

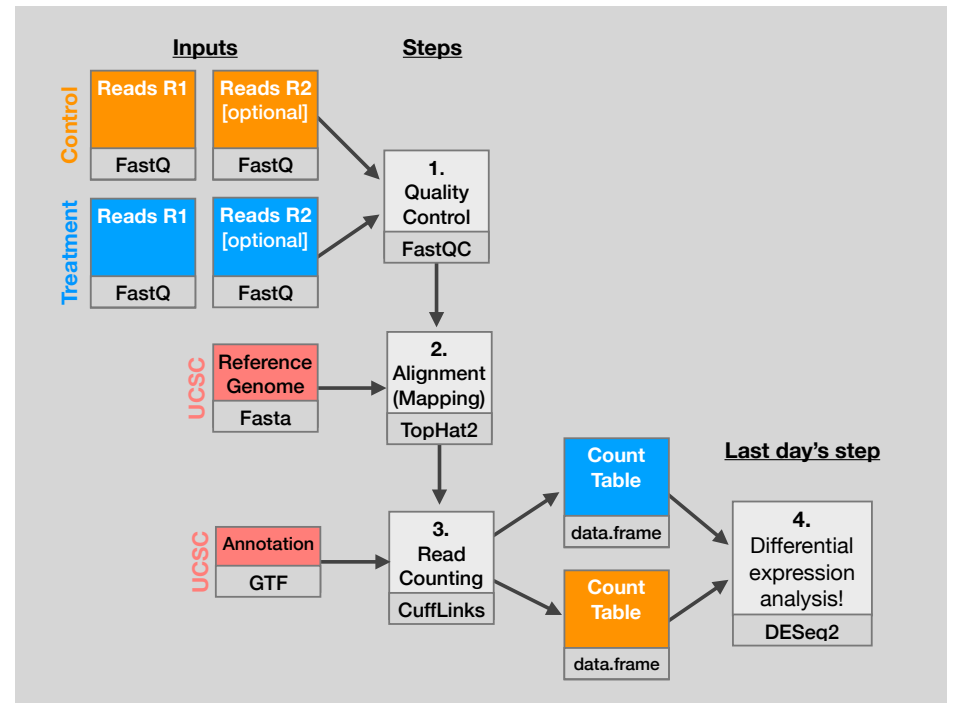
BGGN 213

Pathway Analysis and the Interpretation of Gene Lists

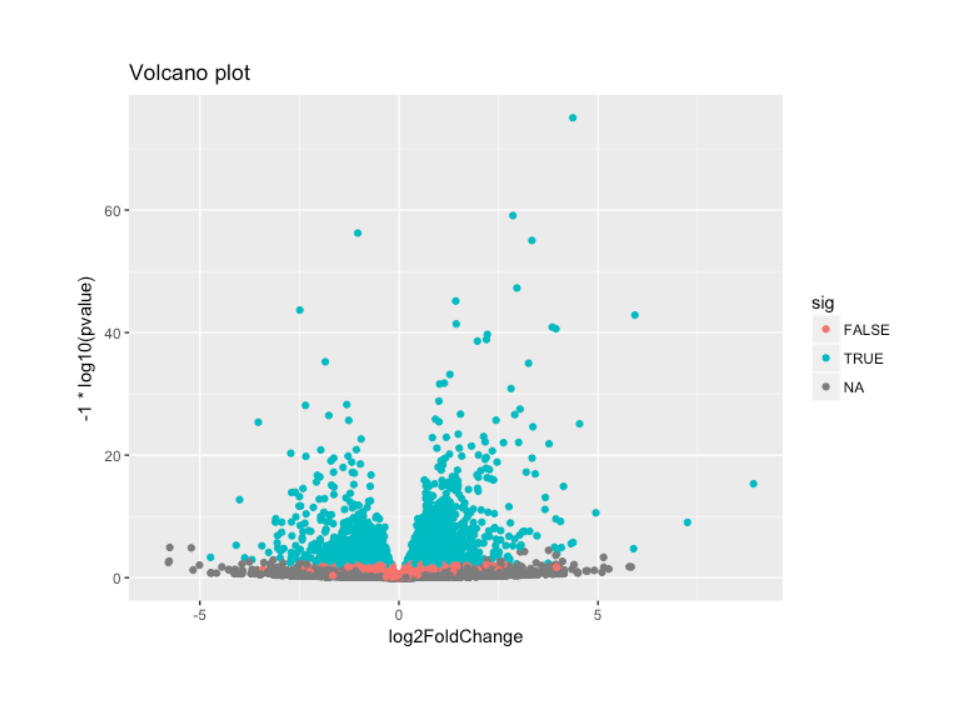
Lecture 15

Barry Grant
UC San Diego

<http://thegrantlab.org/bgg213>



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	ARHGFB2
