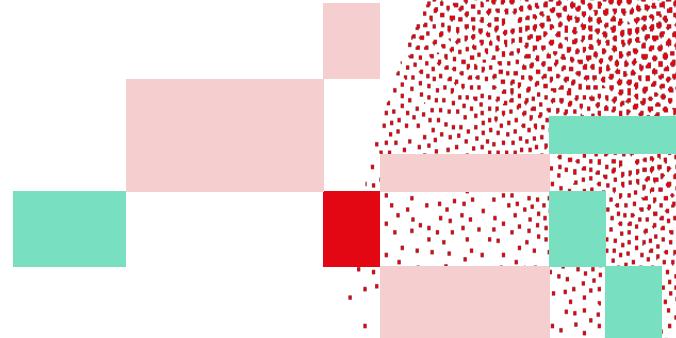




Swiss Institute of
Bioinformatics



Enrichment analysis

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Schedule

- **9:00 - 9:30**
- Introduction
- **9:30 – 10:30**
- Over-representation analysis
- Exercise
- **10:30ish** break
- **10:50 - 12:30**
- Method of gene set enrichment analysis
- Exercise
- **12:30ish - 13:30** lunch break
- **13:30 - 15:30**
- Visualization of enrichment results
- Exercise
- **15:30ish - 15:50** break
- **15:50 - 16:50**
- Ontologies and sources of gene sets
- Exercise
- **16:50 - 17:00** Feedback and end of day

The Translational Data Science group



- Part of the **SIB Swiss Institute of Bioinformatics**
- Located at the AGORA Cancer Research Center in **Lausanne**
- Provides **the statistics, bioinformatics and computational expertise** to molecular biology and applied research labs.
- Participates in fundamental and translational research by providing expertise in **data analysis** of single-cell and bulk multi-omics, spatial transcriptomics, flow cytometry, etc

For core facility service inquiry: nadine.fournier@sib.swiss

<https://agora-cancer.ch/scientific-platforms/translational-data-science-facility/>

<https://www.sib.swiss/raphael-gottardo-group>

Tell us about yourself !

- Write your name and some keywords about yourself and/or your research into the Google doc, to share about yourself.
-  vevox poll



Photo by National Cancer Institute, Unsplash



Photo by Scott Graham, Unsplash

Course material

- <https://sib-swiss.github.io/enrichment-analysis-training/>

The screenshot shows a website for 'Enrichment analysis'. At the top, there's a red header bar with the SIB logo and the text 'Enrichment analysis'. Below the header, on the left, is a sidebar with a navigation menu:

- Enrichment analysis
- Home
- Precourse preparations
- Course schedule
- Materials
- Exercises** (this item is highlighted in red)
- Bonus code
- Useful links

The main content area has a title 'Exercises' with a pencil icon. Below it is a text block: 'In this section, you will find the R code that we will use during the course. We will explain the code and output during correction of the exercises.' Further down, another section titled 'Source of data' contains text about a study by Ercolano et al 2020.

We will work with RNA sequencing data generated by [Ercolano et al 2020](#). This study described the transcriptomes of immune cells that are circulating in the blood of humans in healthy conditions. Different types of immune cells circulate in human blood. In this study, 2 cell types were included: Natural Killer (NK) cells and CD4+ T helper (Th) cells. These 2 types of cells have different functions: NK cells provide a rapid response in the innate immune response at the

- **Feedback:** survey at the end of the day about your opinion on this course (link sent by course organizer).

Credits: 0.25 ECTS

- Please provide answers and R code for an additional exercise (eg 1 Word with answers and figures and 1 script file, or 1 file generated using Rmarkdown)

<https://sib-swiss.github.io/enrichment-analysis-training/exercises/#extra-exercise-for-ects-credits>

- Sign up for credit by adding your name to the google Doc file (email sent by course organizer)
- Send answers to tania.wyss@sib.swiss within 1 week

Questions and Exercises

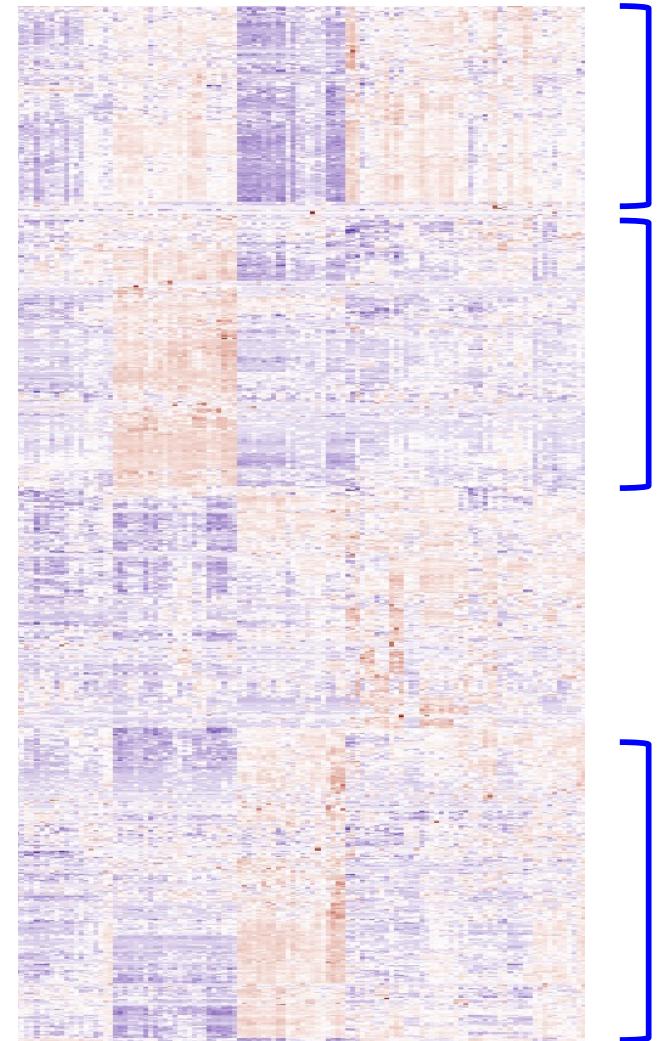
- Feel free to interrupt with questions by asking them directly or raising your (virtual) hand.
- Use the Q&A in Google Doc (or Zoom chat), we will provide answers
- Add a  when you are done with the current exercise
- Exercises in R:
 - We will try to debug as much as possible
 - We are happy if you share your results or alternative code!



Why do we perform enrichment analysis?

- Gene expression analysis yields hundreds to thousands of significant genes
 - We need to summarize the information provided by so many genes
 - Understand their biological relationships
 - Understand the genes' function (**functional analysis**)
 - Identify overarching biological processes or molecular pathways taking place in your system

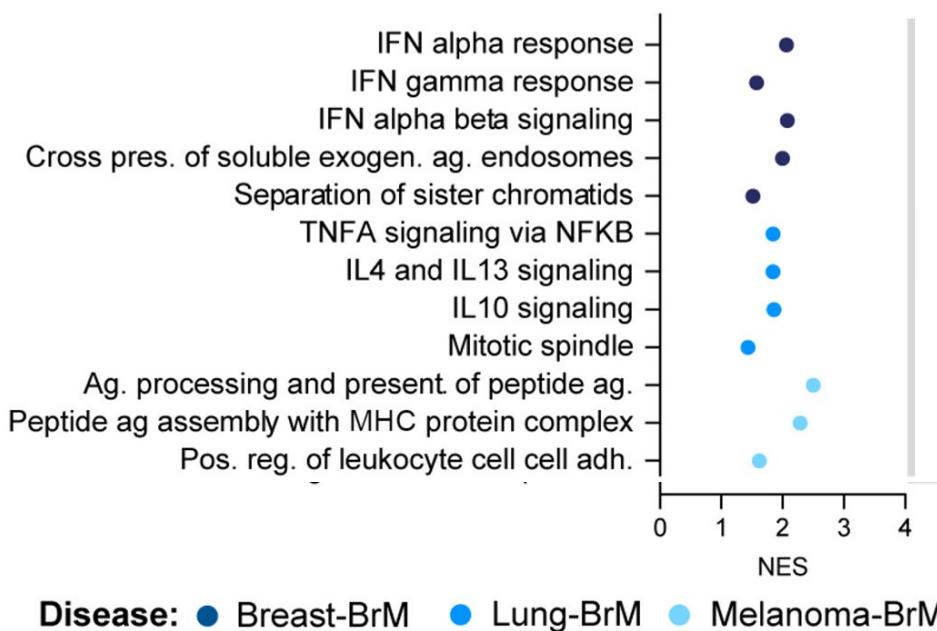
Some genes have similar expression pattern across samples



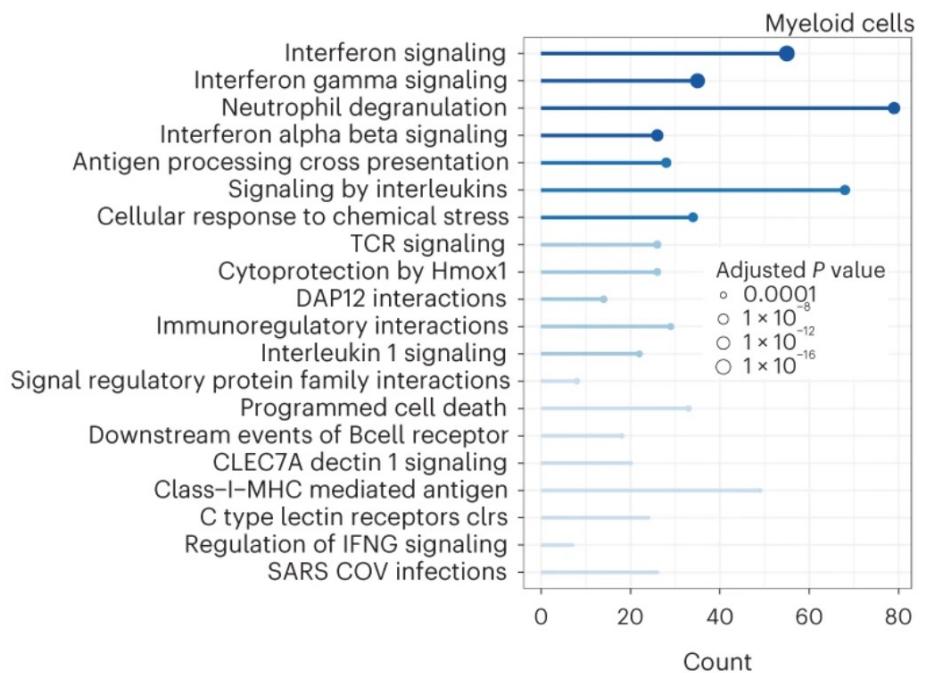
Enrichment analysis in the literature – non-exhaustive examples

Often presented in *omics* studies

Different molecular alterations in vasculature of brain metastasis from different origins, compared to normal brain vasculature



Impact of a treatment on myeloid cells, pathways that could contribute to tumor growth limitation



Bulk RNAseq, GSEA

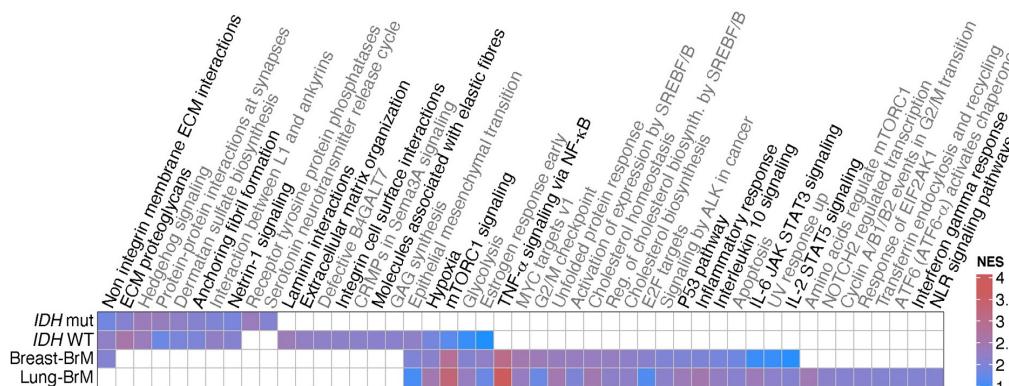
<https://doi.org/10.1016/j.ccell.2023.12.018>

