENSG00000116584	2277.91345	-1.0347000	0.06505273	-15.905557	5.798513e-57	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	1.0295569e-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



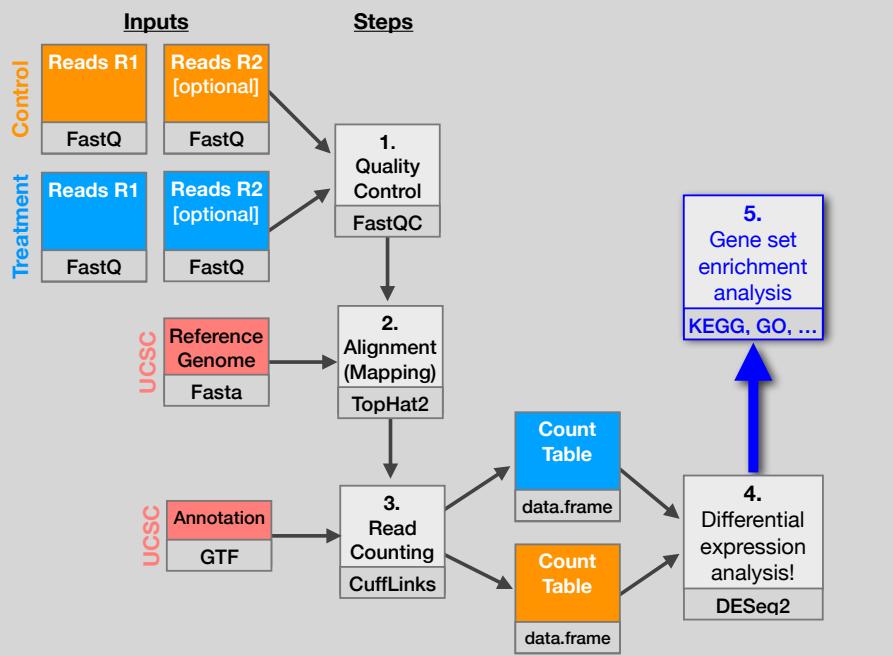
My high-throughput experiment generated a long list of genes/proteins...

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)

Gene ID	Symbol	Log2FC	negLog10PValue	AdjustedPValue	Method
ENSG00000152581	9147.2093	4.3481590	0.21715644	18.421286	0.00070794-71 SPAN2L
ENSG00000179094	741.25248	2.0358350	0.17555853	15.131251	0.00070794-60 PMS2L
ENSG00000116584	227.716345	-1.0149544	0.05005279	13.905357	5.798118e-17 2.027284-53 ARHGAP2
ENSG00000186221	238.735723	3.1950344	0.21454507	15.71200	0.24000000-56 3.000000-52 MACA
ENSG00000177357	1.3951254	0.00000000	0.00000000	1.3951254	0.00000000-57 1.3951254
ENSG00000141175	1349.62037	1.4271683	0.05006663	14.193550	6.030711e-46 1.740174e-42 STOM
ENSG00000176965	2618.40074	-2.4806648	0.17006467	-13.972951	2.008181e-44 4.562374e-41 KCTD12
ENSG00000109450	419.54152	5.0737950	0.41618442	13.641233	3.397558e-41 2.646131e-40 ZEB16
ENSG00000115474	14134.9617	3.4504143	0.24490701	13.514651	1.384000e-41 3.941628e-38 SAMD10
ENSG00000131187	34134.9617	3.4504143	0.24490701	13.514651	1.384000e-41 3.941628e-38 SAMD10
ENSG00000649649	2610.23049	3.9450524	0.29391831	13.641202	2.008070e-41 3.317966e-38 FBXO5
ENSG00000106741	7542.23287	2.2159510	0.16467314	13.131205	1.970000e-40 4.488304e-37 NMNAT
ENSG00000125148	360.57946	2.1895036	0.16170546	13.131205	1.602400e-39 1.613797e-36 MTZA
ENSG00000106076	1.3951254	0.00000000	0.00000000	1.3951254	0.00000000-57 1.3951254
ENSG00000106076	988.06883	-1.8501713	0.14798537	-2.233831	5.861478e-36 5.938130e-33 DNMT3
ENSG00000187131	139.07694	3.2511424	0.26099711	12.478252	1.008146e-31 3.233804e-33 MTIX
ENSG00000262635	11234.97954	1.2801210	0.15047433	12.118979	6.742826e-34 4.027070e-31 SMM3
ENSG00000379568	2619.57020	1.1599497	0.05006884	11.886458	1.784022e-32 1.437936e-30 PMP22
ENSG00000188624	2020.04495	2.8145104	0.24068469	16.094515	1.559815e-31 1.029598e-28 CCDC89
ENSG00000123582	5098.555294	1.0045453	0.08001565	11.285123	1.5594241e-29 1.125904e-26 MORF4L2
ENSG00000144569	1283.77980	-1.3050041	0.11714681	-11.171875	5.473974e-29 3.768338e-26 FAM171B
ENSG00000196157	201.81358	-2.3456577	0.21097936	-11.140401	7.935120e-29 4.995858e-26 SLC2A8
ENSG00000130921	1059.46920	3.9413943	0.27603196	11.030823	4.130702e-28 1.939072e-25 GLB1