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

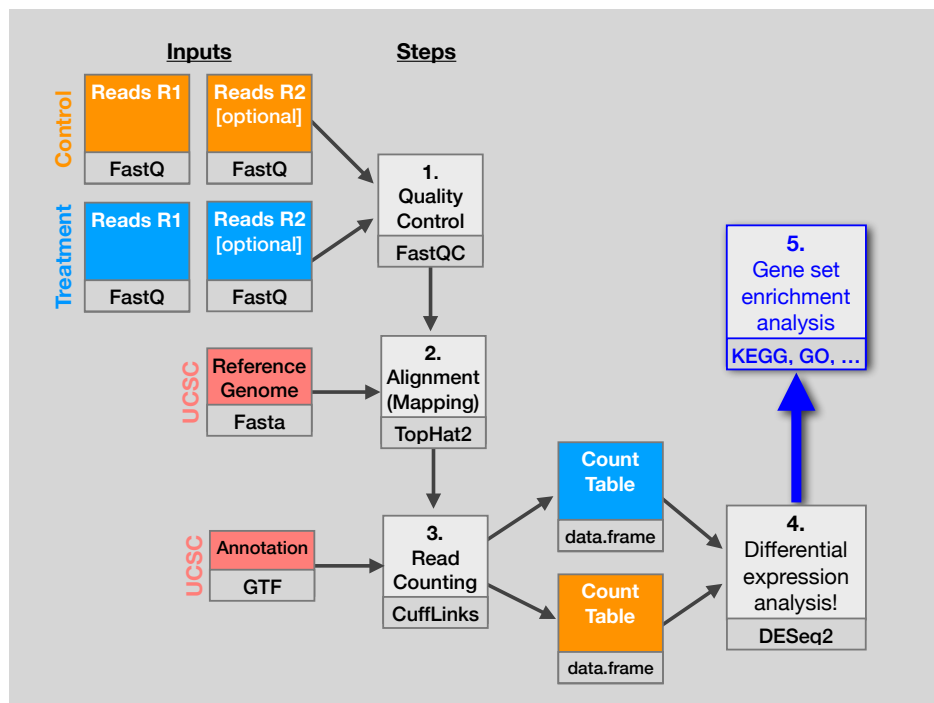


My high-throughput experiment generated a long list of genes/proteins...

What do I do now? 🤔

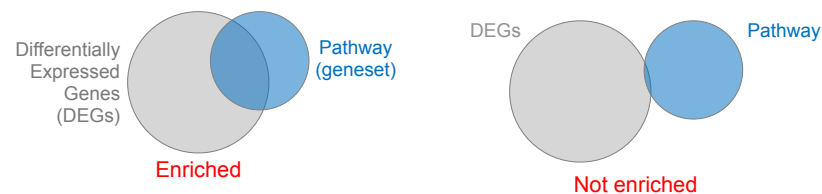
Pathway analysis! (a.k.a. geneset enrichment)