Single-cell RNAseq, ORA

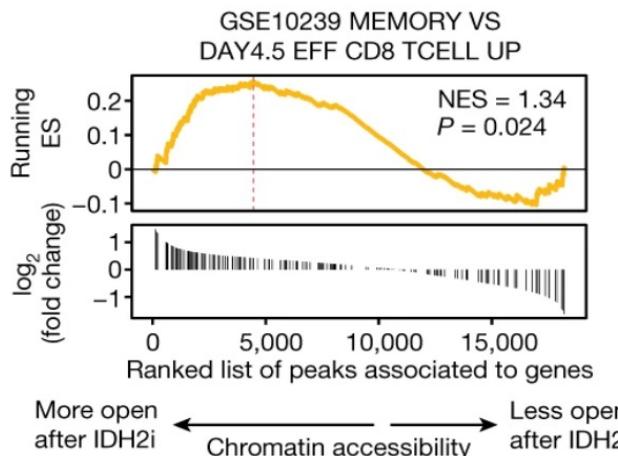
<https://doi.org/10.1038/s43018-023-00668-y>⁹

Enrichment analysis in the literature – non-exhaustive examples

Neutrophils (immune cells) express different pathways depending on the brain tumor origin (primary vs metastatic tumor)



Bulk RNAseq, GSEA <https://doi.org/10.1016/j.cell.2023.08.043>

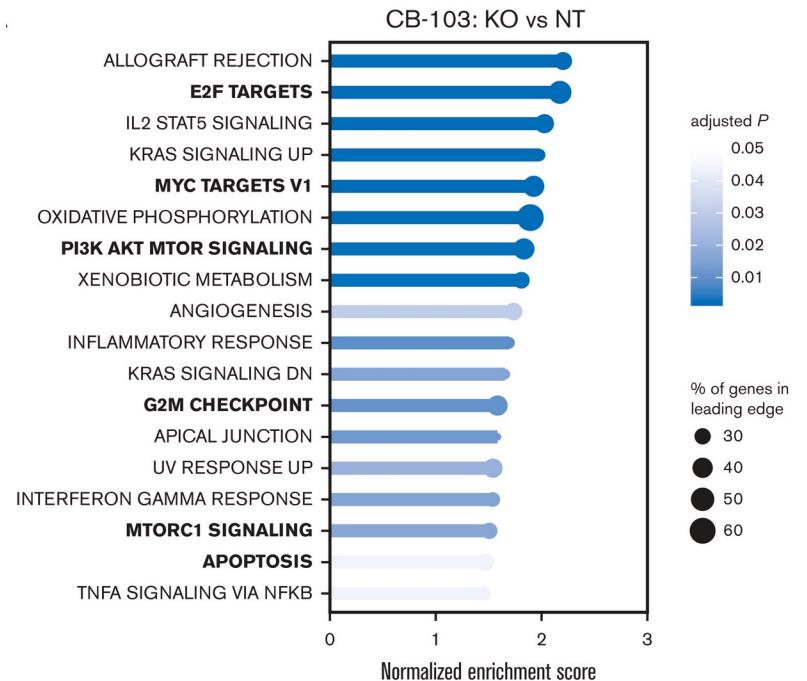


Increased memory phenotype in immune cells exposed to a component.

Bulk ATACseq, GSEA

<https://doi.org/10.1038/s41586-023-06546-y>

Pathways altered upon knocking-out a gene (*PIK3R1*) which confers resistance to treatment. Find new pathways to target with therapy

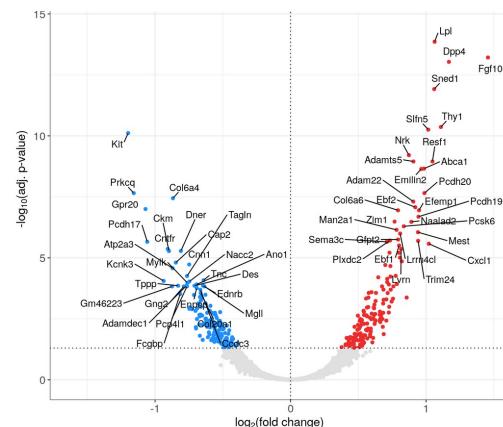


Bulk RNAseq, GSEA
<https://doi.org/10.1182/bloodadvances.2023010380>

Enrichment analysis – input data

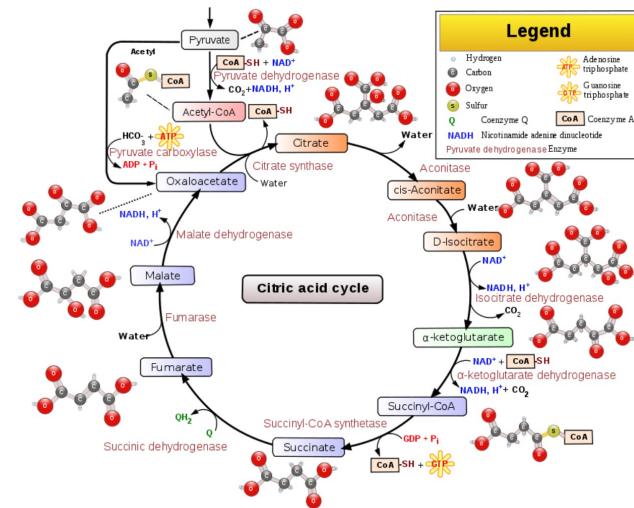
List of genes/proteins that are:

- Differentially expressed between 2 conditions
- Similar expression pattern across samples
- ...
- Either available as a list of gene symbols/IDs or with a score associated to each gene: e.g. T statistic or fold change



Database of gene/protein functional annotation

- Genes need to be grouped into gene sets/pathways/functional annotations.
- Consortia of researchers usually create these gene groupings/annotations



Enrichment analysis in non-model organisms

- Need **functional annotation** of genes: genes need to be grouped into pathways/functions.
- If not available, **convert your genes into the orthologs** of a closely related species that has such a database.
- Will require effort to find a gene functional annotation database. **All statistical analyses** are otherwise the same.

See Useful links:

<https://sib-swiss.github.io/enrichment-analysis-training/links/#tools-for-species-other-than-human-or-mouse>

Once we have identified DE genes, what do we do?

Goal: To gain biologically-meaningful insights from long gene lists

- test if differentially expressed genes are enriched in genes associated with a particular function
- approaches: test a small number of gene sets, or a large collection of gene sets

RNA sequencing pipeline

Differential expression analysis

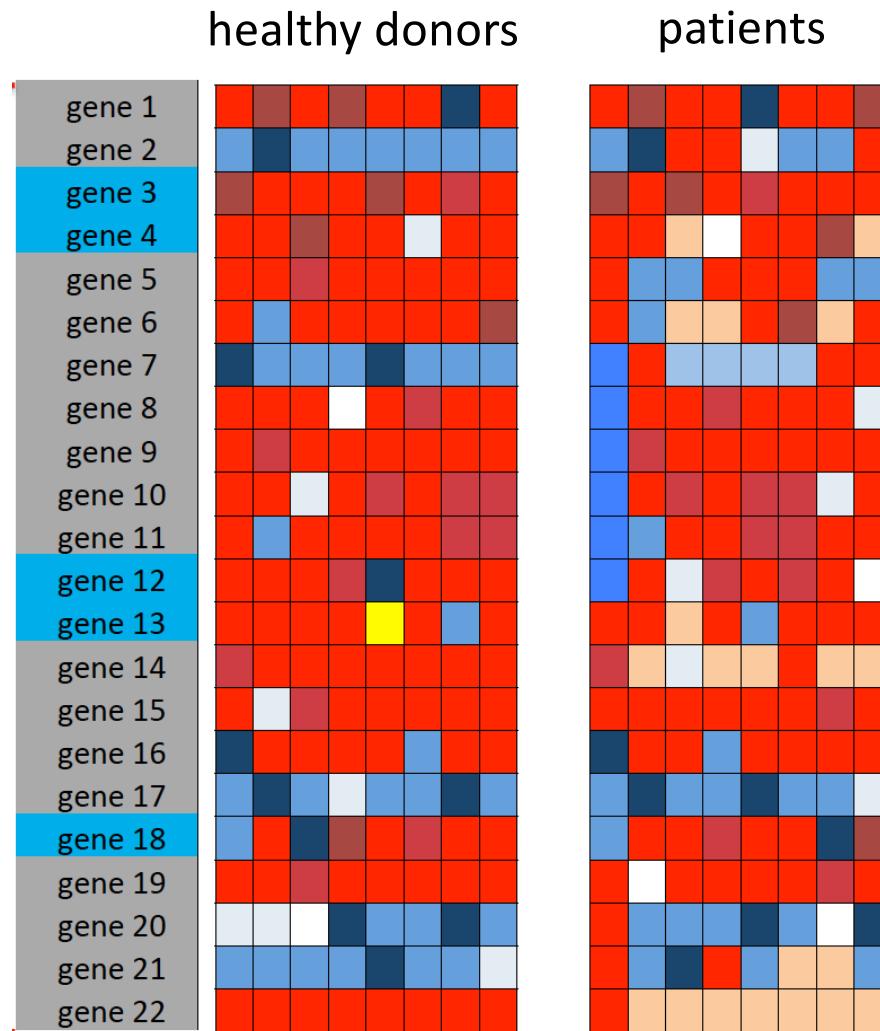
Enrichment analysis

Several methods available, *e.g.*:

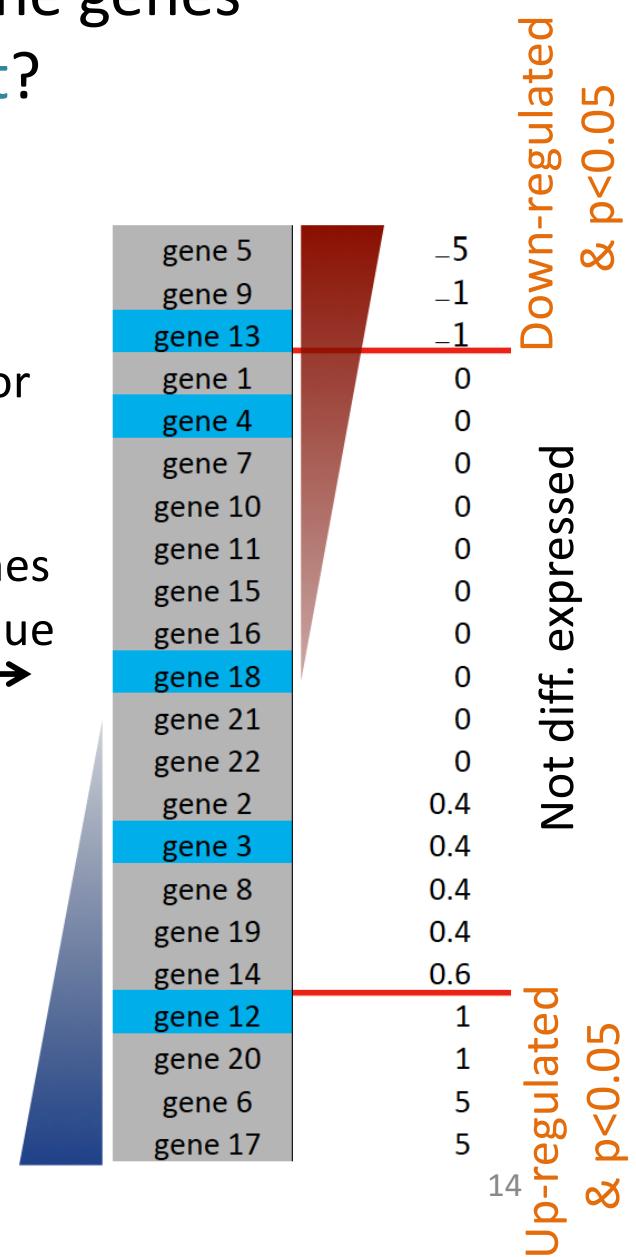
- over-representation analysis (ORA)
- gene set enrichment analysis (GSEA)

Over-representation analysis (ORA)

Are the DE genes overlapping with the genes contained within the blue set?



sort based
on T-statistic or
fold change
and count
significant genes
based on p-value



Fisher's exact test

<i>2x2 count table</i>	Differentially expressed	Not Differentially expressed	total
blue	2	3	5
Not blue	5	12	17
total	7	15	22

contingency table

H_0 : The proportion of blue genes differentially expressed is the same as the proportion of blue genes that are not differentially expressed.

H_1 : The proportion of blue genes differentially expressed is not the same as the proportion of blue genes that are not differentially expressed.