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



Basic idea

Differentially Expressed Genes (DEGs)

	baseMean	logFoldChange	negLog10PValue	padj	symbol
ENSG0000011583	954.77093	3.463556	0.171134	0.0000000000000000	3
ENSG00000117094	743.50000	2.893000	0.175142	0.0000000000000000	4
ENSG0000011654	2277.81345	-1.034700	0.000527	0.0000000000000000	15
ENSG00000182023	2383.73373	1.341554	0.212415	0.0000000000000000	16
ENSG00000182128	1446.70373	2.961216	0.207027	0.0000000000000000	17
ENSG0000014375	13493.40371	1.427748	0.100463	0.0000000000000000	18
ENSG0000014375	13493.40371	1.427748	0.100463	0.0000000000000000	19
ENSG00000139968	418.44142	5.927950	0.428184	0.0000000000000000	20
ENSG00000142462	2933.42426	1.439488	0.158272	0.0000000000000000	21
ENSG00000133487	1414.99177	3.850541	0.248970	0.0000000000000000	22
ENSG00000133487	1414.99177	3.850541	0.248970	0.0000000000000000	23
ENSG00000142699	2030.50000	3.893000	0.214670	0.0000000000000000	24
ENSG00000142699	2030.50000	3.893000	0.214670	0.0000000000000000	25
ENSG00000142699	2030.50000	3.893000	0.214670	0.0000000000000000	26
ENSG00000111448	3095.87946	2.710898	0.146734	0.0000000000000000	27
ENSG00000126126	1646.18314	1.971140	0.150203	0.0000000000000000	28
ENSG00000126126	1646.18314	1.971140	0.150203	0.0000000000000000	29
ENSG00000177662	732.77980	1.859123	0.150203	0.0000000000000000	30
ENSG00000177662	732.77980	1.859123	0.150203	0.0000000000000000	31
ENSG00000176273	1123.47954	1.295119	0.156743	0.0000000000000000	32
ENSG00000176273	1123.47954	1.295119	0.156743	0.0000000000000000	33
ENSG00000176686	2639.37020	1.110994	0.090084	0.0000000000000000	34
ENSG00000141213	7257.00868	1.024852	0.086576	0.0000000000000000	35
ENSG00000140674	2026.04495	2.814104	0.248970	0.0000000000000000	36
ENSG00000140674	2026.04495	2.814104	0.248970	0.0000000000000000	37
ENSG00000144986	1281.77980	-1.359004	0.137146	0.0000000000000000	38
ENSG00000144986	1281.77980	-1.359004	0.137146	0.0000000000000000	39
ENSG00000185157	241.85156	-2.345887	0.210473	0.0000000000000000	40
ENSG00000115821	18075.40029	1.041394	0.270272	0.0000000000000000	41

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

Annotate...



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



- DEGs come from your experiment

> Critical, needs to be as clean as possible

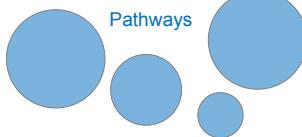
- Pathway genes ("geneset") come from annotations

> Important, but typically not a competitive advantage

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

Differentially Expressed Genes (DEGs)

Overlap...



