

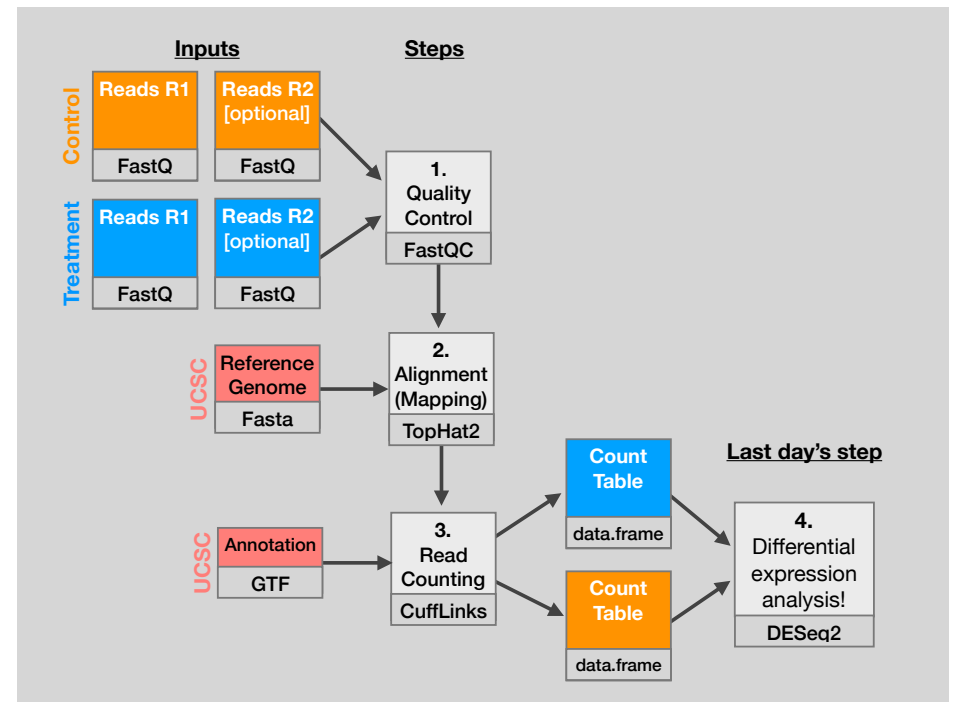
BIMM 143

Pathway Analysis and the Interpretation of Gene Lists

Lecture 15

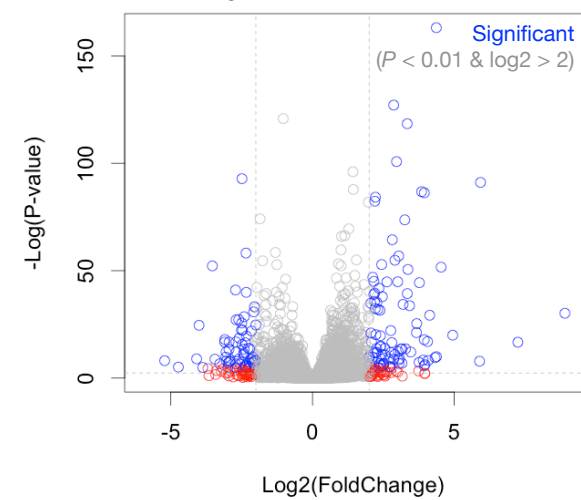
Barry Grant
UC San Diego

<http://thegrantlab.org/bimm143>



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
Fold change vs P-value



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

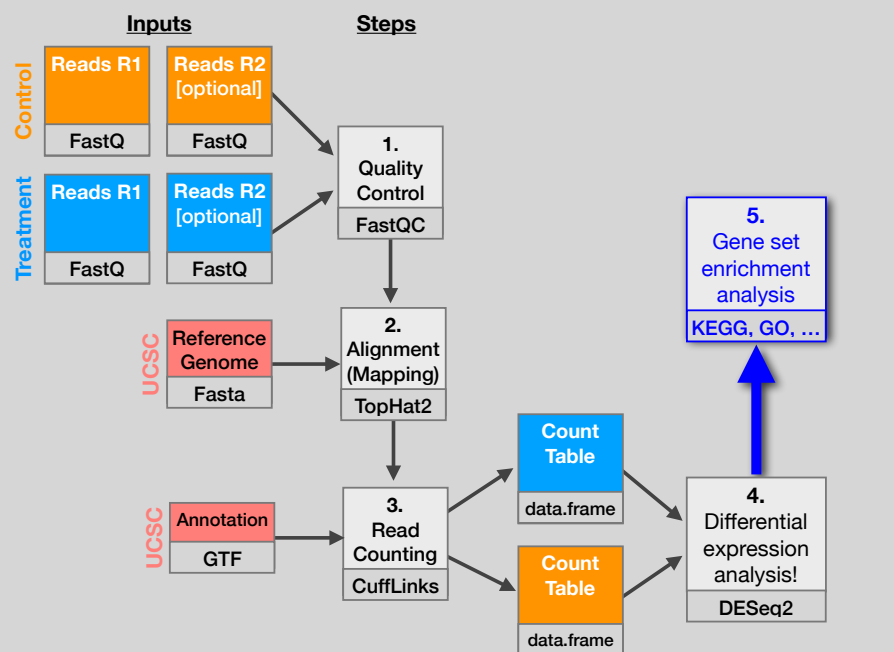
What do I do now?



Pathway analysis!

(a.k.a. geneset enrichment)

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



Basic idea

Differentially Expressed Genes (DEGs)

[illegible]

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

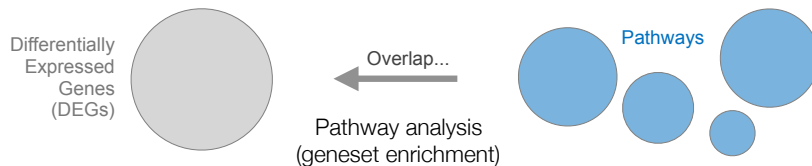
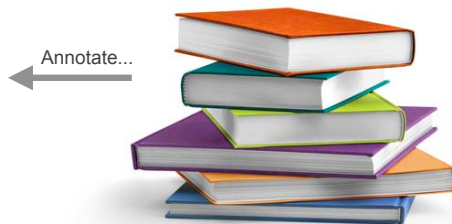


Basic idea

Differentially Expressed Genes (DEGs)

bipolyticity	
20000011291	954.77000
20000011292	4.938000
20000011293	27.11840
20000011294	16.42200
20000011295	6.802700
20000011296	1.542570
20000011297	SPAC13
20000011298	1.000000
20000011299	1.000000
20000011300	1.000000
20000011301	1.000000
20000011302	1.000000
20000011303	1.000000
20000011304	1.000000
20000011305	1.000000
20000011306	1.000000
20000011307	1.000000
20000011308	1.000000
20000011309	1.000000
20000011310	1.000000
20000011311	1.000000
20000011312	1.000000
20000011313	1.000000
20000011314	1.000000
20000011315	1.000000
20000011316	1.000000
20000011317	1.000000
20000011318	1.000000
20000011319	1.000000
20000011320	1.000000