Fisher's exact test in R

```
> cont.table<-matrix(c(2,3,5,12), ncol=2, byrow = T)  
> fisher.test(cont.table)
```

Fisher's Exact Test for Count Data

data: cont.table

p-value = 1

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

0.1012333 18.7696686

sample estimates:

odds ratio

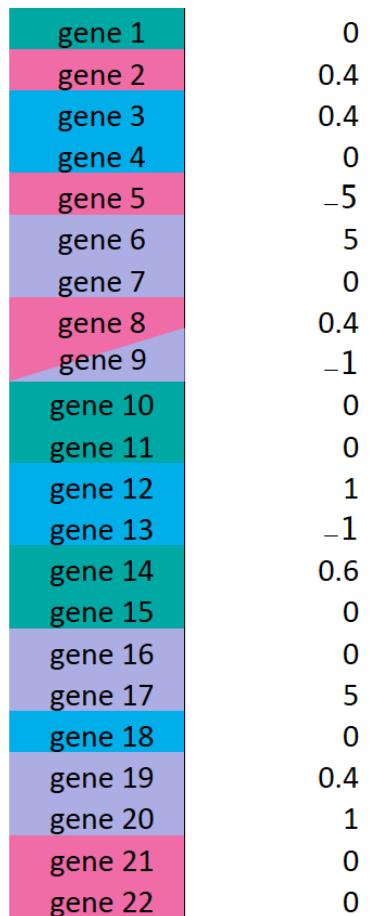
1.56456

2x2 count table	Differentially expressed	Not Differentially expressed	total
blue	2	3	5
Not blue	5	12	17
total	7	15	22

$$2/7 = 0.29$$

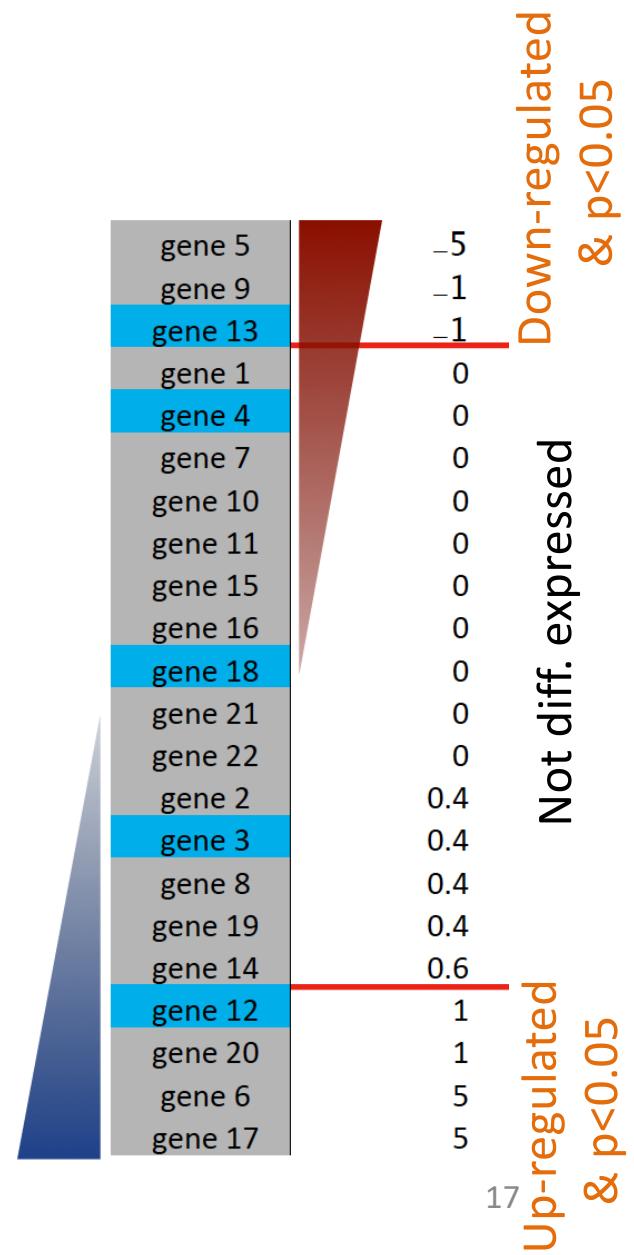
$$3/15 = 0.20$$

Which gene sets are differentially expressed?



Run individual Fisher's exact tests for each gene set, **blue, pink, purple, green**

⇒ Multiple tests need **p-value adjustment.**



Enrichment analysis using R: one possibility among others

clusterProfiler

platforms all rank 41 / 2140 support 1 5 / 2 3 in Bioc 11 years
build ok updated < 1 week dependencies 125

DOI: [10.18129/B9.bioc.clusterProfiler](https://doi.org/10.18129/B9.bioc.clusterProfiler)  

A universal enrichment tool for interpreting omics data

Bioconductor version: Release (3.15)

This package supports functional characteristics of both coding and non-coding genomics data for thousands of species with up-to-date gene annotation. It provides a universal interface for gene functional annotation from a variety of sources and thus can be applied in diverse scenarios. It provides a tidy interface to access, manipulate, and visualize enrichment results to help users achieve efficient data interpretation. Datasets obtained from multiple treatments and time points can be analyzed and compared in a single run, easily revealing functional consensus and differences among distinct conditions.

Author: Guangchuang Yu [aut, cre, cph] , Li-Gen Wang [ctb], Erqiang Hu [ctb], Xiao Luo [ctb], Meijun Chen [ctb], Giovanni Dall'Olio [ctb], Wanqian Wei [ctb]

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

Built-in functions for enrichment analysis

Built-in gene sets for human, mouse, yeast, etc

Built-in GO and KEGG (see later)

- <https://bioconductor.org/packages/release/bioc/html/clusterProfiler.html>
- G Yu, LG Wang, Y Han, QY He. clusterProfiler: an R package for comparing biological themes among gene clusters. *OMICS: A Journal of Integrative Biology* 2012, 16(5):284-287. [doi:\[10.1089/omi.2011.0118\]\(http://dx.doi.org/10.1089/omi.2011.0118\)](https://doi.org/10.1089/omi.2011.0118)
- Full vignette: <http://yulab-smu.top/clusterProfiler-book/>

Functions for Fisher test and for ORA with R and clusterProfiler

Fisher exact test (package stats)

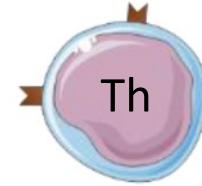
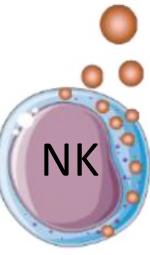
```
fisher.test(x, y = NULL, workspace = 200000, hybrid = FALSE,  
           hybridPars = c(expect = 5, percent = 80, Emin = 1),  
           control = list(), or = 1, alternative = "two.sided",  
           conf.int = TRUE, conf.level = 0.95,  
           simulate.p.value = FALSE, B = 2000)
```

enricher(): implementation of hypergeometric test (one-sided Fisher test) for user defined gene list and gene set annotations (package clusterProfiler)

```
enricher(  
  gene,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  universe,  
  minGSSize = 10,  
  maxGSSize = 500,  
  qvalueCutoff = 0.2,  
  TERM2GENE,  
  TERM2NAME = NA  
)
```

Eg genes that are markers of cell clusters of single-cell RNA seq





Recap and exercise 1

- Once we have identified differentially expressed (DE) genes, we can use an over-representation analysis to determine whether or not the genes of a gene set of interest are over-represented among the DE genes or not.
- Exercise 1:**
- Results table of differential gene expression analysis between 2 human immune cell types, natural killer (NK) cells and CD4 T helper cells (Th):

ensembl_gene_id	symbol	logFC	t	P.Value	p.adj
ENSG00000000003	TSPAN6	-5.643604444	-4.67212847	4.260000e-05	7.358019e-04
ENSG00000000419	DPM1	-0.181898089	-1.10183079	2.780198e-01	5.176076e-01
ENSG00000000457	SCYL3	0.496987374	1.49103508	1.448691e-01	3.449889e-01
ENSG00000000460	C1orf112	1.121799095	1.44589945	1.570599e-01	3.630935e-01
ENSG00000000938	FGR	10.670687340	7.21234165	1.980000e-08	1.718657e-06
ENSG00000000971	CFH	-3.412927673	-2.78888655	8.480300e-03	4.610083e-02

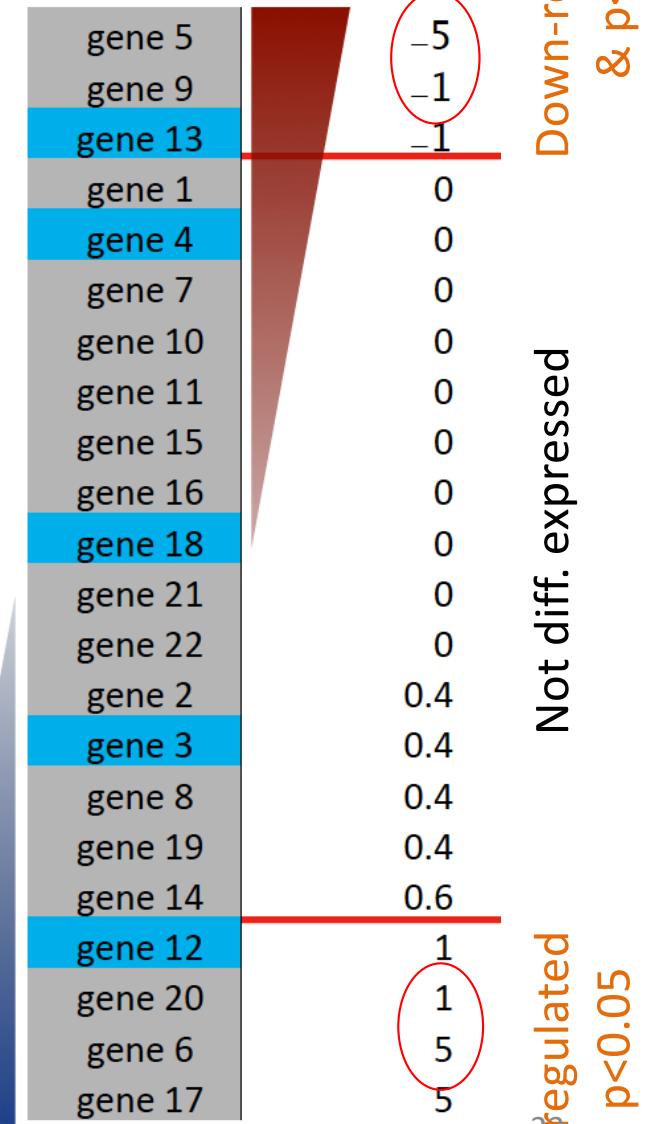
Positive logFC = higher in NK
Negative logFC = lower in NK

- Run a **Fisher's exact test** to determine whether genes involved in the **adaptive immune response** are over-represented among the genes up-regulated in Th cells.

Fisher's exact test is threshold-based

2x2 count table	Differentially expressed	Not Differentially expressed	total
blue	2	3	5
Not blue	5	12	17
total	7	15	22

Contingency table with count of genes,
without taking into account the **magnitude**
of the change of each gene.

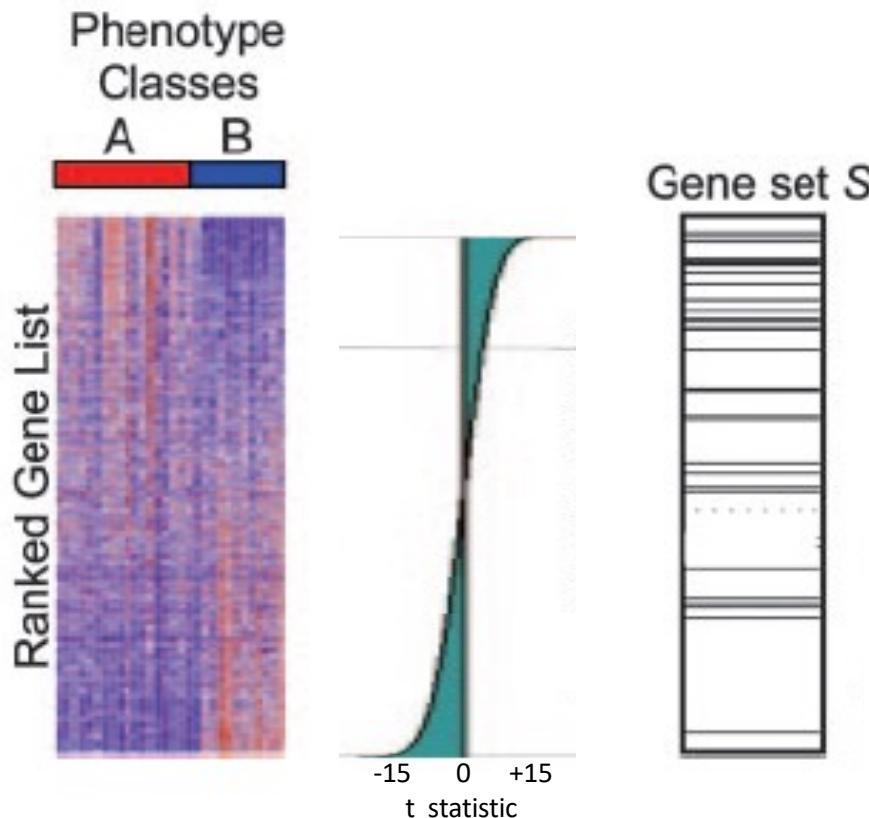


Gene set enrichment analysis (GSEA)

- **Threshold-free:** the whole list of genes detected in the RNA sequencing experiment is used.
- GSEA is a computational method that determines whether an *a priori* defined set of genes shows statistically significant, concordant differences between two biological states (MSigDB)
- Rank all genes based on score (eg t-statistic) and calculate an enrichment score (ES) that reflects the degree to which the members of a gene set are overrepresented at the top or bottom of the ranked genes.

