

Swiss Institute of
Bioinformatics

Introduction to RNA-Seq – Enrichment analysis

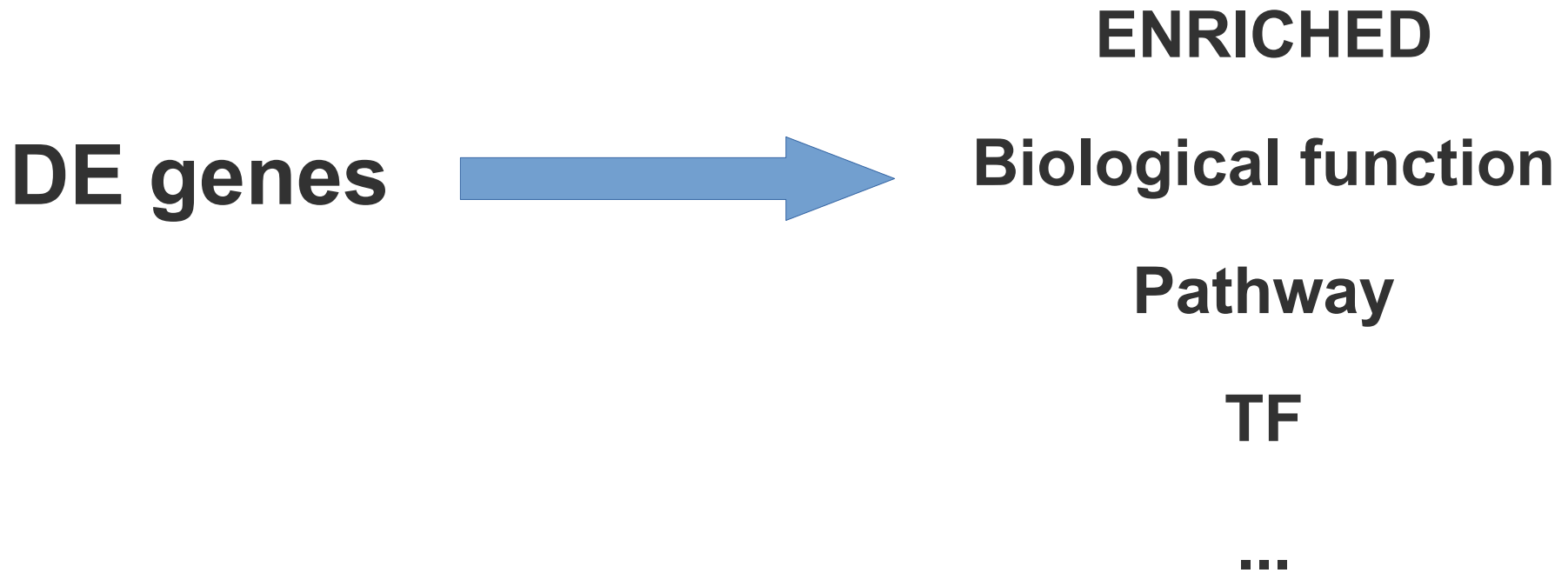
Wandrille Duchemin

Enrichment analysis

- **What to do with your list of differentially expressed gene ?**
- **Interpretation can be difficult, especially when many genes are DE**