20000011321	1.000000
20000011322	1.000000
20000011323	1.000000
20000011324	1.000000
20000011325	1.000000
20000011326	1.000000
20000011327	1.000000
20000011328	1.000000
20000011329	1.000000
20000011330	1.000000
20000011331	1.000000
20000011332	1.000000
20000011333	1.000000
20000011334	1.000000
20000011335	1.000000
20000011336	1.000000
20000011337	1.000000
20000011338	1.000000
20000011339	1.000000
20000011340	1.000000
20000011341	1.000000
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20000011346	1.000000
20000011347	1.000000
20000011348	1.000000
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20000011365	1.000000
20000011366	1.000000
20000011367	1.000000
20000011368	1.000000
20000011369	1.000000
20000011370	1.000000
20000011371	1.000000
20000011372	1.000000
20000011373	1.000000
20000011374	1.000000
20000011375	1.000000
20000011376	1.000000
20000011377	1.000000
20000011378	1.000000
20000011379	1.000000
20000011380	1.000000
20000011381	1.000000
20000011382	1.000000
20000011383	1.000000
20000011384	1.000000
20000011385	1.000000
20000011386	1.000000
20000011387	1.000000
20000011388	1.000000
20000011389	1.000000
20000011390	1.000000
20000011391	1.000000
20000011392	1.000000
20000011393	1.000000
20000011394	1.000000
20000011395	1.000000
20000011396	1.000000
20000011397	1.000000

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



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

Side-note:

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*

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

228018	ENSGG000000090339	NP_000192	C20orf58
226	ENSGG000000003030	NP_057219	
207	ENSGG00000003383	055029	
225	ENSGG0000000151513	000585	
221	ENSGG00000003613	006125	01
1553	ENSGG00000007124	89495	03
2184	ENSGG0000000757	01032249	08
2049	ENSGG000000092370	78870	11
2026	ENSGG000000079646	4515	orf112
23095	ENSGG000000056892	8339	orf58
22801	ENSGG000000125450	412	NMB
15540	ENSGG000000253982	069	PA2
20312	ENSGG000000140688	83	MEM50B
22518	ENSGG00000010457	01	MP2
225079	ENSGG00000009518	05340	MS12
243010	ENSGG00000002013	5	C20orf58
230668	ENSGG00000004050	033666	C8orf4
218541	ENSGG000000033666	NP_002332	ETV7
242225	ENSGG000000033666		LTB
207339	ENSGG000000033666		ITC1
202637	s at W03F8.6		

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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 - UniProt < www.uniprot.org>; IDConverter < idconverter.biinfo.cnio.es >

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

The screenshot shows the UniProt website's ID Mapping tool. At the top, there is a navigation bar with links for 'Downloads', 'Contact', and 'Documentation/Help'. Below this is a search bar with a 'Query' field and a 'Search' button. A dropdown menu is open, showing 'Protein Knowledgebase (UniProtKB)' as the selected option. To the right of the search bar, there are buttons for 'Search', 'Blast', 'Align', 'Retrieve', and 'ID Mapping', with 'ID Mapping' highlighted by a red rectangle. Below the search bar, there are sections for 'WELCOME' and 'NEWS'. The main part of the interface is titled 'Identifiers' and contains a large empty text box for input. To the right of this box, there are two dropdown menus: 'From' (set to 'EMBL/GenBank/DDBJ') and 'To' (set to 'UniProtKB AC'). Below these are buttons for 'Map', 'Swap', and 'Clear'. At the bottom, there is a section for 'or Choose File' with 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)

Edit			Font			Alignment			Number		
		Calibri (Body)	12						abc		General
Paste		B	<i>I</i>	<u>U</u>							

B3 fx =VLOOKUP(A3,SG\$3:\$O\$30490,2,FALSE)

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	1.44699053	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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- Use the **merge()** or **mapIds()** functions in R - *fast, versatile & reproducible!*
 - Also **clusterProfiler::bitr()** function and many others... [\[Link to clusterProfiler vignette\]](#)

```

# Using the merge() function
> anno <- read.csv("data/annotables_grch38.csv")
> merge(mygenes, anno, by.x="row.names", by.y="ensgene")
    
```

This is our differential expressed genes

```

# Using mapIds() function from bioconductor
> library("AnnotationDbi")
> library("org.Hs.eg.db")
> mygenes$symbol <- mapIds(org.Hs.eg.db,
    
```

Load the required Bioconductor packages

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", "FXRD", "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:

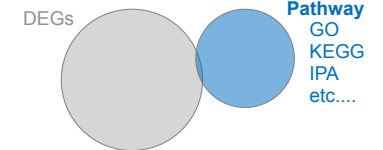
<https://bioconductor.org/packages/release/bioc/html/clusterProfiler.html>

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*

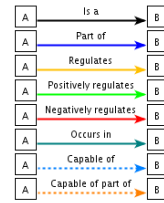
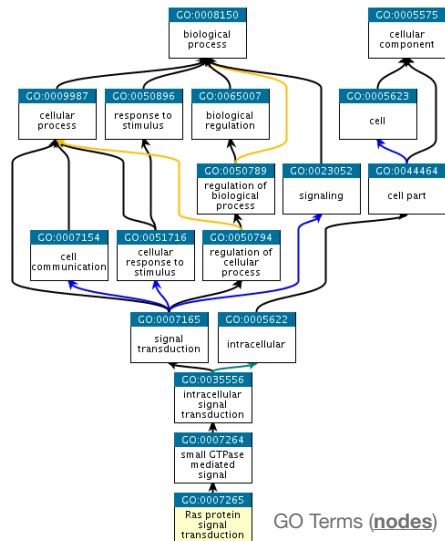
- **Ontology** => a structured and controlled vocabulary that allows us to annotate gene products consistently, interpret the relationships among annotations, and can easily be *handled by a computer*

- 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 >

GO is structured as a “directed graph”



Relationships (edges)