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



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

Principle



- 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

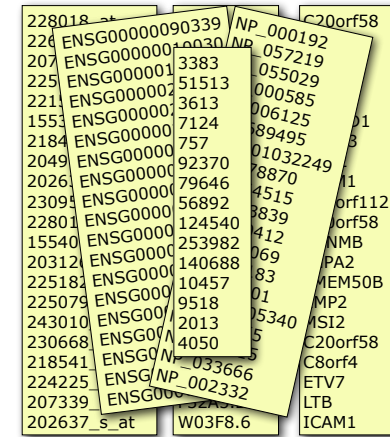
Side-note:

- **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-κB 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-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



228018	at	90339	NP_000192	C20orf58
226	ENSG00000000000	10030	NP_057219	
207	ENSG00000000000	3383	055029	
225	ENSG00000000000	51513	000585	
221	ENSG00000000000	3613	006125	01
1553	ENSG00000000000	7124	89495	8
2184	ENSG00000000000	757	01032249	
2049	ENSG00000000000	92370	8870	11
2026	ENSG00000000000	79646	4515	orf112
2309	ENSG00000000000	56892	8839	orf58
22801	ENSG00000000000	124540	412	NMB
15540	ENSG00000000000	253982	069	PA2
20312	ENSG00000000000	140688	83	MEM50B
22518	ENSG00000000000	10457	01	MP2
225079	ENSG00000000000	9518	5340	SI2
243010	ENSG00000000000	2013	5	C20orf58
230668	ENSG00000000000	4050	5	C8orf4
218541	ENSG00000000000	033666	002332	ETV7
224225	ENSG00000000000	002332		LTB
207339	ENSG00000000000			ICAM1
202637	s_at	W03F8.6		

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

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

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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)

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	Cgln1	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	1.44699053	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

Translating between identifiers

- Many different identifiers exist for genes and proteins, e.g. UniProt, Entrez, etc.
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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 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... [\[Link to clusterProfiler vignette\]](#)

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", "MCM", "SPP1", "LAMC1", "COL4A2", "COL4A1", "MYOC",
      "ANXA4", "TFPI2", "CST6", "SLPI", "TIMP2", "CPM", "GGT1", "NNMT",
      "MAL", "EEF1A2", "HGD", "TCN2", "CDA", "PCCA", "CRYM", "PDXK",
      "STC1", "WARS", "HMOX1", "FXD2", "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?

• 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)

GO database < www.geneontology.org >

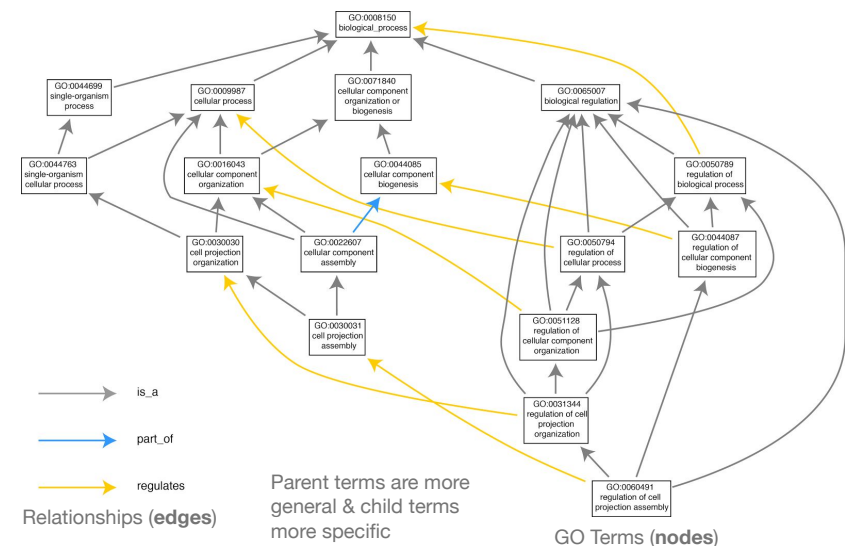
• What function does HSF1 perform?