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

Side-note:

- **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-κB 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-κB, AP-1, IRF3/7, NFAT

Starting point for pathway analysis: Your gene list

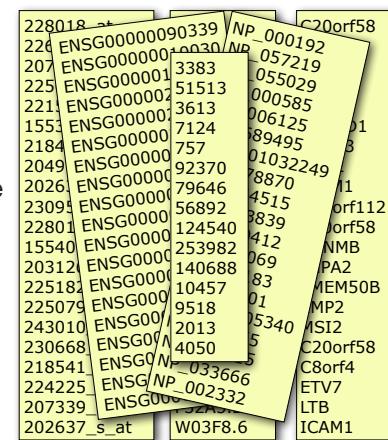
- You have a list of genes/proteins of interest
- You have quantitative data for each gene/protein

- Fold change

- p-value

- Spectral counts

- Presence/absence



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
 - 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>; IDConverter <idconverter.bioinfo.cnio.es>

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

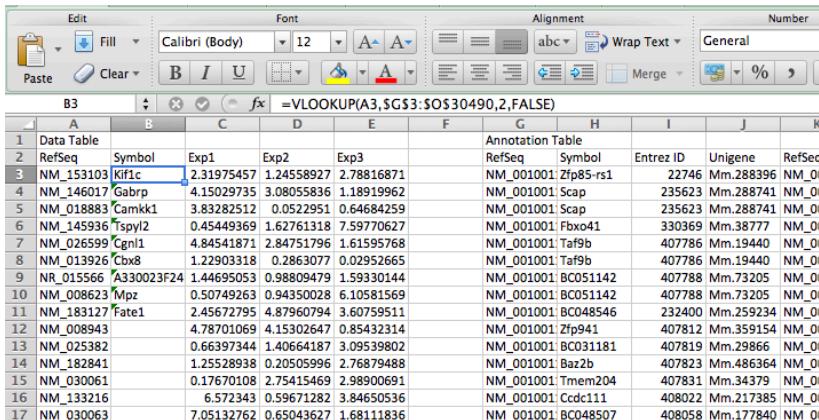
The screenshot shows the UniProt homepage. At the top, there is a search bar with dropdown menus for 'Search in' (Protein Knowledgebase (UniProtKB)) and 'Query'. Below the search bar are buttons for 'Search', 'Clear', 'Fields', 'Blast', 'Align', 'Retrieve', and 'ID Mapping'. The 'ID Mapping' button is highlighted with a red box. The main area is titled 'WELCOME' and 'NEWS'. Below this, there is a form for 'Identifiers' mapping. It has two dropdown menus: 'From' (set to 'EMBL/GenBank/DDBJ') and 'To' (set to 'UniProtKB AC'). There is also a file upload field labeled 'Choose File' with the placeholder 'no file selected'. To the right of the dropdowns are three buttons: 'Map', 'Swap', and 'Clear'.

Translating between identifiers

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 - UniProt <www.uniprot.org>; IDConverter <idconverter.bioinfo.cnio.es>
- **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 first table, 'Data Table', has columns A through F. The second table, 'Annotation Table', has columns G through K. Cell B3 contains the formula =VLOOKUP(A3,\$G\$3:\$O\$30490,2, FALSE). The 'Annotation Table' is sorted by RefSeq.

A	B	C	D	E	F	G	H	I	J	K
RefSeq	Symbol	Exp1	Exp2	Exp3		RefSeq	Entrez ID	Unigene	RefSeq	
NM_153103	Kif1c	2.31975457	1.24558927	2.78816871		NM_001001	Zfp85-rs1	22746	Mm.288396	NM_001
NM_146017	Gabbrp	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	232408	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

Translating between identifiers

- Many different identifiers exist for genes and proteins, e.g. UniProt, Entrez, etc.
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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 two ids you want to convert between; Use vlookup to translate your list

- 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
```

Reminder

2. class-material (bash)

```
# 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", "T0B1", "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", "FXYD2", "RBP4", "SLC6A12", "KDELR3", "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:

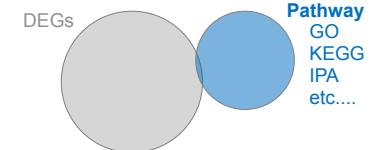
<https://bioconductor.org/packages/release/bioc/html/clusterProfiler.html>

Alternative...