Parent terms are more general & child terms more specific

GO Terms (nodes)

GO evidence codes

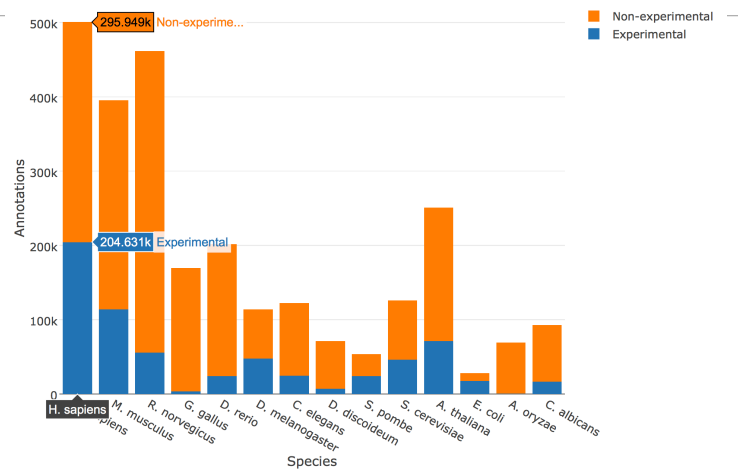
Evidence code	Evidence code description	Source of evidence	Manually checked	Current number of annotations*
IDA	Inferred from direct assay	Experimental	Yes	71,050
IEP	Inferred from expression pattern	Experimental	Yes	4,598
IGI	Inferred from genetic interaction	Experimental	Yes	8,311
IMP	Inferred from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

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

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](#)

[Rerun Using Options](#) [Create Sublist](#)

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
Current Background: HOMO SAPIENS
2320 DAVID IDs
Check Defaults ☒ [Clear All](#)

☐ 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

[Functional Annotation Clustering^{new!}](#) [Functional Annotation Chart](#) [Functional Annotation Table](#)

DAVID Functional Annotation Clustering

- Based on shared genes between functional sets

Functional Annotation Clustering

Current Gene List: Uploaded List_3
2320 DAVID IDs

Options: Classification Stringency: Medium

Download File

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

Want more?

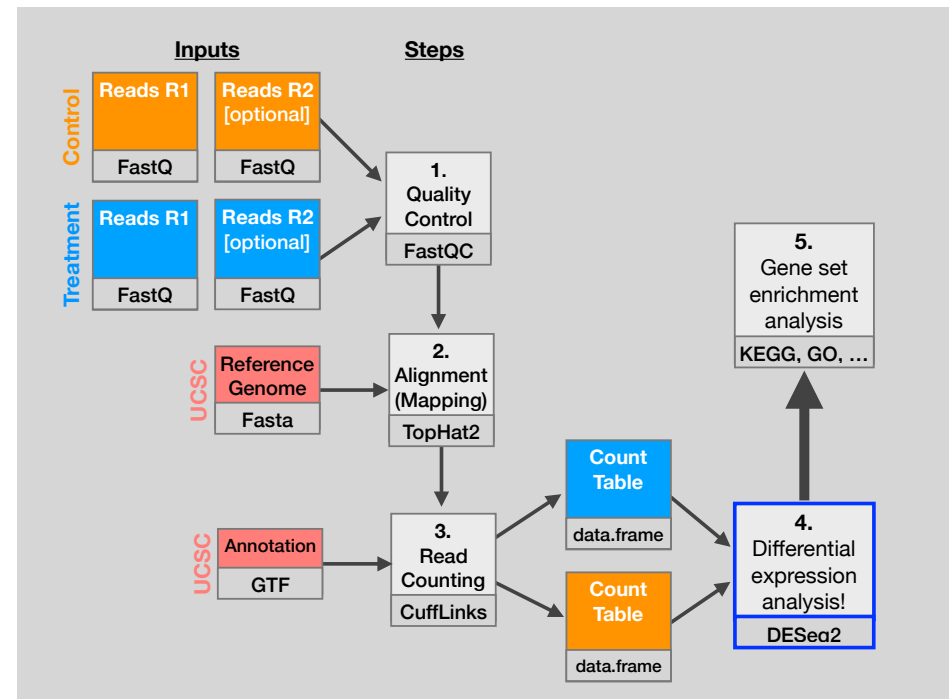


- GeneGO** < portal.genego.com >
 - MD/PhD curated annotations, great for certain domains (eg, Cystic Fibrosis)
 - Nice network analysis tools
 - Email us for access
- Oncomine** < www.oncomine.org >
 - Extensive cancer related expression datasets
 - Nice concept analysis tools
 - Research edition is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

Hands-on time!