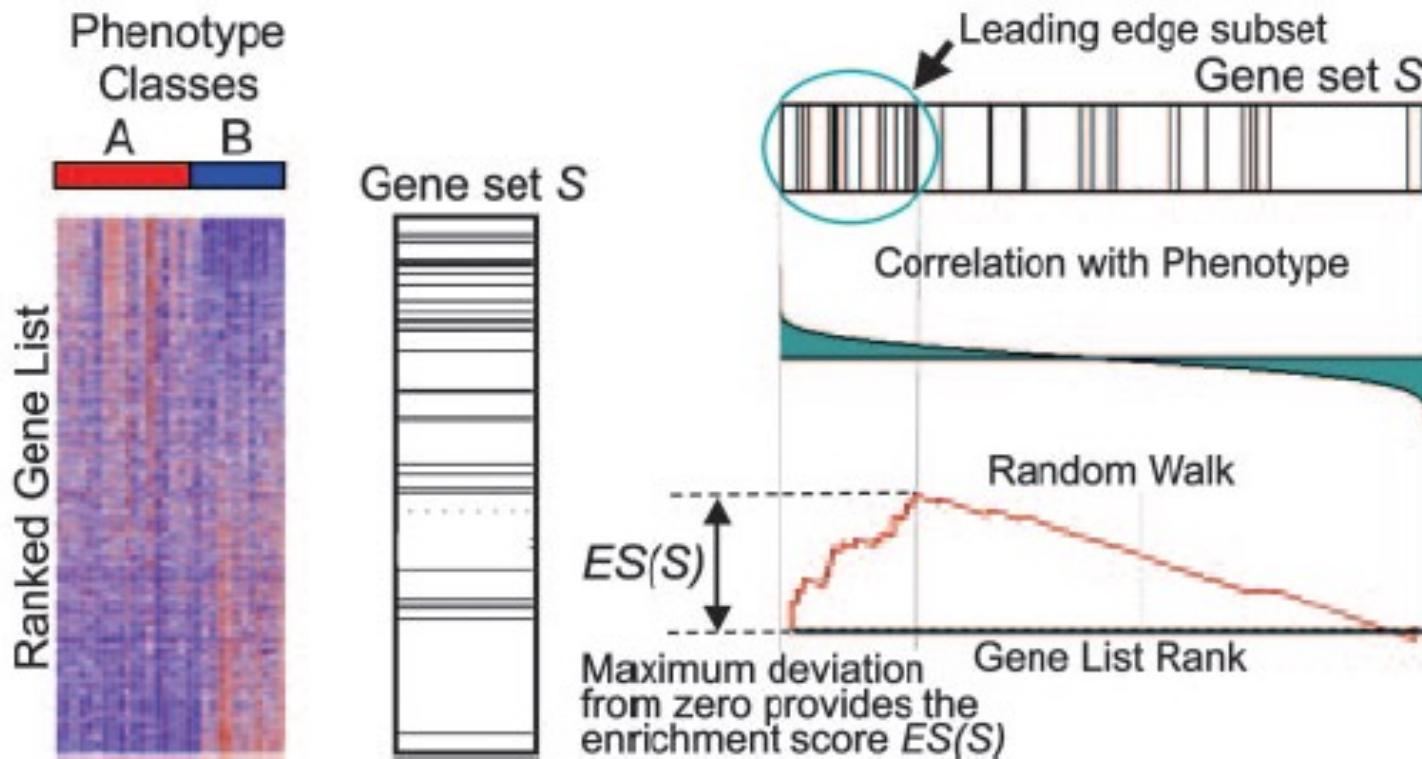
Method of GSEA

Goal: determine whether the members of a gene set **S** are randomly distributed throughout a ranked gene list or if they are located at the top or bottom of the ranked gene lists



1. Sort the genes based on the t statistic (=weight)

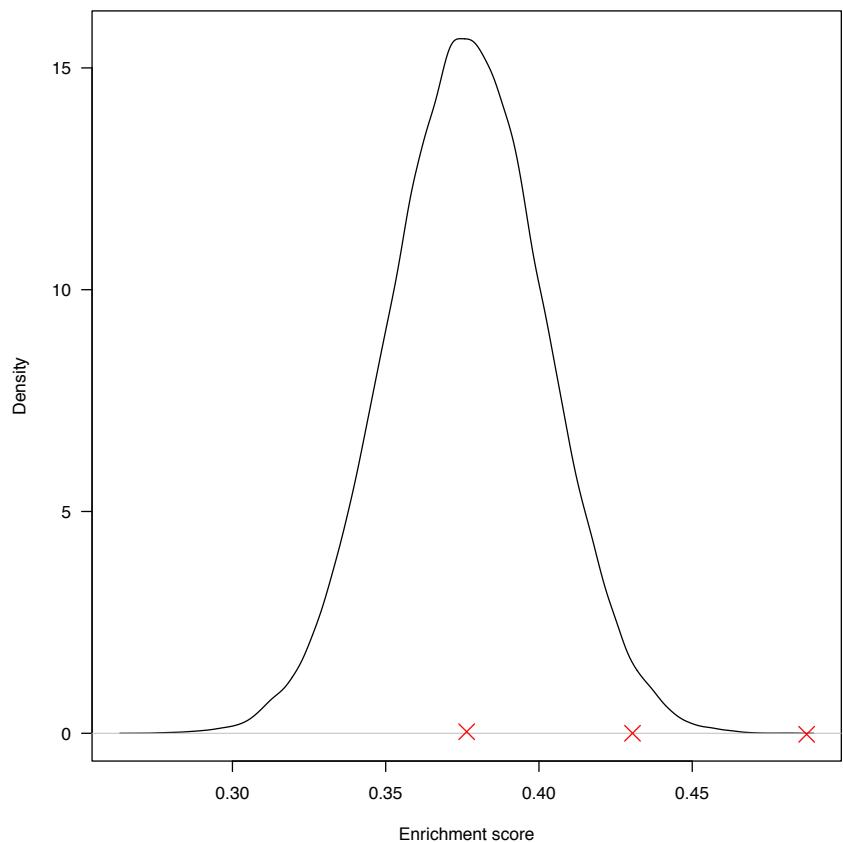
Method of GSEA



1. Sort the genes based on the t statistic (=weight)
2. Calculate enrichment score ES using weight. The ES for a set is the maximum value reached (pos. or neg.)

Method of GSEA

1. Sort the genes based on the t statistic (=weight)
2. Calculate enrichment score ES using weight. The ES for a set is the maximum value reached (pos. or neg.)
3. Perform permutations of samples and/or genes to recalculate random ES scores
4. Calculate Normalized ES (NES) and estimate p-value of each gene set based on randomized ES scores
5. Adjust p-value



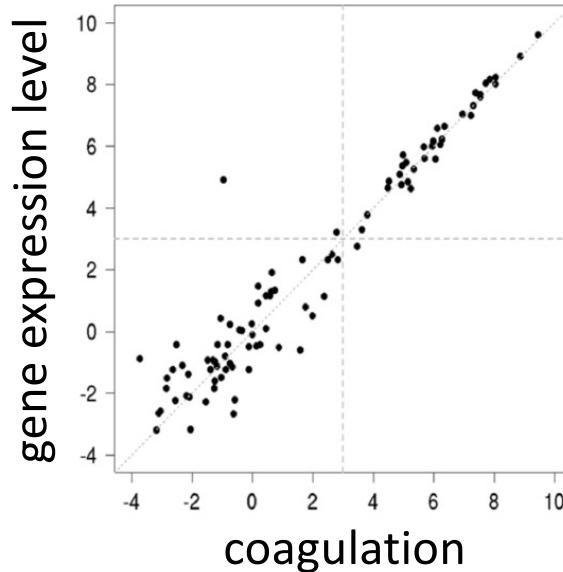
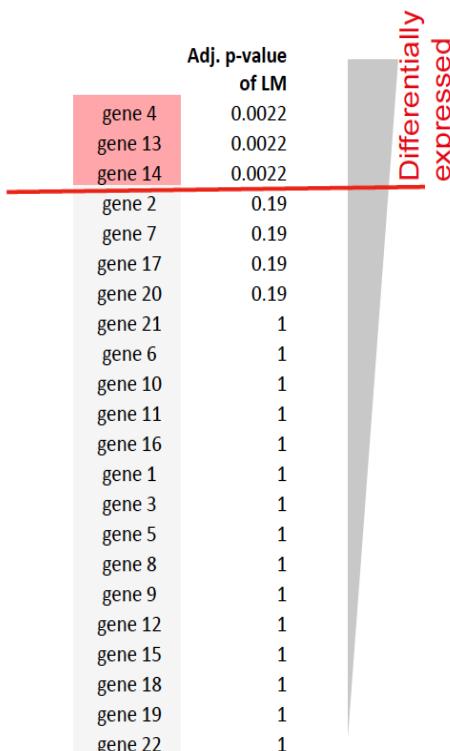
$$\text{NES} = \frac{\text{actual ES}}{\text{mean(ESs against all permutations of the dataset)}}$$

Do not forget p-value
adjustment if more than 1
gene set is tested!

NES: 1 NES: 1.16 NES: 1.32
p: 0.5 p: 0.05 p: 0.001

Apply GSEA to other type of data or score

- Use t-statistic from paired t-test
- Use F statistic of one way or two way ANOVA
- Use coefficients of linear model



GSEA for linear model implemented in `romer()` function of the `limma` package

Functions for GSEA with clusterProfiler

GSEA(): GSEA of user-defined gene sets using all ranked genes

```
GSEA(  
  geneList,  
  exponent = 1,  
  minGSSize = 10,  
  maxGSSize = 500,  
  eps = 1e-10,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  TERM2GENE,  
  TERM2NAME = NA,  
  verbose = TRUE,  
  seed = FALSE,  
  by = "fgsea",  
  ...  
)
```

TERM2GENE:

term	gene
GOBP_ADAPTIVE_IMMUNE_RESPONSE	ZC3H12A
GOBP_ADAPTIVE_IMMUNE_RESPONSE	ZNF683
GOBP_ADAPTIVE_IMMUNE_RESPONSE	ZP3
GOBP_HAIR_CELL_DIFFERENTIATION	ATOH1
GOBP_HAIR_CELL_DIFFERENTIATION	CDH23
GOBP_HAIR_CELL_DIFFERENTIATION	CLRN1

gseGO(): GSEA of GO gene sets using all ranked genes

```
gseGO(  
  geneList,  
  ont = "BP",  
  OrgDb,  
  keyType = "ENTREZID",  
  exponent = 1,  
  minGSSize = 10,  
  maxGSSize = 500,  
  eps = 1e-10,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  verbose = TRUE,  
  seed = FALSE,  
  by = "fgsea",  
  ...  
)
```