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...

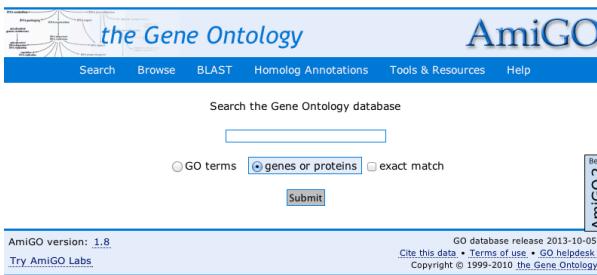
- **Enzyme Classification, PFAM, Reactome,**
- Disease Ontology, MSigDB, Chemical Entities of Biological Interest, Network of Cancer Genes etc...
- See: Open Biomedical Ontologies (www.obofoundry.org)

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**

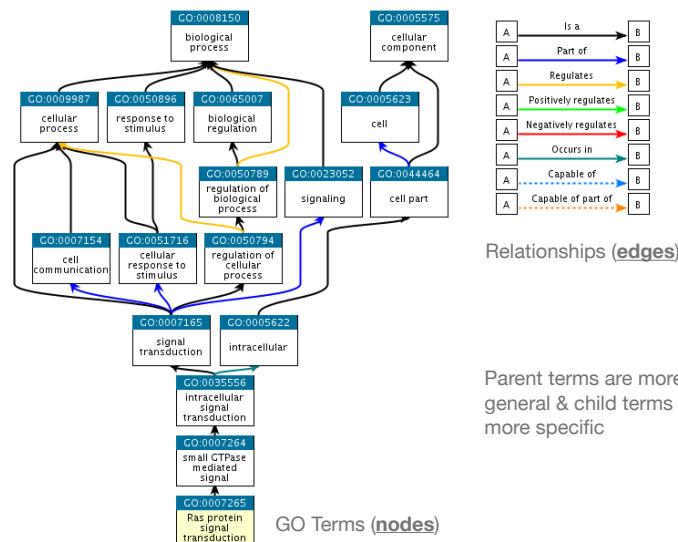
GO Annotations

- 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's a navigation bar with links for 'Search', 'Browse', 'BLAST', 'Homolog Annotations', 'Tools & Resources', and 'Help'. Below the navigation bar is a search bar labeled 'Search the Gene Ontology database'. Underneath the search bar are three radio buttons: 'GO terms' (selected), 'genes or proteins', and 'exact match'. A 'Submit' button is located below the search bar. At the bottom of the page, there's footer information including 'AmiGO version: 1.8', 'GO database release 2013-10-05', 'Try AmiGO Labs', 'Cite this data', 'Terms of use', 'GO Helpdesk', 'Copyright © 1999-2010 the Gene Ontology', and a 'Beta' badge.

GO is structured as a “directed graph”



Relationships (edges)

Parent terms are more general & child terms more specific

GO Terms (nodes)

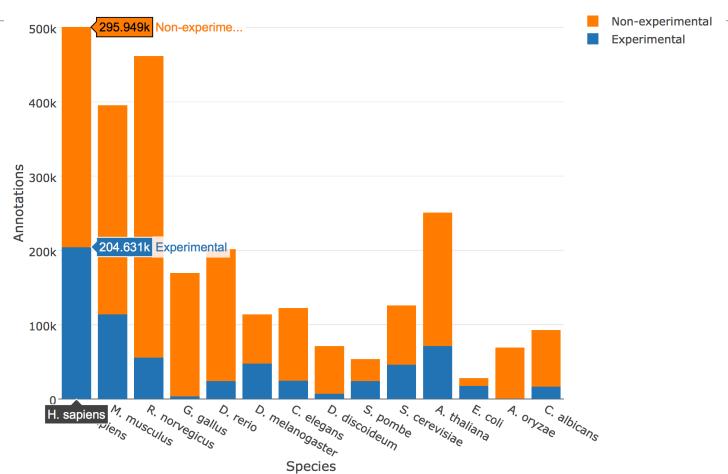
GO evidence codes

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	15,687,387
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 the PANTHER Classification System interface for Gene List Analysis. The main form includes fields for Enter IDs, Upload IDs, Select List Type, Select organism, and Select Analysis.