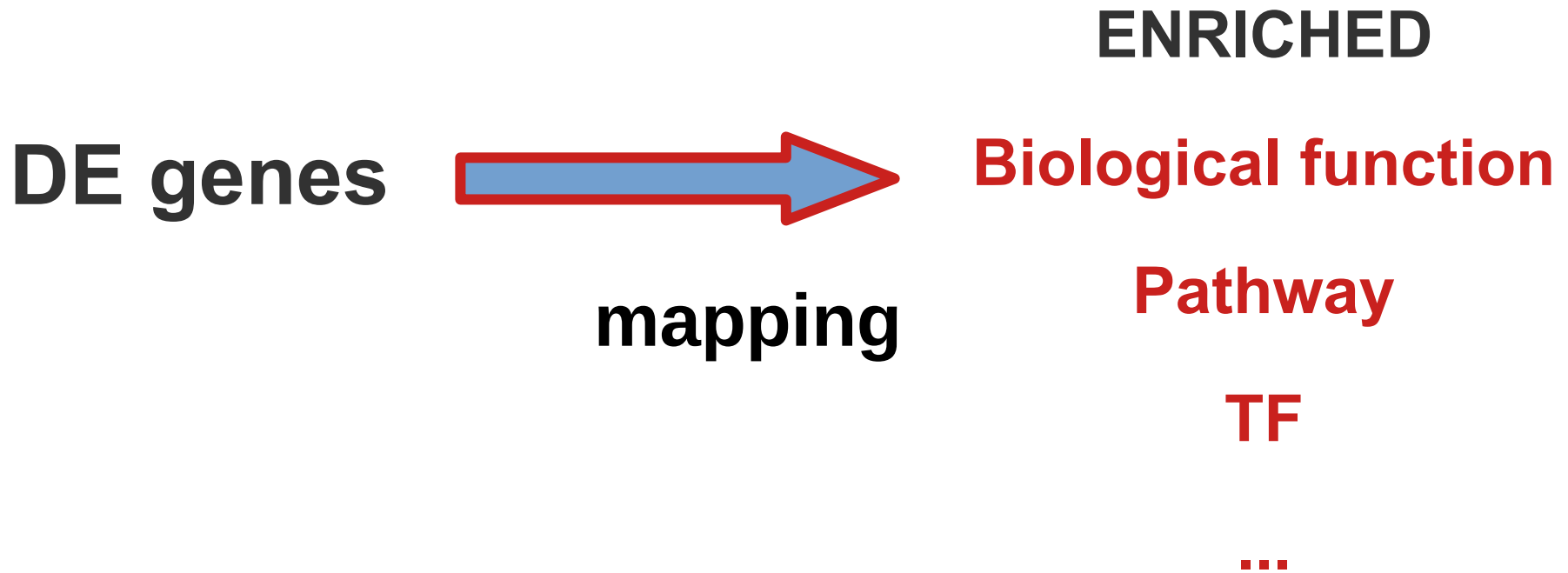
Enrichment analysis

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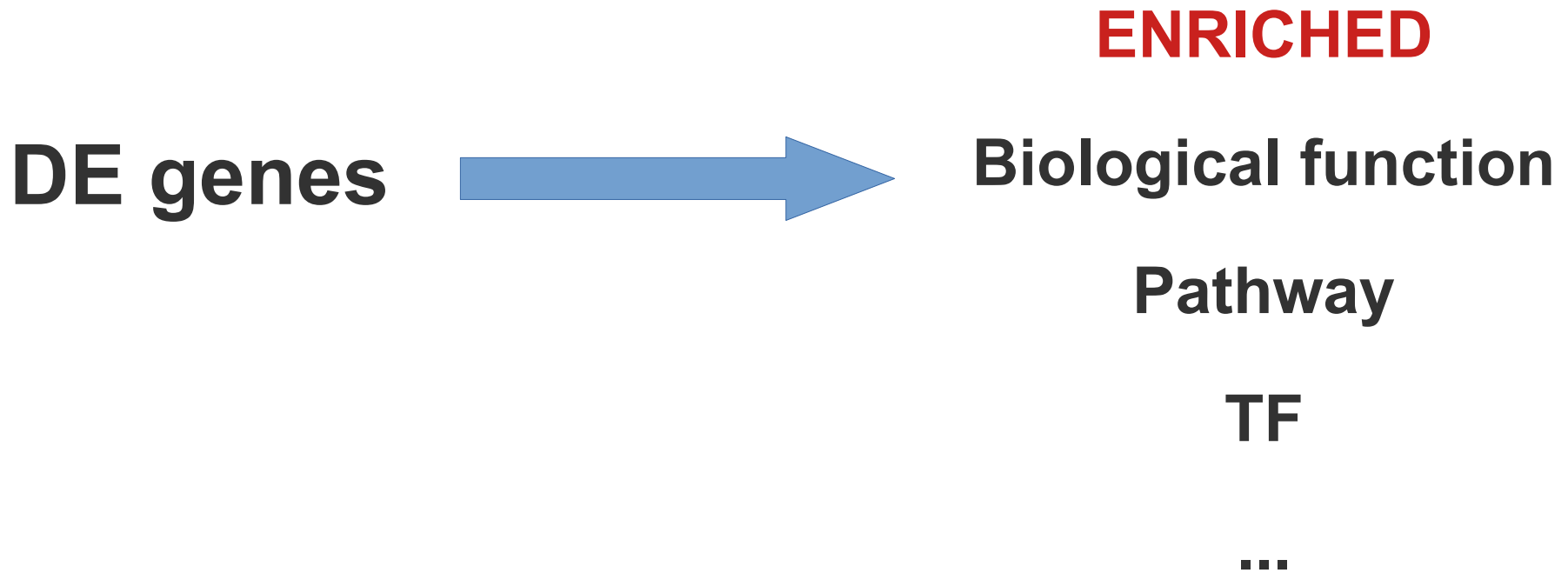
Enrichment analysis