Bioconductor orgDb packages



Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

About Learn Packages Developers

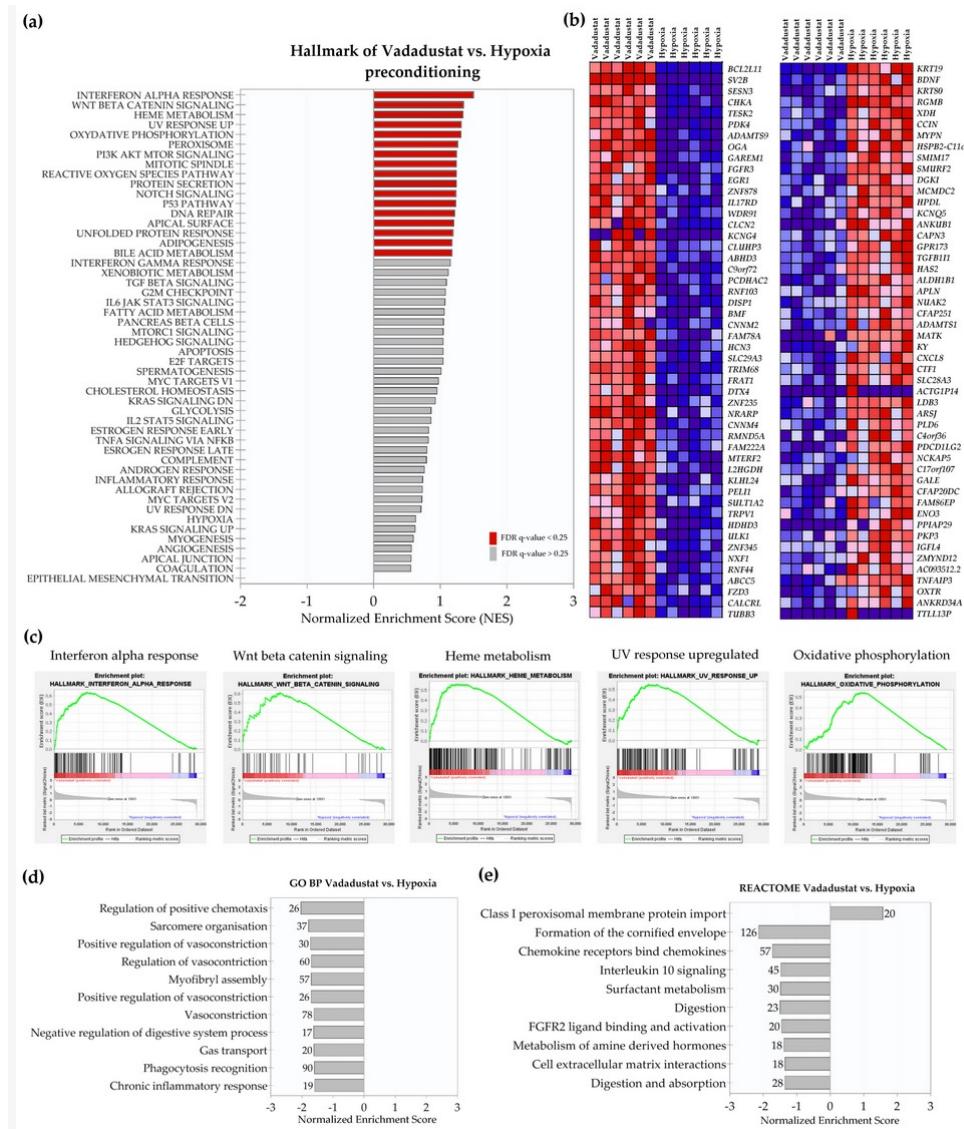
<u>org.Sc.sgd.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Yeast	42
<u>org.Ce.eg.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Worm	45
<u>org.Bt.eg.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Bovine	48
<u>org.Ss.eg.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Pig	50
<u>org.Gg.eg.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Chicken	51
<u>org.Cf.eg.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Canine	52
<u>org.Mmu.eg.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Rhesus	53
<u>org.Xl.eg.db</u>	Bioconductor Package Maintainer	Genome wide annotation for Xenopus	60



Recap and exercise 2

- Fisher test is a threshold-based method, while GSEA is a threshold-free enrichment method. Both can be used for single or multiple gene sets.
- Exercise 2: use functions of clusterProfiler and data provided in Ex. 1
 - Run a GSEA for the Gene Ontology gene sets (more details on this collection later)
 - Explore the results: how many gene sets are significant? Are the gene sets up-regulated or down-regulated in NK cells?

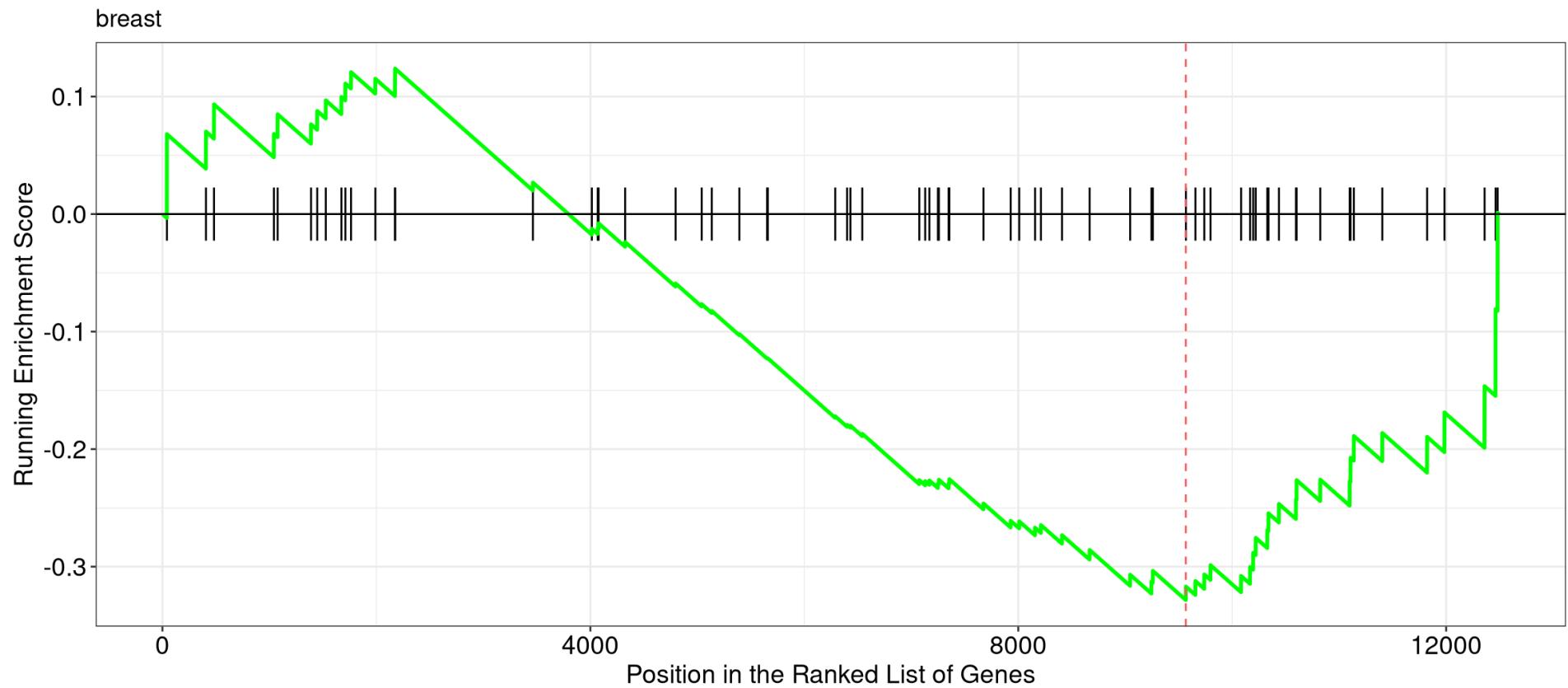
How to show the results of an enrichment analysis?



Visualizations available in clusterProfiler

- barcode plot

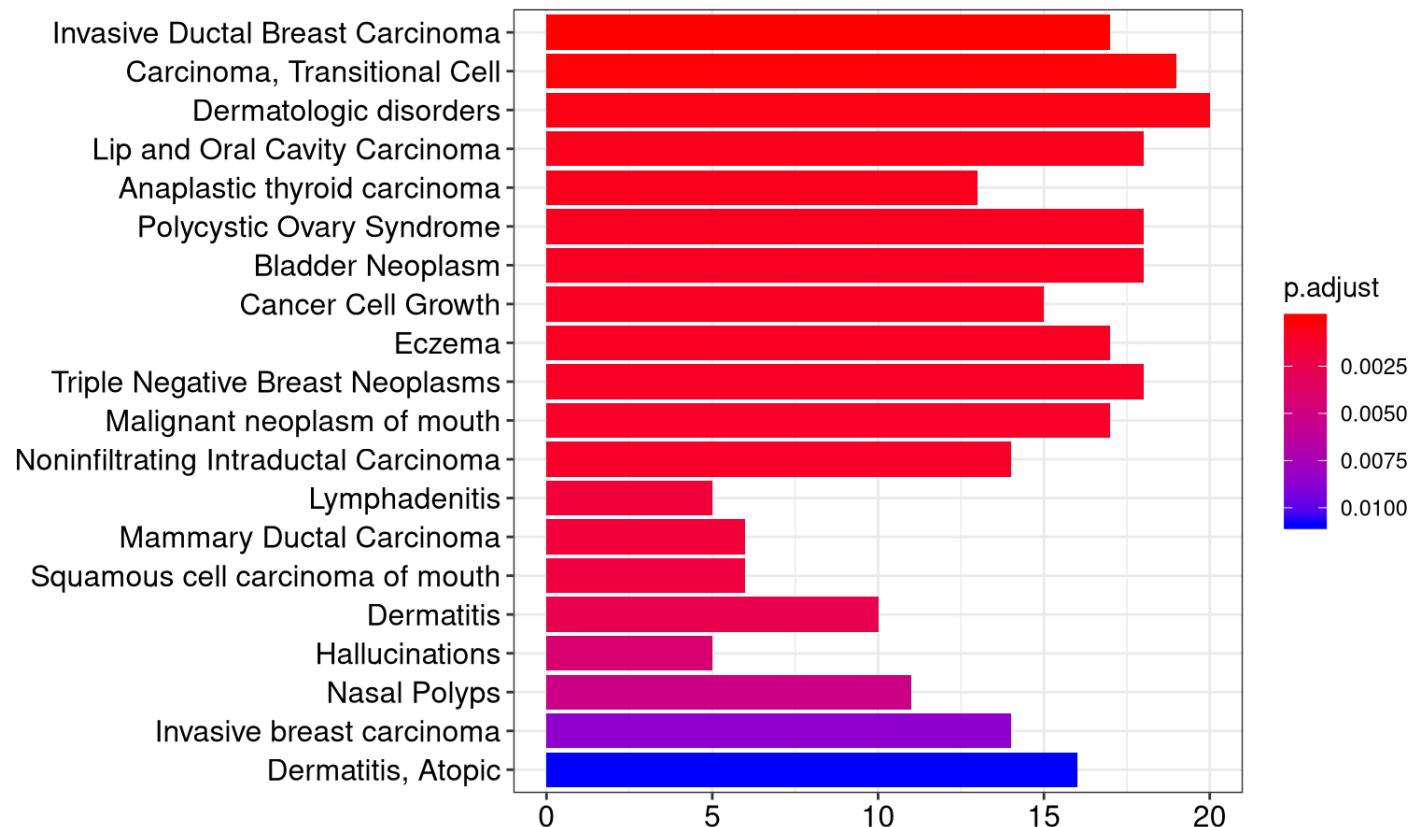
```
gseaplot(h_NK_vs_Th, geneSetID =  
"BREAST", title=" BREAST")
```



Visualizations available in clusterProfiler

- **barplot**

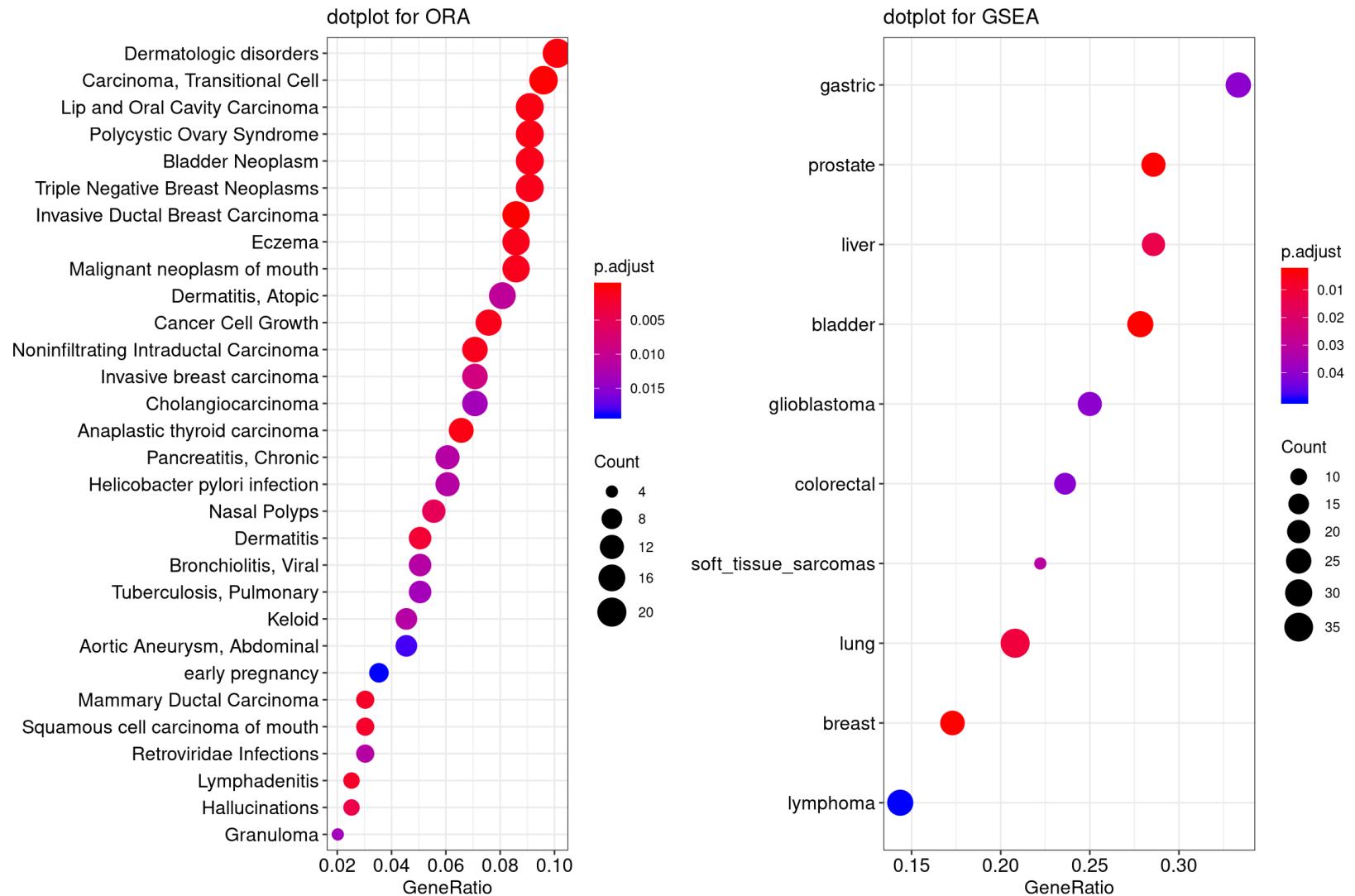
```
ego <- enrichGO(de, OrgDb=org.Hs.eg.db, ont="BP", keyType = "SYMBOL")
barplot(ego, showCategory=20)
```