• *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*

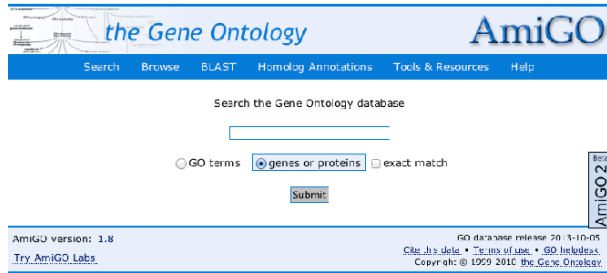
• GO database consists of 3 ontologies that describe gene products in terms of their associated **biological processes, cellular components** and **molecular functions**

GO is structured as a “directed graph”



GO Annotations

- 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 >



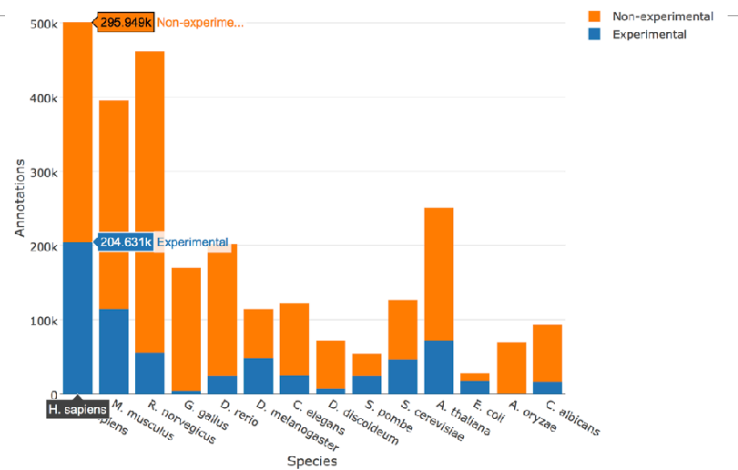
GO evidence codes

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

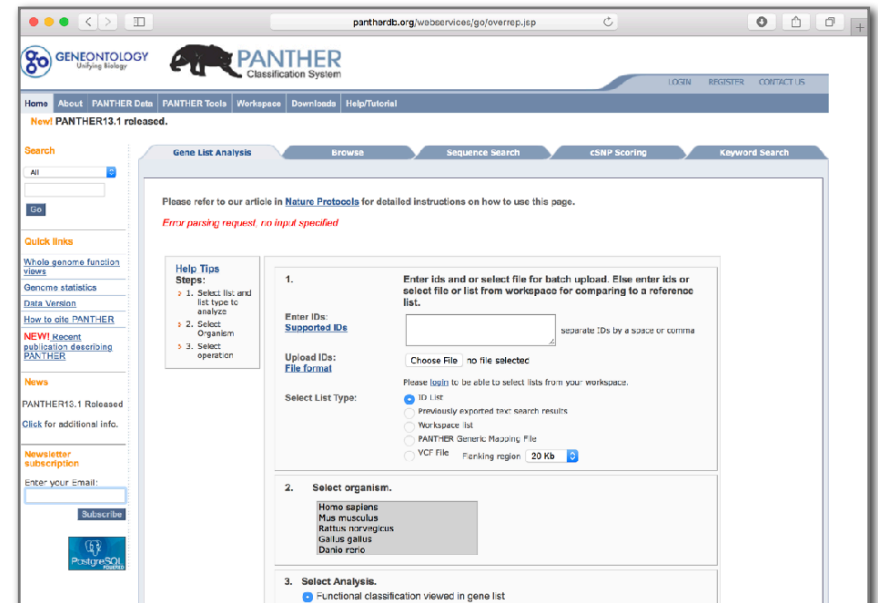
Use and misuse of the gene ontology annotations
Seung Yon Rhee, Valerie Wood, Kara Dolinski & Sorin Draghici
Nature Reviews Genetics 9, 509-515 (2008)