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Enrichment analysis

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Enrichment analysis - mapping

- **The goal is to regroup certain genes together in meaningful sets**
- **Genes involved in the same pathway (eg. DNA repair)**
- **Genes located in the same biological compartment**
- **Genes with a similar molecular function**
- **Genes regulated by the same transcription factor**
- **...**

Enrichment analysis - mapping

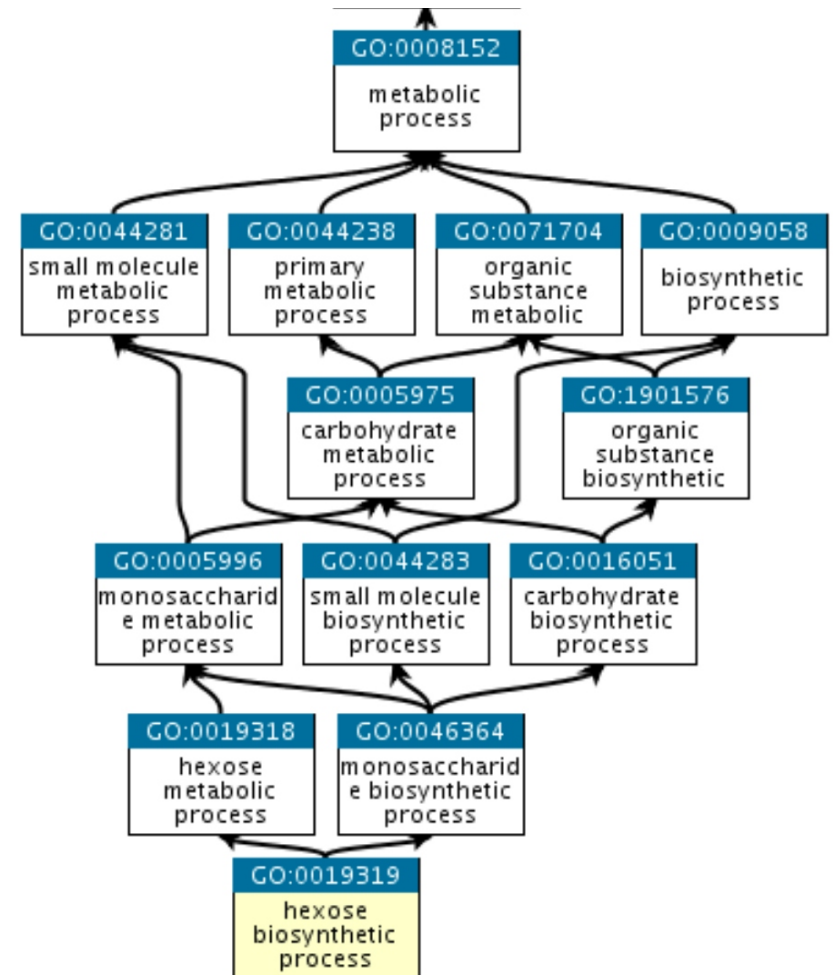
- **A few of the possibilities :**
- **Gene Ontology**
- **Reactome**
- **KEGG**
- **MSigDB**
- **Custom set**
- **...**