Key elements visible:

- Enter IDs:** Supported IDs, File format (Choose File: no file selected).
- Select List Type:** ID List, Previously exported text search results, Workspace list, PANTHER Generic Mapping File, VCF File Flanking region | 20 Kb.
- Select organism:** Homo sapiens, Mus musculus, Rattus norvegicus, Gallus gallus, Danio rerio.
- Select Analysis:** Functional classification viewed in gene list.

Another popular online tool: **DAVID** at NIAID < david.abcc.ncifcrf.gov >

The screenshot shows the DAVID Analysis Wizard interface. At the top, it says "Analysis Wizard" and "DAVID Bioinformatics Resources 2008, NIAID/NIH". Below that is a navigation bar with links like Home, Start Analysis, Shortcut to DAVID Tools, Technical Center, Downloads & APIs, Term of Service, Why DAVID?, and About Us. The main area is titled "Analysis Wizard" and has a sub-section "Step 1: Submit your gene list through left panel". It includes a text input field for "Gene List" with a "Clear" button, a "Choose From a File" section, and a dropdown for "Step 2: Select Identifier" set to "AFFY_ID". A note says "Note: Affy Exon IDs and Affy Gene Array IDs are now supported in DAVID, as *affy_id* type." Below this is a list of gene identifiers: 1007_s_at, 1008_s_at, 117_at, 121_at, 1255_g_at, 1316_at, 1320_at, 1431_at, 1438_at, 1487_at, 1494_f_at, 1598_g_at. At the bottom, there's a "Submit List" button.

DAVID

- Functional Annotation Chart



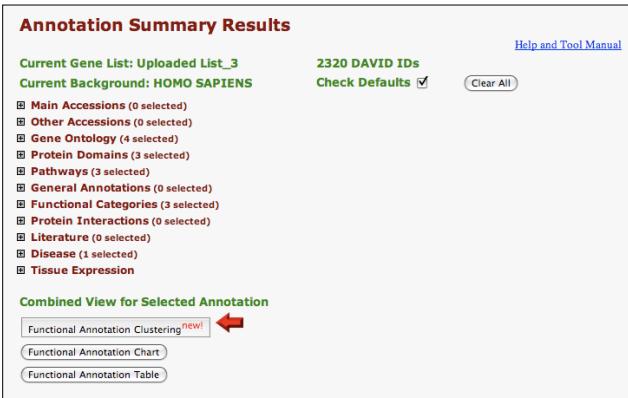
Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources
Da Wei Huang, Brad T Sherman & Richard A Lempicki
Nature Protocols 4, 44 - 57 (2009)

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

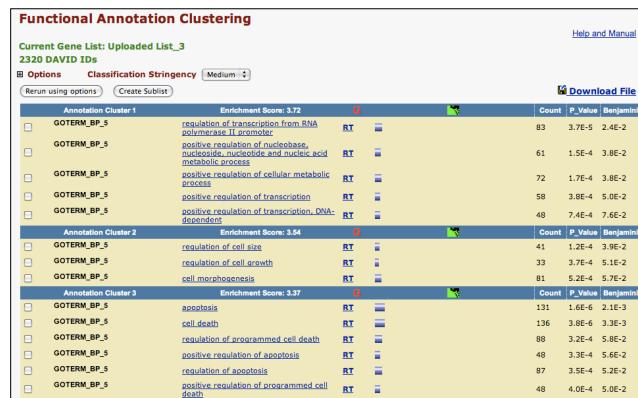
DAVID

- DAVID now offers functional annotation clustering:



DAVID Functional Annotation Clustering

- Based on shared genes between functional sets



Hands-on time!

https://bioboot.github.io/bimm143_F18/lectures/#16

Also: R Quiz Online

Want more?