Experimental annotations by species



- See AmiGO for details: http://amigo.geneontology.org/amigo/base_statistics

Can now do gene list analysis with GeneGO



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

Upload | List | Background

Upload Gene List

Demolist 1 Demolist 2
Upload Help

Step 1: Enter Gene List
A: Paste a list

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

Analysis Wizard

Tell us how you like the tool
Contact us for questions

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

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
1304_at
1316_at
1320_at
1405_f_at
1431_at
1438_at
1487_at
1494_f_at
1598_g_at

DAVID

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

Analysis Wizard

Tell us how you like the tool
Contact us for questions

Gene List Manager

Select to limit annotations by one or more species Help

Use All Species -
HOMO SAPIENS (442)
SYNTHETIC CONSTRUCT(S)

Select

List Manager Help

Uploaded List_2

Select List to:

Use Rename
Remove Combine

Show Gene List^{new!}

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

- *Functional Annotation Tool*

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

- Specify functional sets

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 (1 selected)

Gene Ontology Term	Percentage	DAVID IDs	Chart
GOTERM_BP_1	71%	1669	Chart
GOTERM_BP_2	71%	1652	Chart
GOTERM_BP_3	69%	1609	Chart
GOTERM_BP_4	65%	1519	Chart
<input checked="" type="checkbox"/> GOTERM_BP_5	61%	1432	Chart
GOTERM_BP_ALL	71%	1669	Chart
GOTERM_CC_1	75%	1754	Chart
GOTERM_CC_2	75%	1741	Chart
GOTERM_CC_3	75%	1741	Chart
GOTERM_CC_4	70%	1634	Chart
GOTERM_CC_5	69%	1605	Chart
GOTERM_CC_ALL	75%	1754	Chart
GOTERM_MF_1	75%	1745	Chart
GOTERM_MF_2	73%	1716	Chart
GOTERM_MF_3	65%	1523	Chart

DAVID

- 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 Clear All

Main Accessions (0 selected)
 Other Accessions (0 selected)
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 Protein Domains (3 selected)
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 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

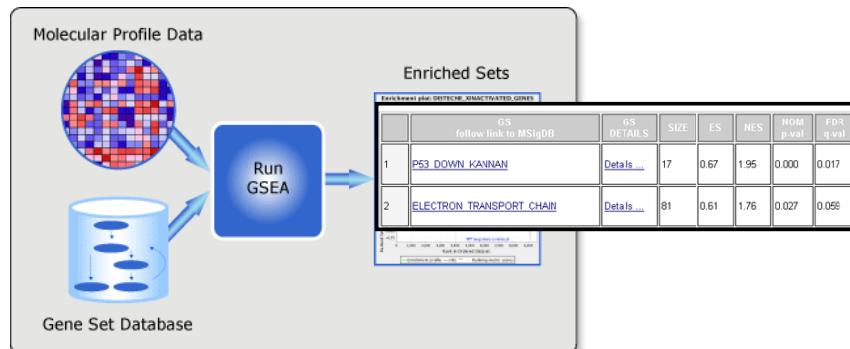
Options [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_5	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 nucleoside, nucleotide, 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)

GSEA < www.broadinstitute.org/gsea >

- Download GSEA desktop application



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

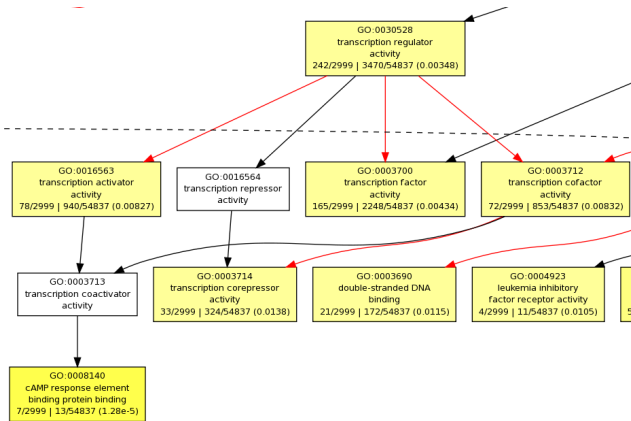
Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles
 Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, ...
PNAS 102, 15545-15550 (2005)