<http://thegrantlab.org/bimm143>

Do it Yourself!



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
...

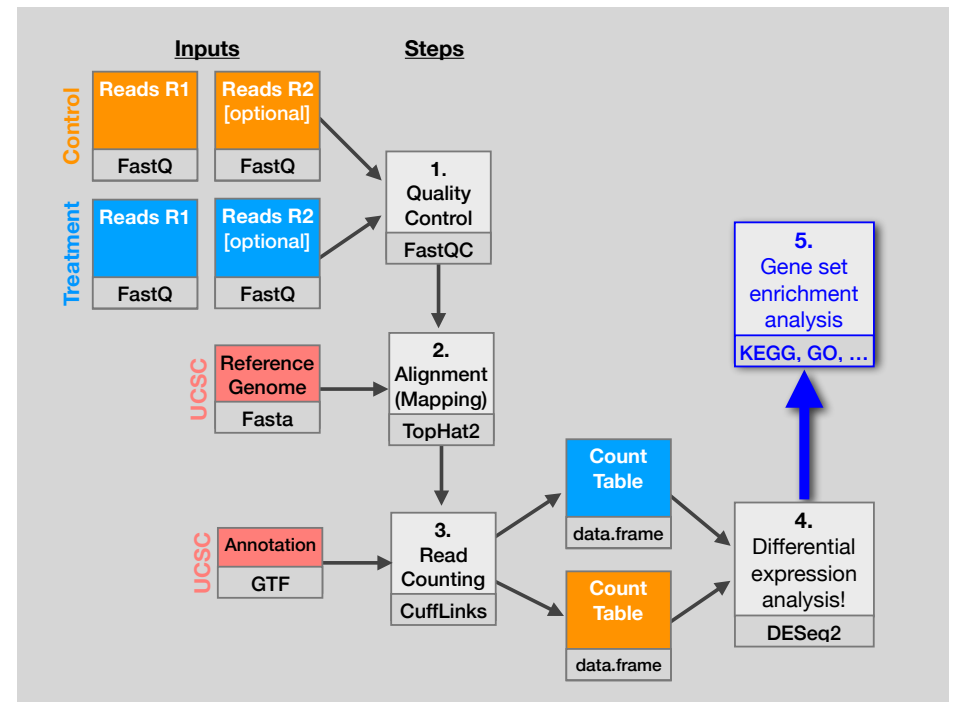
countData is the count matrix
(Number of reads coming from each gene for each sample)

2 colData

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

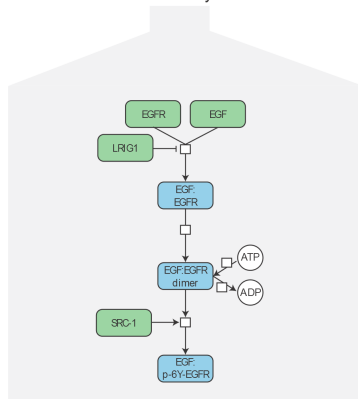
colData describes metadata about the columns of countData