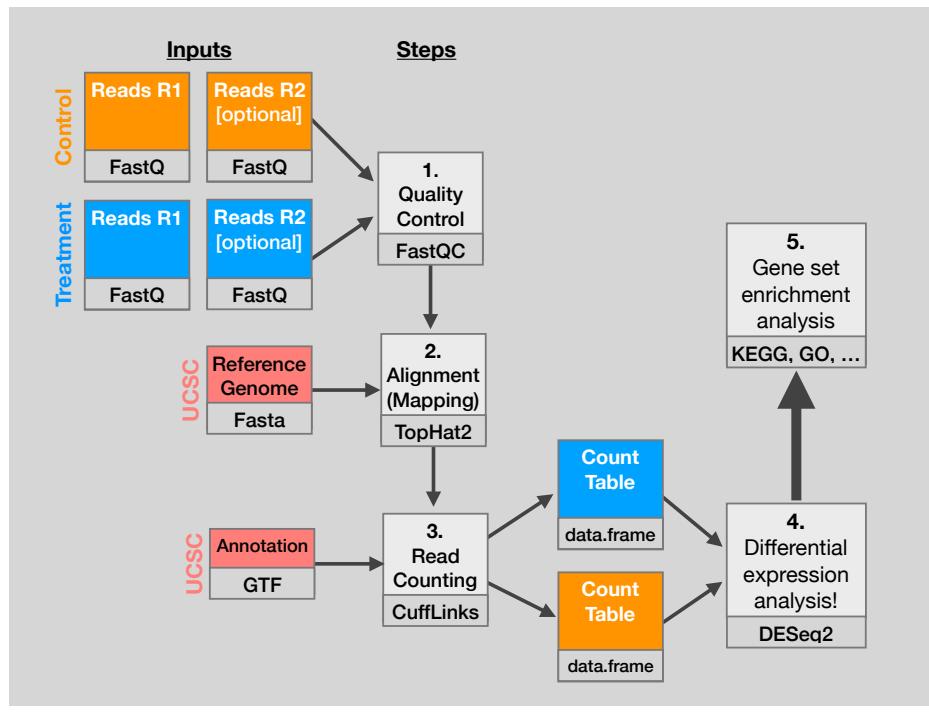
- GeneGO** < portal.genego.com >
 - MD/PhD curated annotations, great for certain domains (eg, Cystic Fibrosis)
 - Nice network analysis tools
 - Email us for access
- Oncomine** < www.oncomine.org >
 - Extensive cancer related expression datasets
 - Nice concept analysis tools
 - Research edition is 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/bimm143_F18/lectures/#16

Also: R Quiz Online



Data structure: counts + metadata

countData

gene	ctrl_1	ctrl_2	exp_1	exp_1
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)

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

colData

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

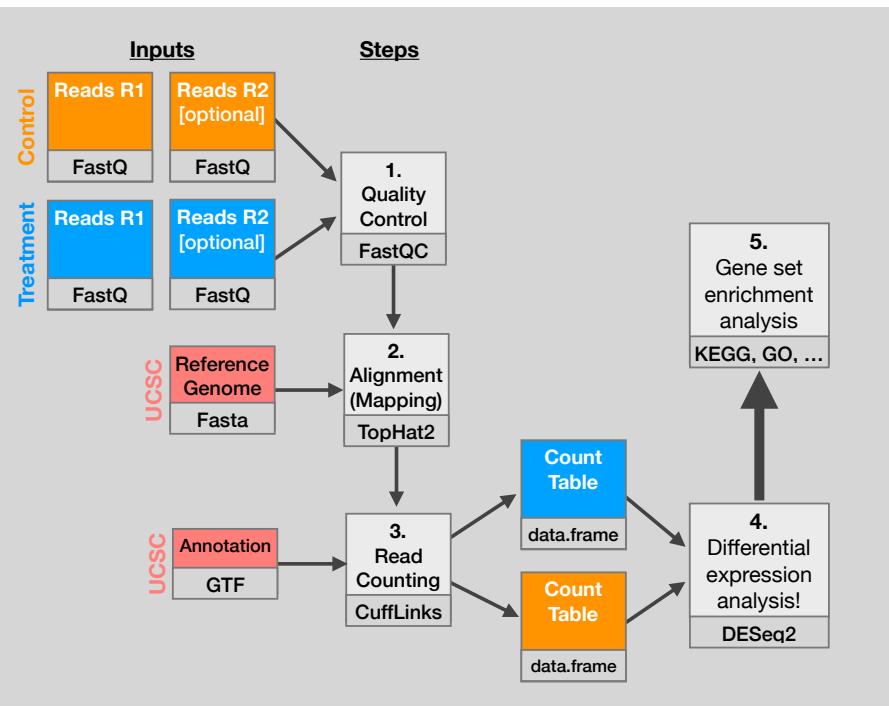
Sample names:
ctrl_1, ctrl_2, exp_1, exp_2