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 >

- Graphical view of enriched GO terms and their relationships



GO SLIMs

- 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

Download File

Annotation Cluster	Enrichment Score	Count	P-Value	Benjamini
Annotation Cluster 1 (Enrichment Score: 3.72)				
GOTERM_BP_5	regulation of transcription from DNA 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	121	1.6E-6	2.1E-3
GOTERM_BP_5	cell death	126	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	3.3E-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!!!**

Do it Yourself!

Hands-on time!

https://bioboot.github.io/bggn213_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
...

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

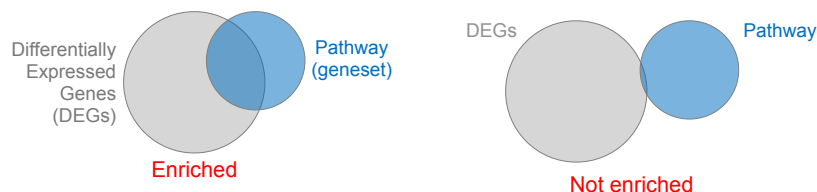
countData is the count matrix
(number of reads coming from
each gene for each sample)

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



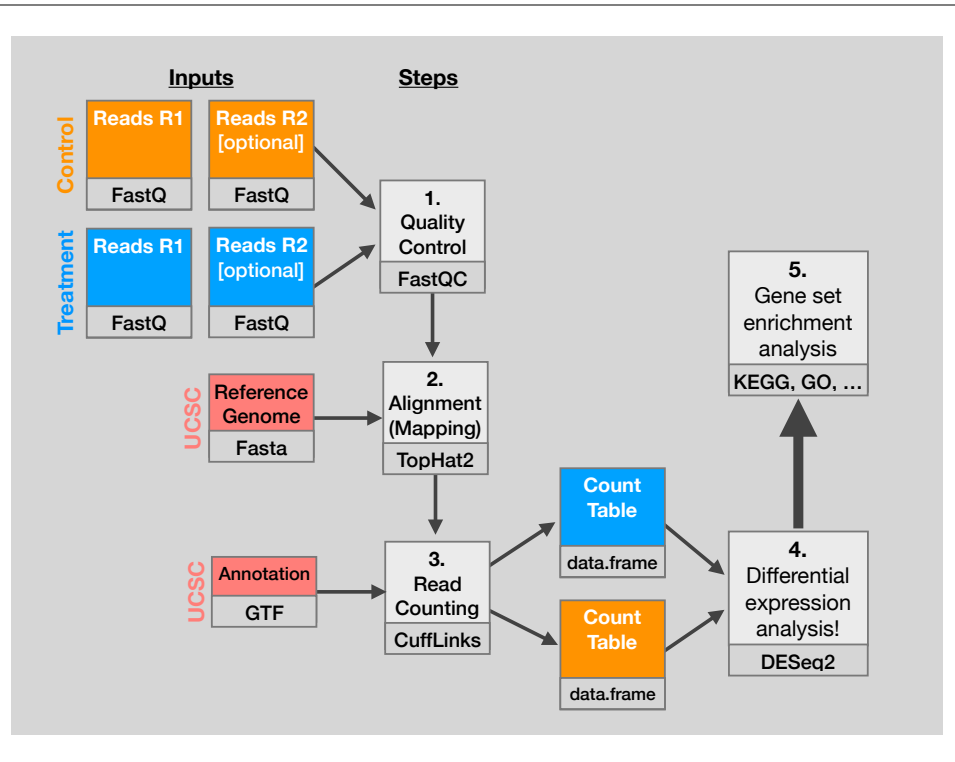
- Variations of the math: overlap, ranking, networks... > *Not critical, different algorithms show similar performances*
- DEGs come from your experiment > *Critical, needs to be as clean as possible*
- Pathway genes ("geneset") come from annotations > *Important, but typically not a competitive advantage*