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



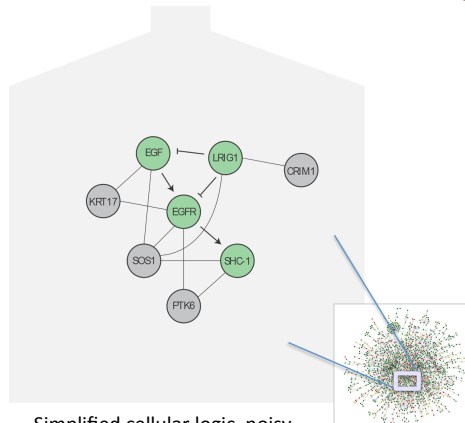
Pathways vs Networks

EGFR-centered Pathway



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

EGFR-centered Network



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

Next Class

Goal

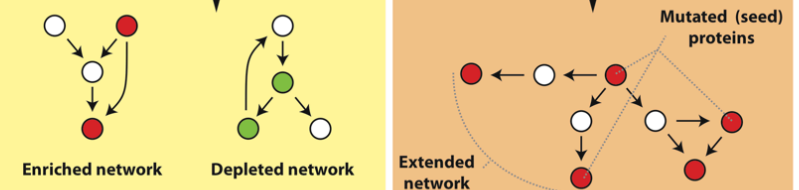
1 Enrichment of fixed gene sets

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

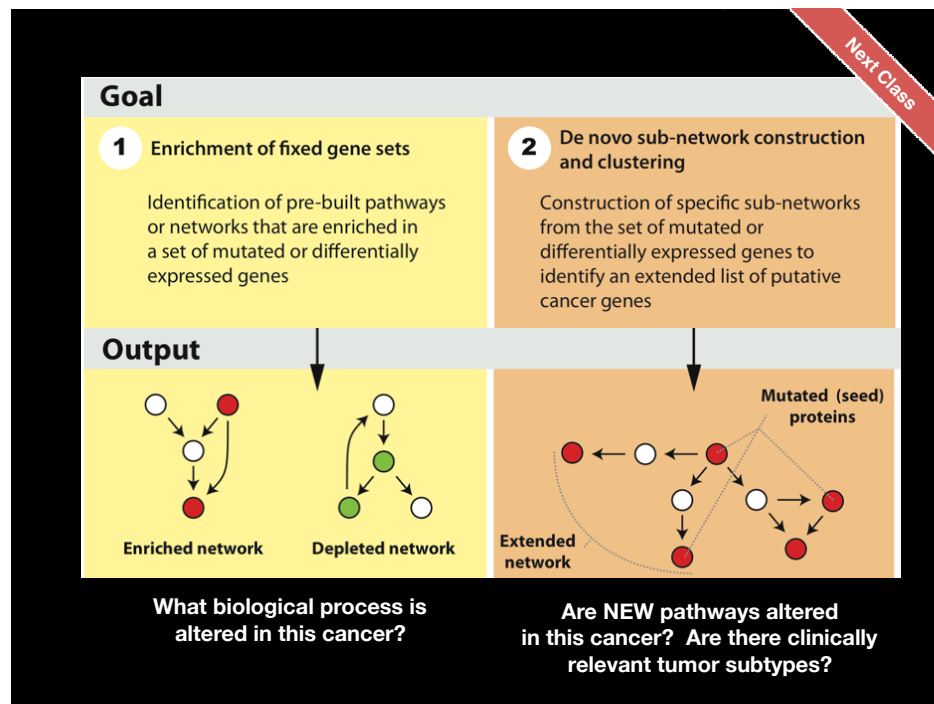
2 De novo sub-network construction and clustering

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

Output



Next Class



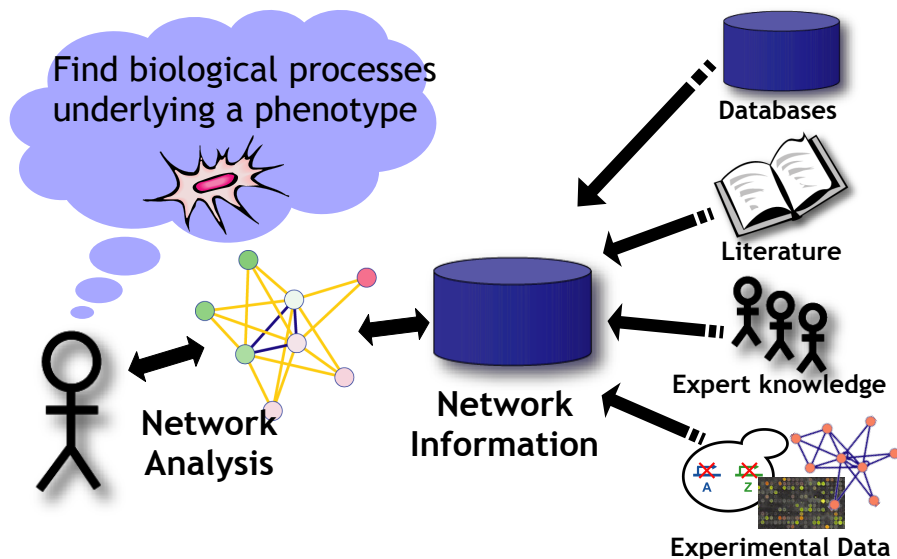
Pathway analysis (a.k.a. geneset enrichment)

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-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

Pathway & Network Analysis Overview



R Knowledge Check For BIMM-143 Quiz

Do it Yourself!

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

Time Limit: 40 mins