Visualizations available in clusterProfiler

- dotplot

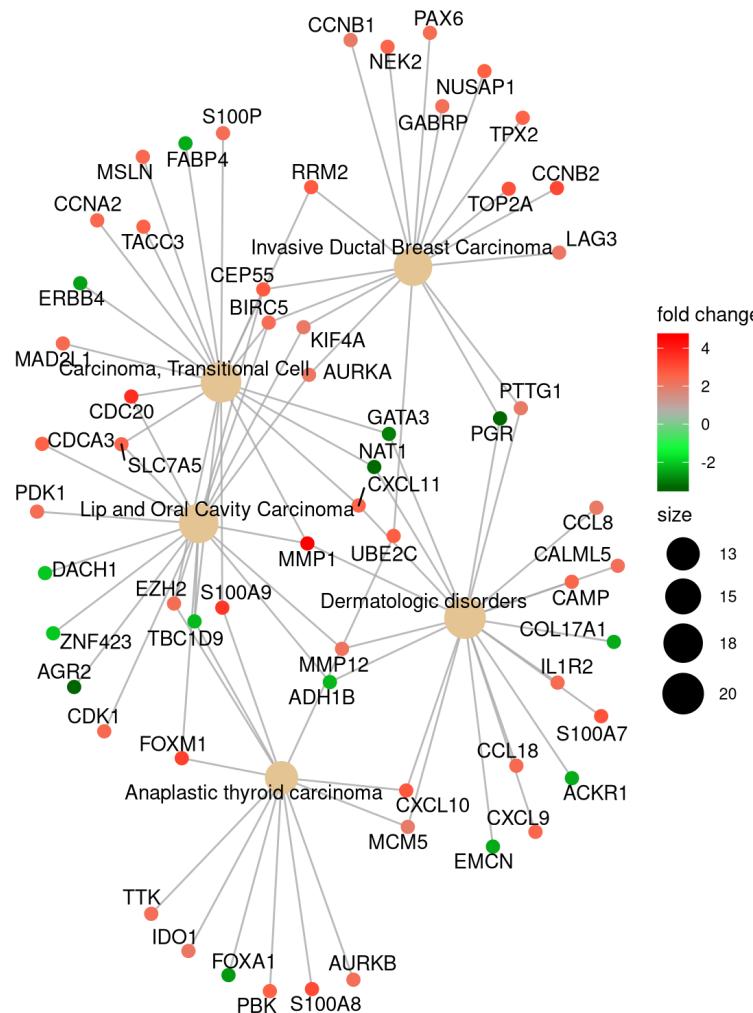
```
ego <- enrichGO(de)
dotplot(ego, showCategory=20)
```



Visualizations available in clusterProfiler

```
cnetplot(edox, categorySize="pvalue", foldChange=toList)
```

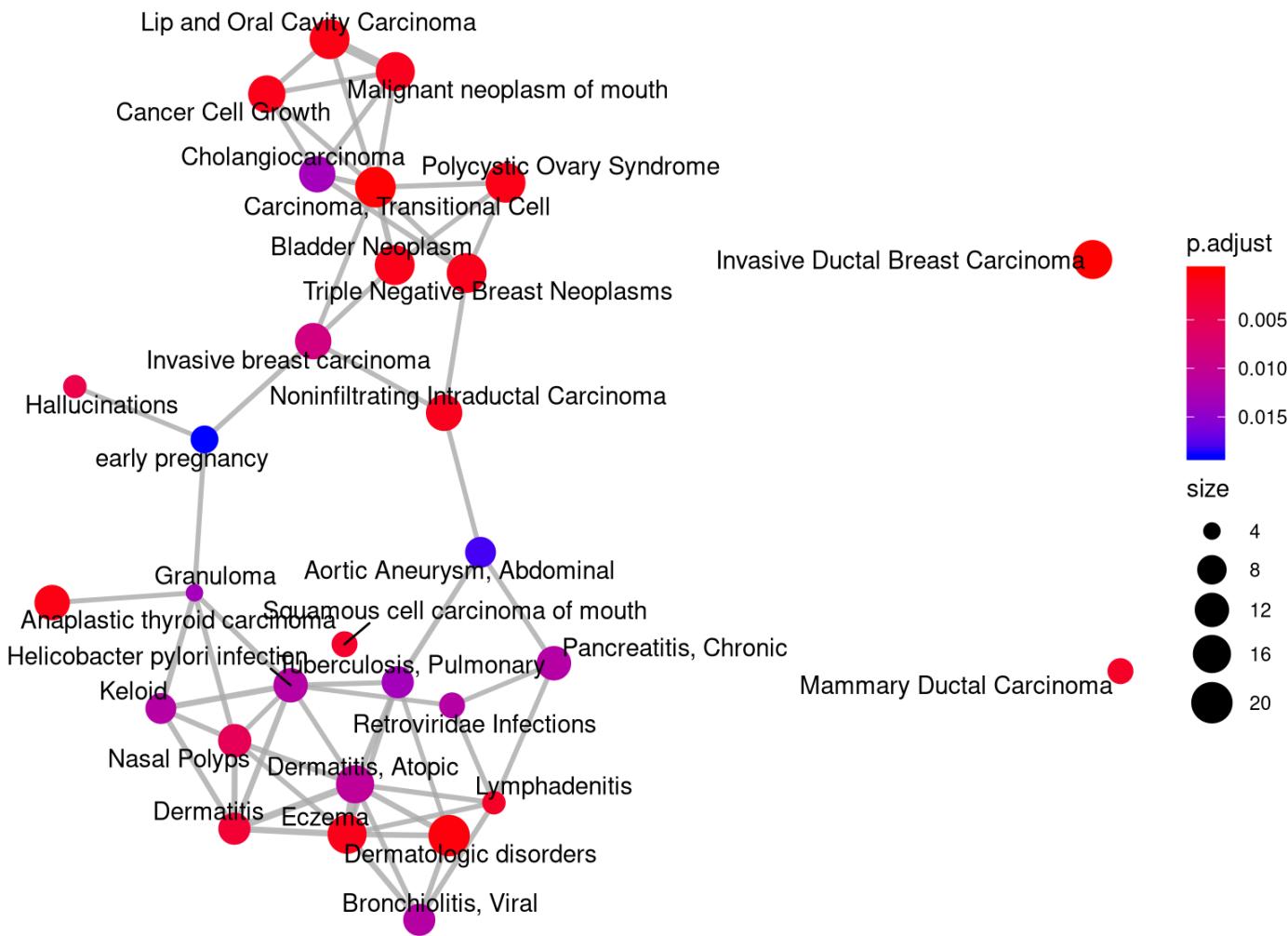
- Gene-concept network



Visualizations available in clusterProfiler

- Enrichment map

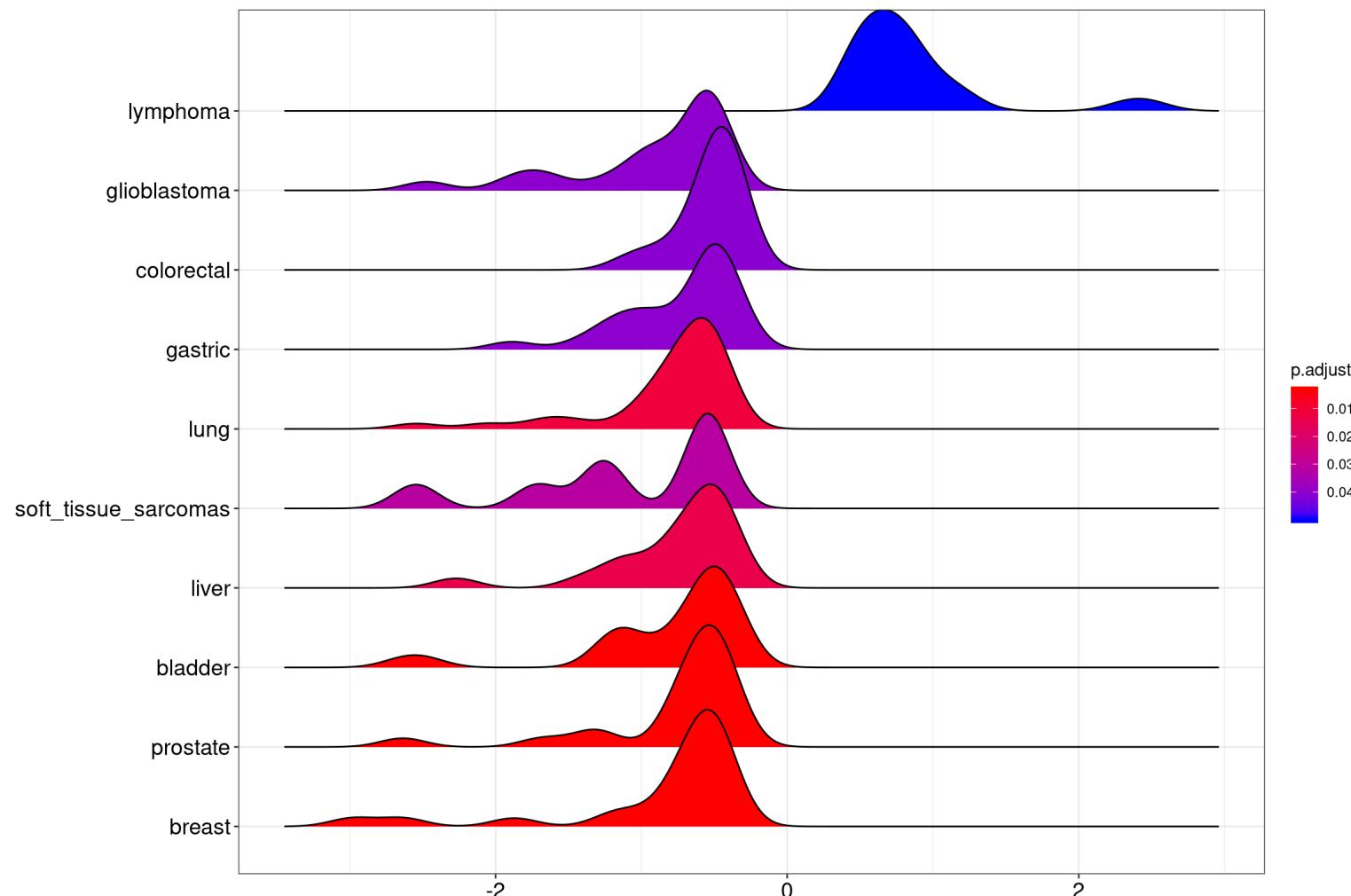
```
ego <- enrichGO(de)
emapplot(ego)
```



Visualizations available in clusterProfiler

- Ridgeplot

```
ego <- gseGO(de)  
ridgeplot(ego)
```





Recap and Exercise 3

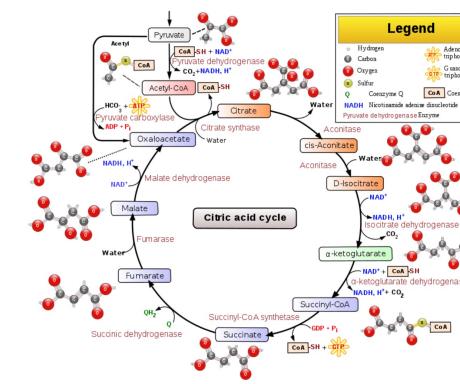
Several visualization methods can be used to represent the results, either for single gene sets (barcode plot) or for several gene sets (barplots, etc).