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

Limitations

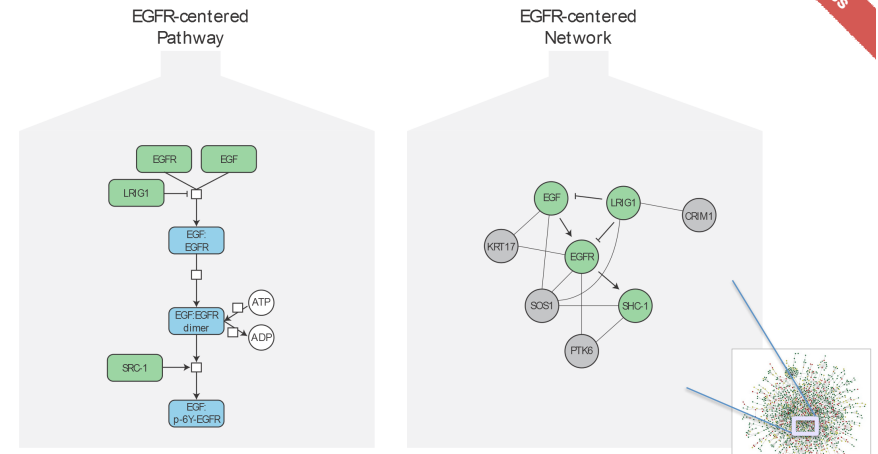
Side-note:

- **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-κB 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-κB, AP-1, IRF3/7, NFAT