colData describes metadata about the *columns* of countData

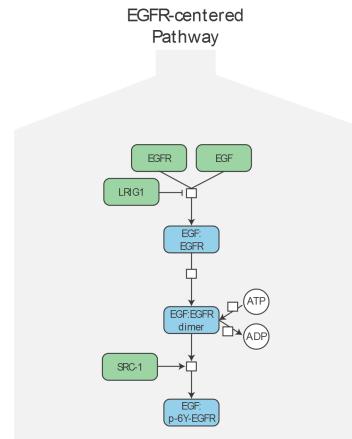
Advice:

Figure out “**What do I want to do with my list?**”

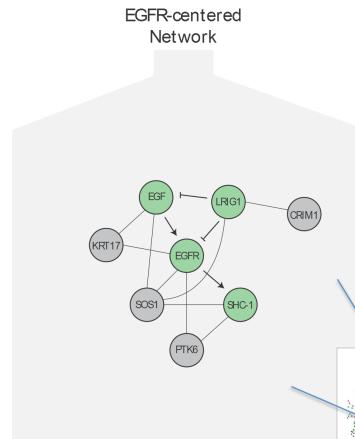
- Organize/summarize data for presentation or manuscript
 - DAVID: GO_FAT -> Functional Annotation Clustering -> Pick threshold
- Infer biological processes from the list
 - DAVID: Functional Annotation Chart -> explore functional databases and see which make sense
 - GSEA: Select MSigDB sets of interest -> e.g., immunologic signatures
 - Use domain specific database it at all possible!
- Find “missing” genes/proteins not detected by experiment
 - ConceptGen: Gene-gene enrichment



Pathways vs Networks



- 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

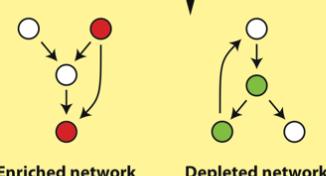
Next Class

Goal

1 Enrichment of fixed gene sets

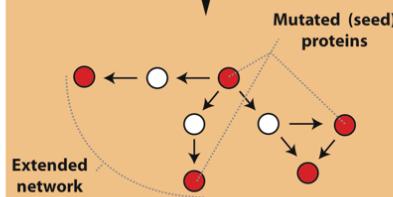
Identification of pre-built pathways or networks that are enriched in a set of mutated or differentially expressed genes

Output



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



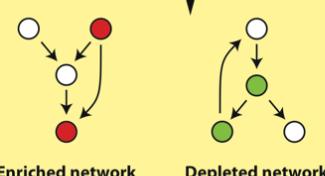
Next Class

Goal

1 Enrichment of fixed gene sets

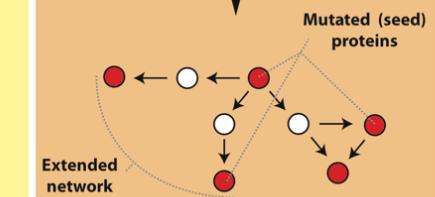
Identification of pre-built pathways or networks that are enriched in a set of mutated or differentially expressed genes

Output



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



What biological process is altered in this cancer?

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

Next Class

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

Limitations

Side-note:

- **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

Network Analysis Overview