Exercise 3: Create figures for the enrichment results:

- barplot of $-\log_{10}(\text{p-value})$ of the p-values of the top 10 GO gene sets, or of positive and negative NES values
- Enrichment maps, gene-concept networks, ridge plots, etc

What is a gene set?

- Genes working together in a pathway (e.g. energy release through Krebs cycle)
- Genes located in the same compartment in a cell (e.g. all proteins located in the cell nucleus)
- Proteins that are all regulated by a same transcription factor
- Custom gene list that comes from a publication and that are down-regulated in a mutant
- List of SNPs associated with a disease
- ... etc!
- Several gene sets are grouped into Knowledge bases

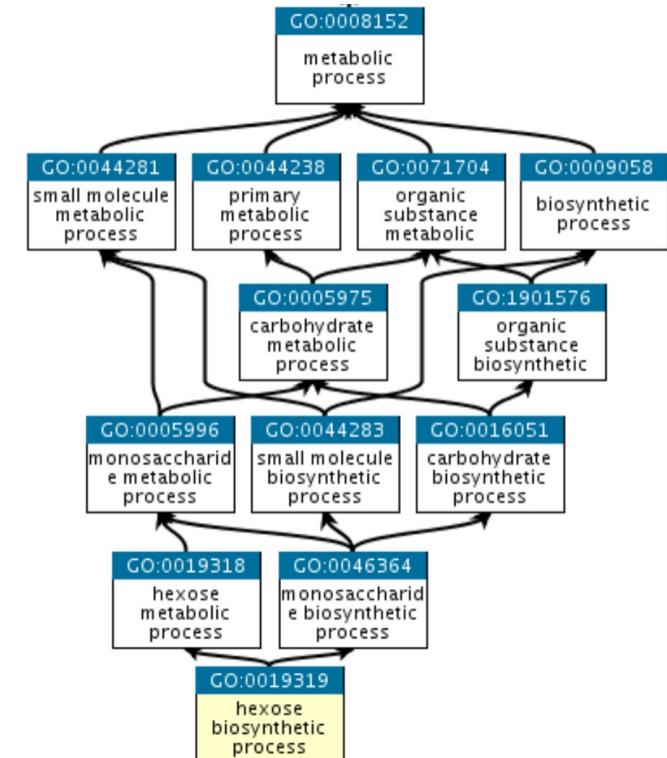


Gene ontology

- <http://geneontology.org/>

Collaborative effort to address the need for consistent descriptions of gene products across databases

- GO Consortium: develop a comprehensive, computational model of biological systems, ranging from the molecular to the organism level, across the multiplicity of species in the tree of life
- GO terms = GO categorizations
- GO term: each with a name (DNA repair) and a unique accession number (GO:0005125)



The Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes.

Gene ontology

GO ontologies: GO terms organized in 3 independent controlled vocabularies

- **Molecular function:** represents the biochemical activity of the gene product, such activities could include "ligand", "GTPase", and "transporter".
- **Cellular component:** refers to the location in the cell of the gene product. Cellular components could include "nucleus", "lysosome", and "plasma membrane".
- **Biological process:** refers to the biological role involving the gene or gene product, and could include "transcription", "signal transduction", and "apoptosis". A biological process generally involves a chemical or physical change of the starting material or input.

KEGG

<https://www.genome.jp/kegg/pathway.html>

KEGG Databases Mapper Auto annotation Kanehisa Lab



KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions and relations

KEGG2 PATHWAY BRITE MODULE KO GENES COMPOUND DISEASE DRUG

Select prefix Enter keywords Help

[New pathway maps | Update history]

Pathway Maps

KEGG PATHWAY is a collection of manually drawn [pathway maps](#) representing our knowledge of the molecular interaction, reaction and relation networks for:

1. Metabolism

Global/overview Carbohydrate Energy Lipid Nucleotide Amino acid Other amino Glycan
Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiotics Chemical structure

2. Genetic Information Processing

3. Environmental Information Processing

4. Cellular Processes

5. Organismal Systems

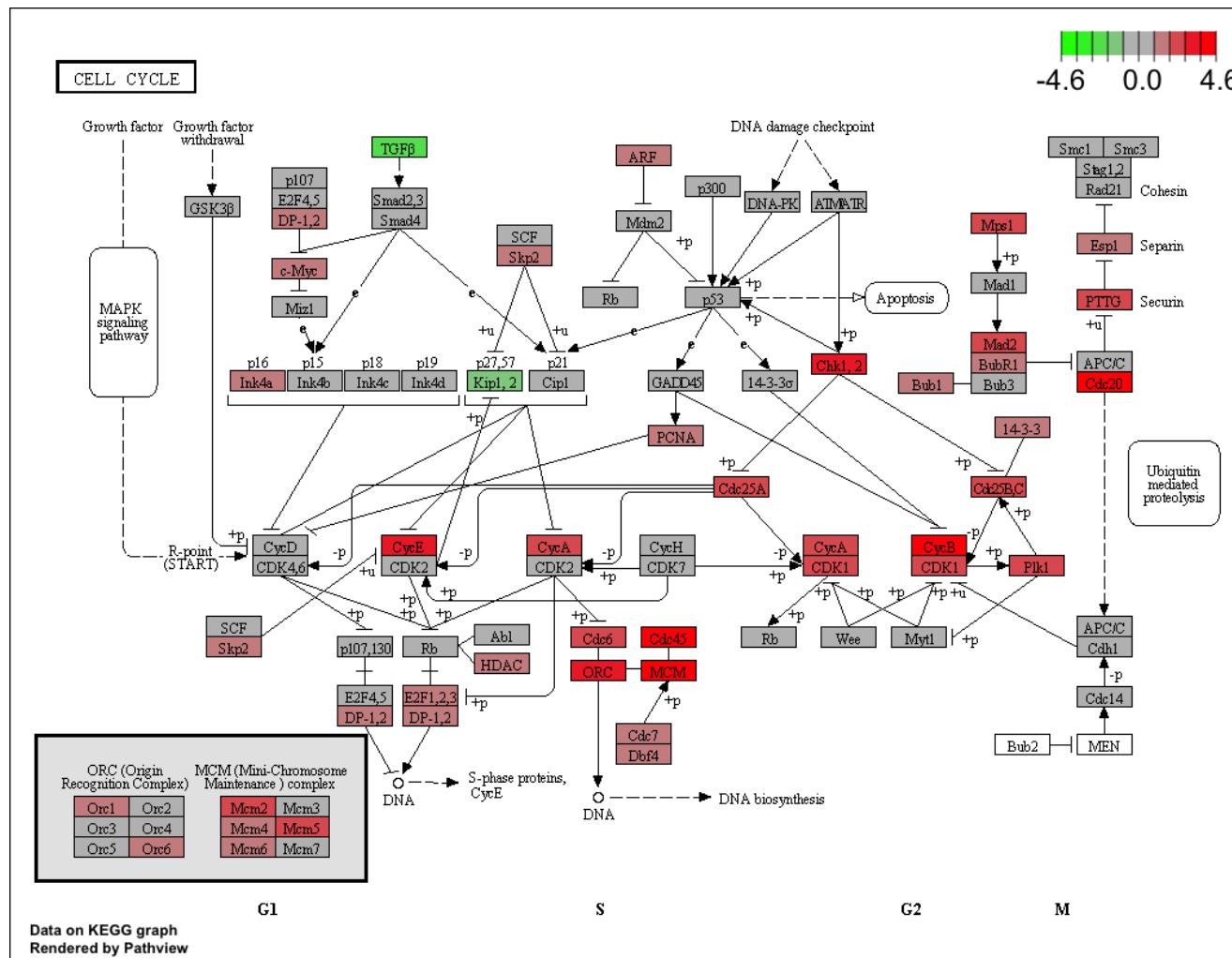
6. Human Diseases

7. Drug Development

KEGG PATHWAY is the reference database for pathway mapping in **KEGG Mapper**.

Visualizations available - pathview package

```
hsa04110 <- pathview(gene.data = geneList, pathway.id = "hsa04110", species = "hsa",
limit = list(gene=max(abs(geneList)), cpd=1))
```



Reactome

<https://reactome.org/>



The screenshot shows the Reactome website homepage. At the top left is the Reactome logo. At the top right are navigation links: About, Content, Docs, Tools, Community, and Download. Below the navigation is a search bar with the placeholder "Find Reactions, Proteins and Pathways" and a "Go!" button. Below the search bar are four large blue rounded squares, each containing a white icon and a title: "Pathway Browser" (with a network icon), "Analysis Tools" (with a bar chart icon), "ReactomeFIViz" (with a network node icon), and "Documentation" (with a document icon).

Pathway Browser	Analysis Tools	ReactomeFIViz	Documentation
Visualize and interact with Reactome biological pathways	Merges pathway identifier mapping, over-representation, and expression analysis	Designed to find pathways and network patterns related to cancer and other types of diseases	Information to browse the database and use its principal tools for data analysis

MSigDB

<https://www.gsea-msigdb.org/gsea/msigdb/index.jsp>

H **hallmark gene sets** are coherently expressed signatures derived by aggregating many MSigDB gene sets to represent well-defined biological states or processes.

C1 **positional gene sets** for each human chromosome and cytogenetic band.

C2 **curated gene sets** from online pathway databases, publications in PubMed, and knowledge of domain experts.

C3 **regulatory target gene sets** based on gene target predictions for microRNA seed sequences and predicted transcription factor binding sites.

C4 **computational gene sets** defined by mining large collections of cancer-oriented microarray data.

C5 **ontology gene sets** consist of genes annotated by the same ontology term.

C6 **oncogenic signature gene sets** defined directly from microarray gene expression data from cancer gene perturbations.

C7 **immunologic signature gene sets** represent cell states and perturbations within the immune system.

C8 **cell type signature gene sets** curated from cluster markers identified in single-cell sequencing studies of human tissue.

Download gmt files with version number:

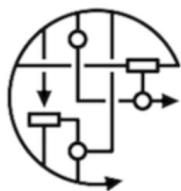
<https://www.gsea-msigdb.org/gsea/downloads.jsp>

The Hallmark collection:

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4707969/>

WikiPathways

<https://www.wikipathways.org/index.php/WikiPathways>



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- Help
- About us
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- Development
- WikiPathways Blog
- Curation Events

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- Download files
- Other file formats
- Web service API
- WikiPathways RDF
- Embed code

activity

- Browse pathways
- Recent changes
- New releases
- New pathways
- Edit pathways

page discussion view source history Log in / create account

Share your pathway knowledge in the fight against COVID-19

ACCESS the rapidly growing collection of COVID-19 pathways, CONTRIBUTE your time and domain knowledge about pathway biology as a pathway author, and USE these pathways in your research.

Welcome to WikiPathways

WikiPathways is a database of biological pathways maintained by and for the scientific community. Read about our 12-year journey so far and [official exit from beta](#) or our [2021 NAR paper](#).

Find Pathways

Search

You can search by:

- Pathway name (*Apoptosis*)
- Gene or protein name (*p53*)
- Any page content (*cancer*)

Browse

Browse pathways

Browse by species and category

Today's Featured Pathway

COVID-19, thrombosis and anticoagulation (Homo sapiens)

Curator of the Week

Kristina Hanspers (Gladstone Institutes)

Get Pathways

Download

Growth

The screenshot shows the main interface of the WikiPathways website. On the left, there's a sidebar with links for Help, About us, Contact us, etc. The main content area has a banner for COVID-19 pathways. Below it, there are sections for 'Welcome to WikiPathways' (describing the database as maintained by the scientific community), 'Find Pathways' (with a search bar and options to search by pathway name, gene/protein name, or page content), 'Browse' (with a grid of pathway thumbnails), and 'Today's Featured Pathway' (showing a complex pathway diagram for COVID-19, thrombosis, and anticoagulation). At the bottom, there's a 'Curator of the Week' section featuring Kristina Hanspers from the Gladstone Institutes. On the far left, there's a small circular logo with nodes and arrows, and below it are sections for 'search', 'download', and 'activity'.