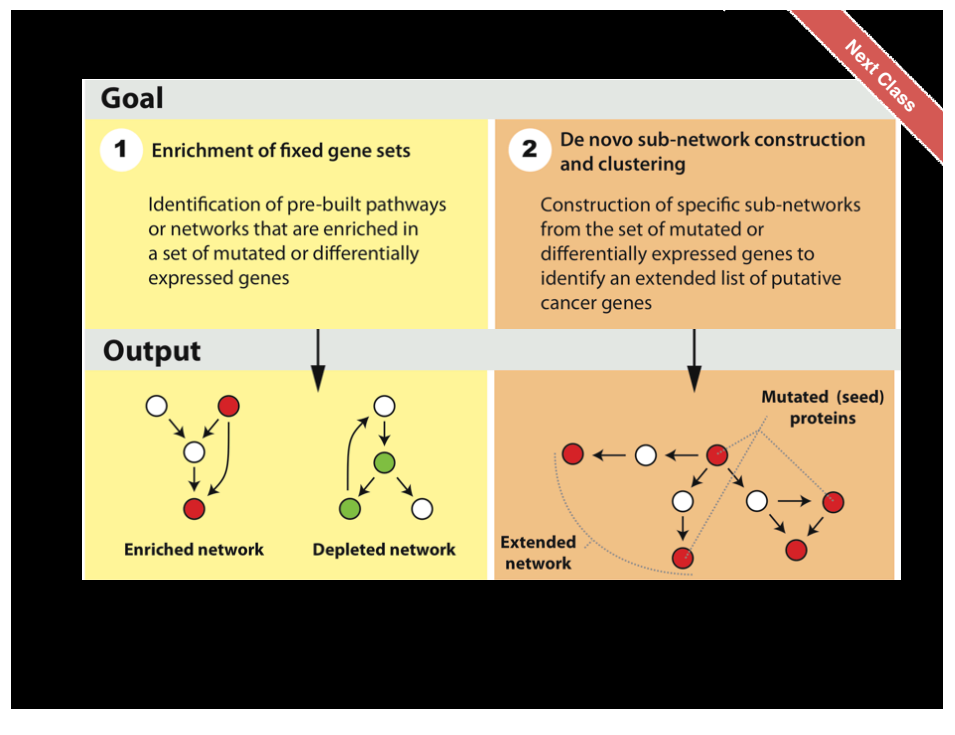


Pathways vs Networks

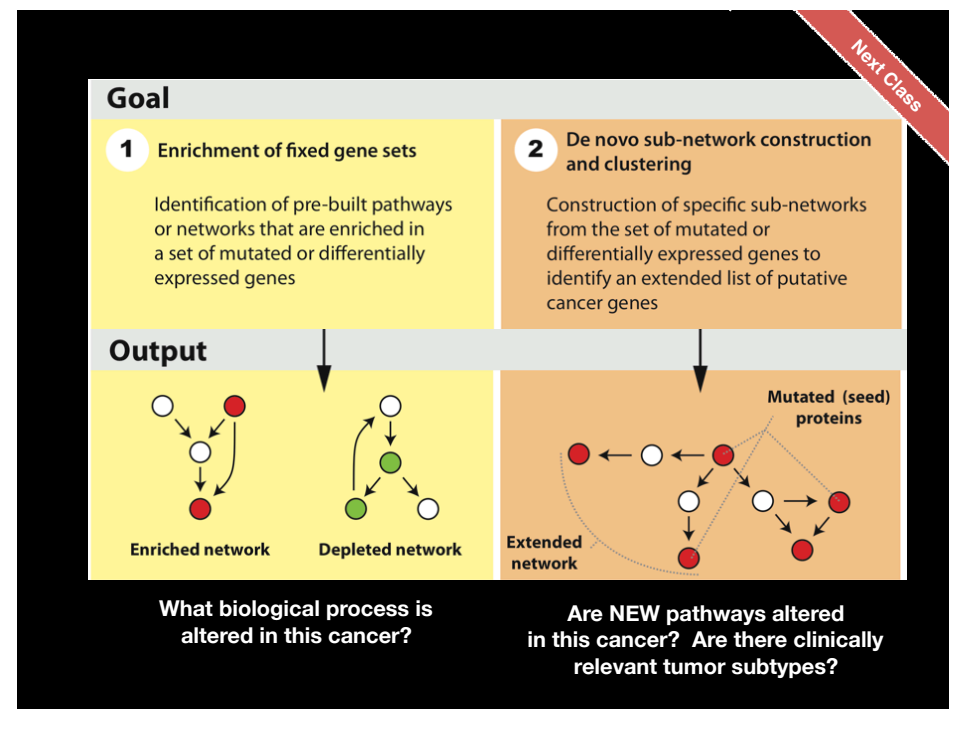
Next Class



- 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



Next Class

Next Class

Network analysis approaches

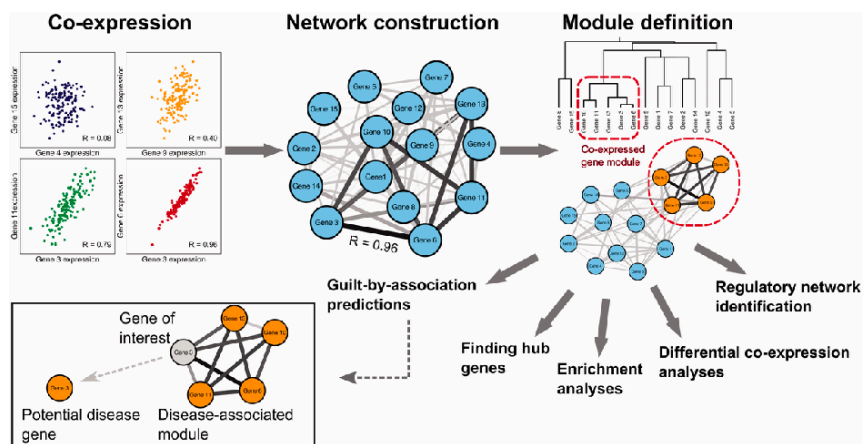


Image from: van Dam et al. (2017) <https://doi.org/10.1093/bib/bbw139>

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