GSEA of other gene sets in R

ClusterProfiler: GSEA for KEGG pathways

```
gseKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,  
nPerm = 1000, minGSSize = 10, maxGSSize = 500,  
pvalueCutoff = 0.05, pAdjustMethod = "BH", verbose = TRUE,  
use_internal_data = FALSE, seed = FALSE, by = "fgsea")
```

Import a .gmt file of gene sets and convert to format needed for clusterProfiler

```
read.gmt(gmtfile)  
  
> head(term2gene_h)  
      ont      gene  
1 HALLMARK_TNFA_SIGNALING_VIA_NFKB JUNB  
2 HALLMARK_TNFA_SIGNALING_VIA_NFKB CXCL2  
3 HALLMARK_TNFA_SIGNALING_VIA_NFKB ATF3  
4 HALLMARK_TNFA_SIGNALING_VIA_NFKB NFKBIA  
5 HALLMARK_TNFA_SIGNALING_VIA_NFKB TNFAIP3  
6 HALLMARK_TNFA_SIGNALING_VIA_NFKB PTGS2  
.
```

conversion of gene ID types with clusterProfiler (or biomaRt package)

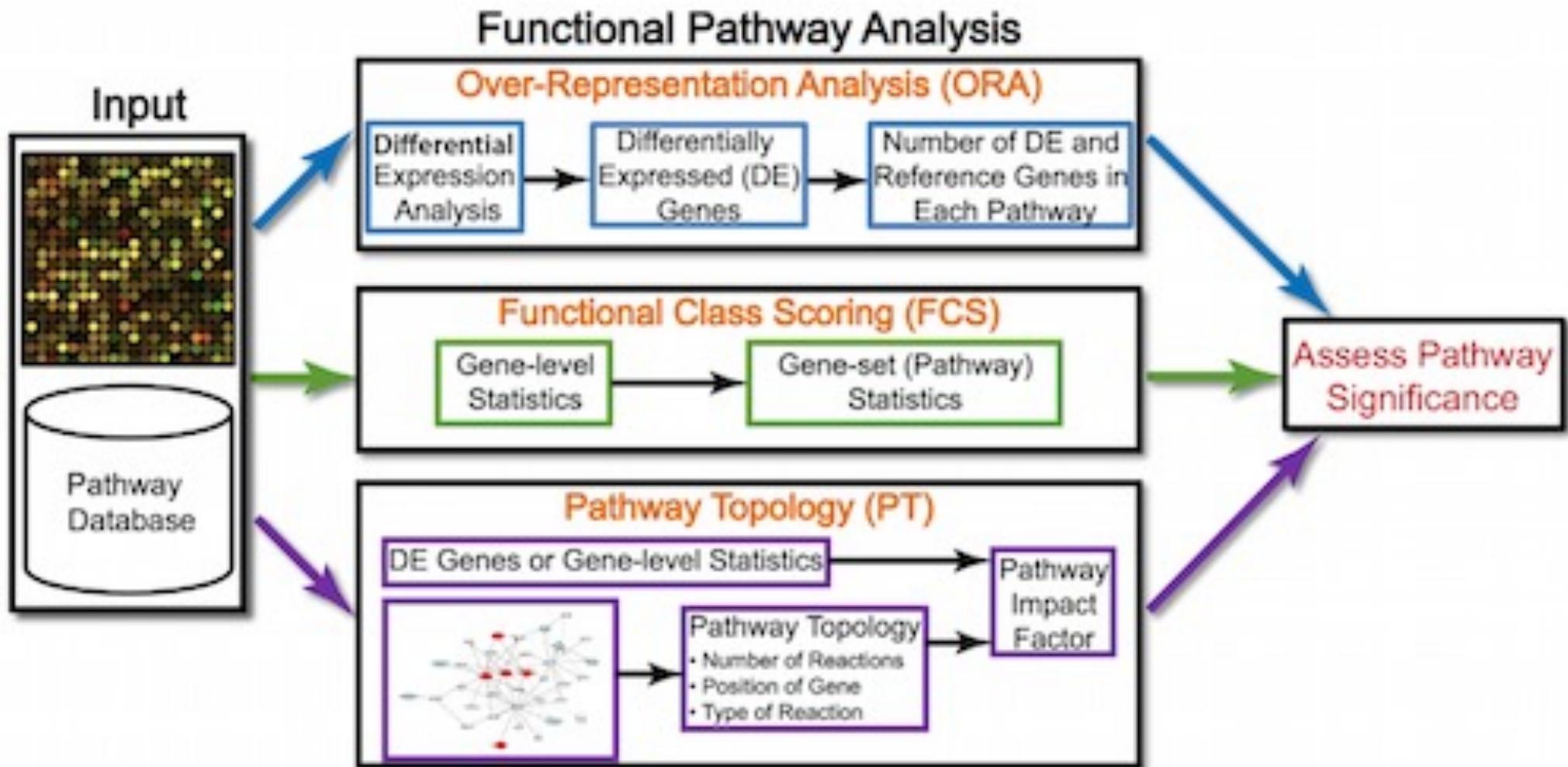
```
bitr(geneID, fromType, toType, OrgDb, drop = TRUE)
```

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

Recap and exercise 4

- We have seen how to perform GSEA using the built-in GO gene sets. Please perform GSEA with the built-in KEGG pathways, as well as with the hallmark gene sets obtained from MSigDB.
- Exercise 4: use functions of clusterProfiler and data provided in Ex. 1, and hallmark gene sets downloaded from MSigDB
 - First convert the gene symbols to EntrezID to perform a GSEA of KEGG pathways (with argument minGSSize=30).
 - Explore the results. Is there a KEGG immune-related gene set coming up? Is there a KEGG Natural killer gene set coming up?
 - Import the hallmark gene sets and run a GSEA. How many significant gene sets are there?

Enrichment/functional analysis - summary



Functional analysis: Pathway topology tools

Signaling pathway impact analysis (SPIA)

Identification of dys-regulated pathways: taking into account gene interaction information + fold changes and adjusted p-values from differential expression analysis

KEGG pathway	P_{NDE}	P_{PERT}	P_G	P_{FDR}	P_{FWER}	Status
Focal adhe..4510	0.0001	0.0000	0.0000	0.00000	0.00000	Act.
ECM-recept..4512	0.0001	0.0004	0.0000	0.00001	0.00002	Act.
PPAR signa..3320	0.0000	0.1240	0.0000	0.00011	0.00034	Inh.
Alzheimers..5010	0.0000	0.7260	0.0001	0.00059	0.00235	Act.
Adherens j..4520	0.0001	0.0852	0.0001	0.00090	0.00452	Act.
Axon guida..4360	0.0002	0.2324	0.0006	0.00487	0.02922	Act.
MAPK signa..4010	0.0001	0.7112	0.0007	0.00504	0.03527	Inh.
Tight junc..4530	0.0007	0.5156	0.0032	0.02073	0.16585	Act.

$$P_{NDE} = P(X \geq N_{DE} | H_0)$$

P_{PERT} : probability to observe a larger perturbation than observed

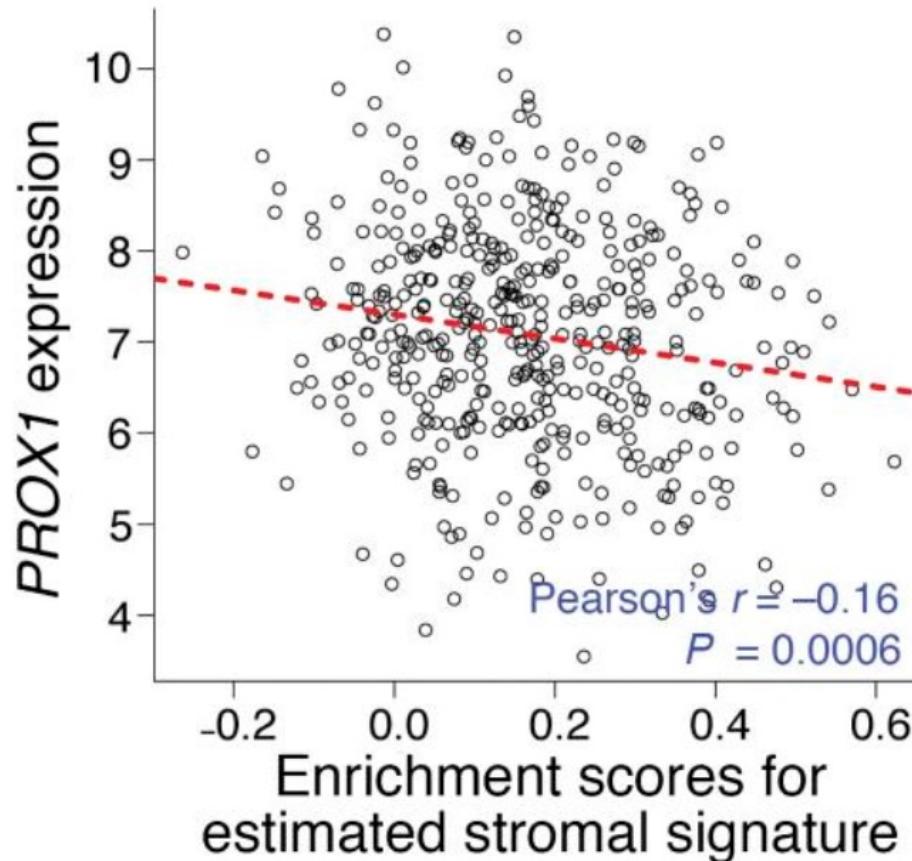
P_G : combination of P_{NDE} and P_{PERT}

P_{FDR} : adjusted FDR p-value

P_{FWER} : adjusted FDR p-value (more conservative)

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

Single-sample gene set variation analysis



GSVA:

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

<https://www.jci.org/articles/view/129558>

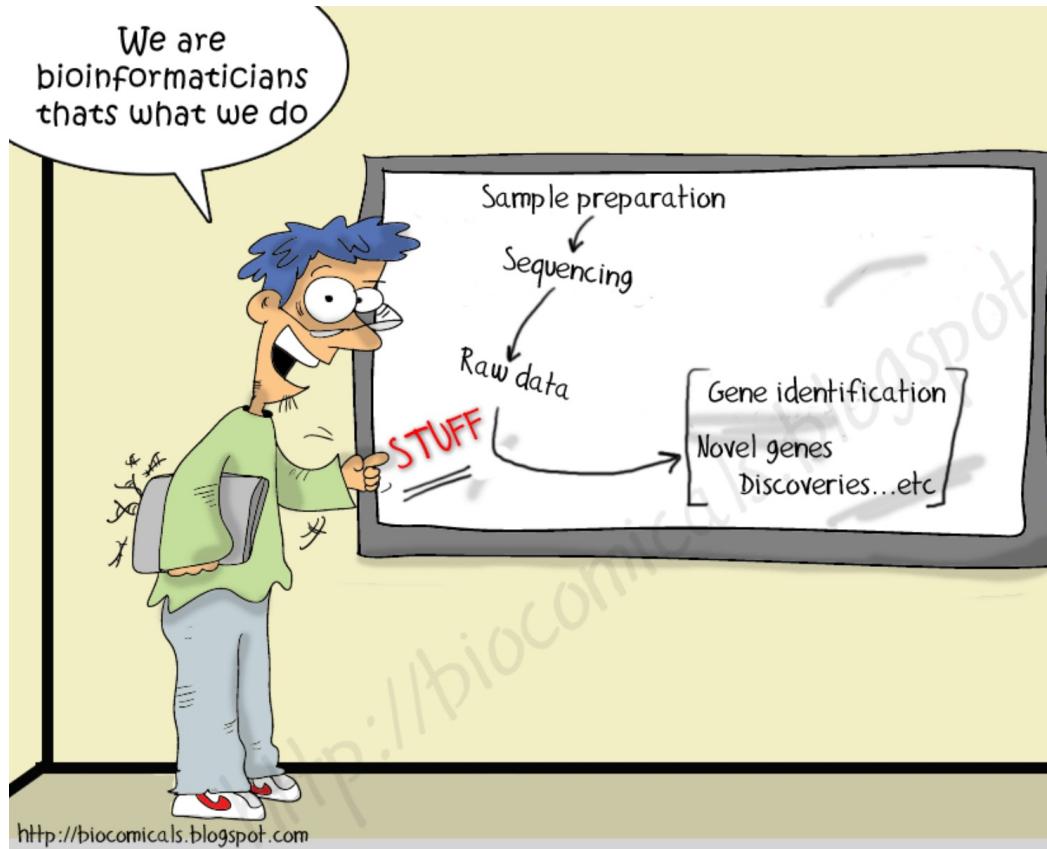
Credits: 0.25 ECTS

- Please provide answers and R code for an additional exercise (eg 1 Word with answers and figures and 1 script file, or 1 file generated from Rmarkdown)

<https://sib-swiss.github.io/enrichment-analysis-training/exercises/#extra-exercise-for-ects-credits>

- Sign up for credit by adding your name to the google Doc file (email sent by course organizer)
- Send answers to tania.wyss@sib.swiss within 1 week

Thank you for your attention!



Please fill in the **feedback** sent by the course organizer.
We thank Isabelle Dupanloup and Linda Dib for
providing course material.