Enrichment analysis - mapping

Gene ontology : <http://geneontology.org>

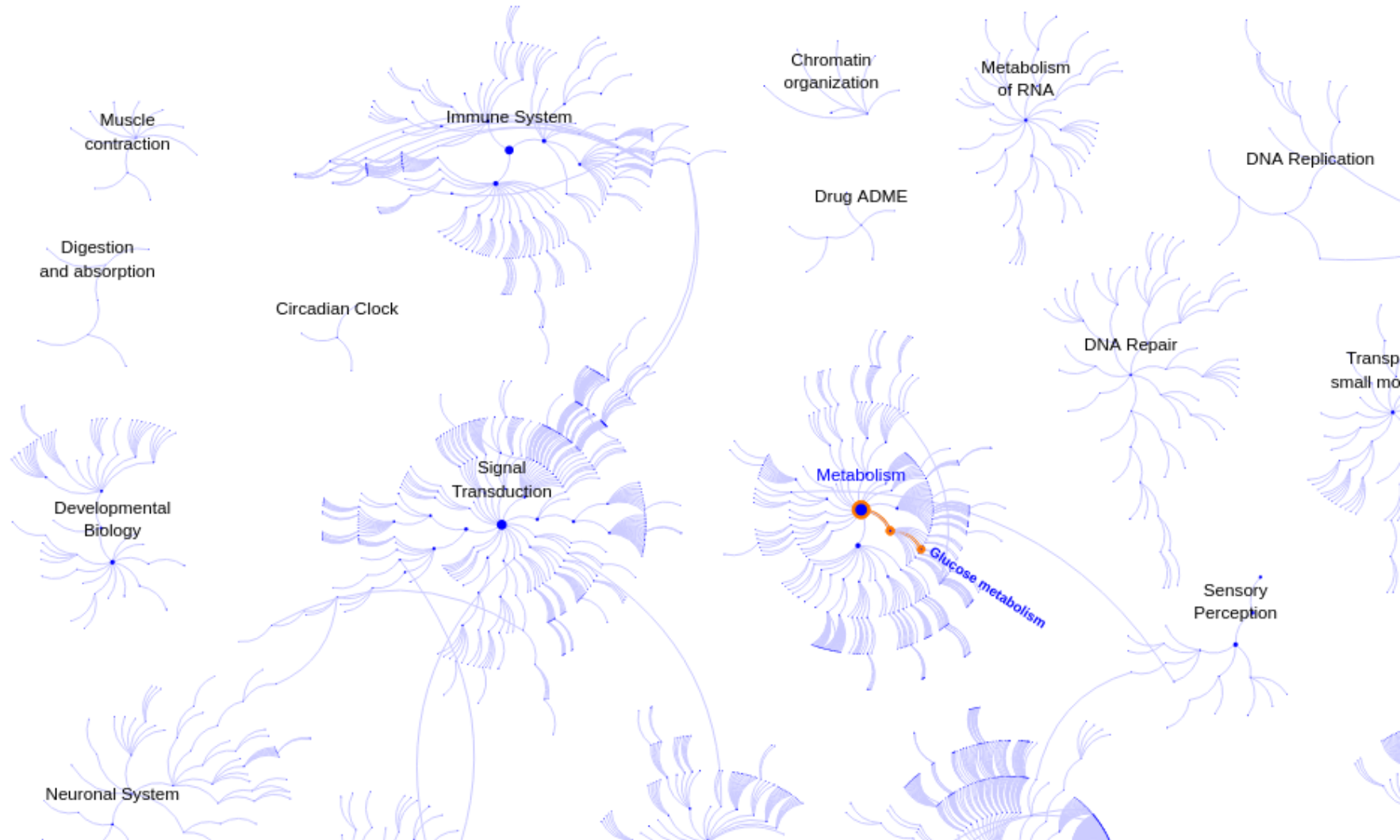
3 domains of nested terms:

- **Molecular Function**
- **Cellular Component**
- **Biological Process**



Enrichment analysis - mapping

Reactome : <https://reactome.org>



Enrichment analysis - mapping

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

Human mouse and rat only

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

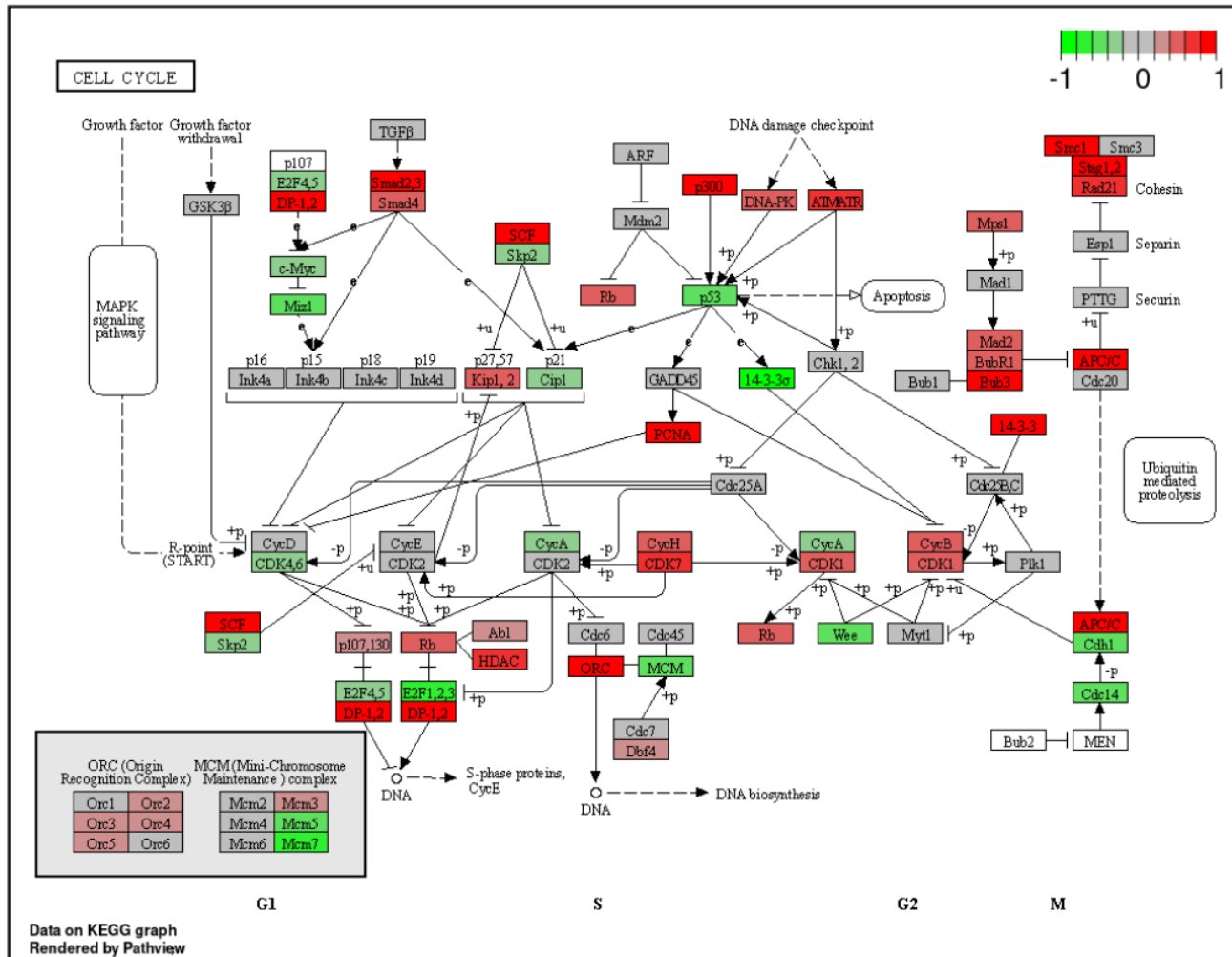
immunologic signature gene sets represent cell states and perturbations within the immune system.

C8

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

Enrichment analysis - mapping

KEGG : <https://www.genome.jp/kegg/> - KEGG PATHWAY



Projection of DE data
onto a KEGG pathway map
With R package pathview

Enrichment analysis - mapping

- **Custom gene sets :**
- **Derived from specialized literature**
- **Tentative annotation**
- **Understudied organisms**
- **...**

Enrichment analysis – computing enrichment

- **2 possible approaches (among many!)**
- **Over-representation analysis**
- **Gene Set Enrichment Analysis**

Enrichment analysis – computing enrichment

- 2 possible approaches (among many!)
- Over-representation analysis
 - Fisher's exact test (with p-val correction)

	DE	Not DE
in gene set	A	B
not in gene set	C	D

$N = A+B+C+D$ # total genes
 $M = A+B$ # genes in set

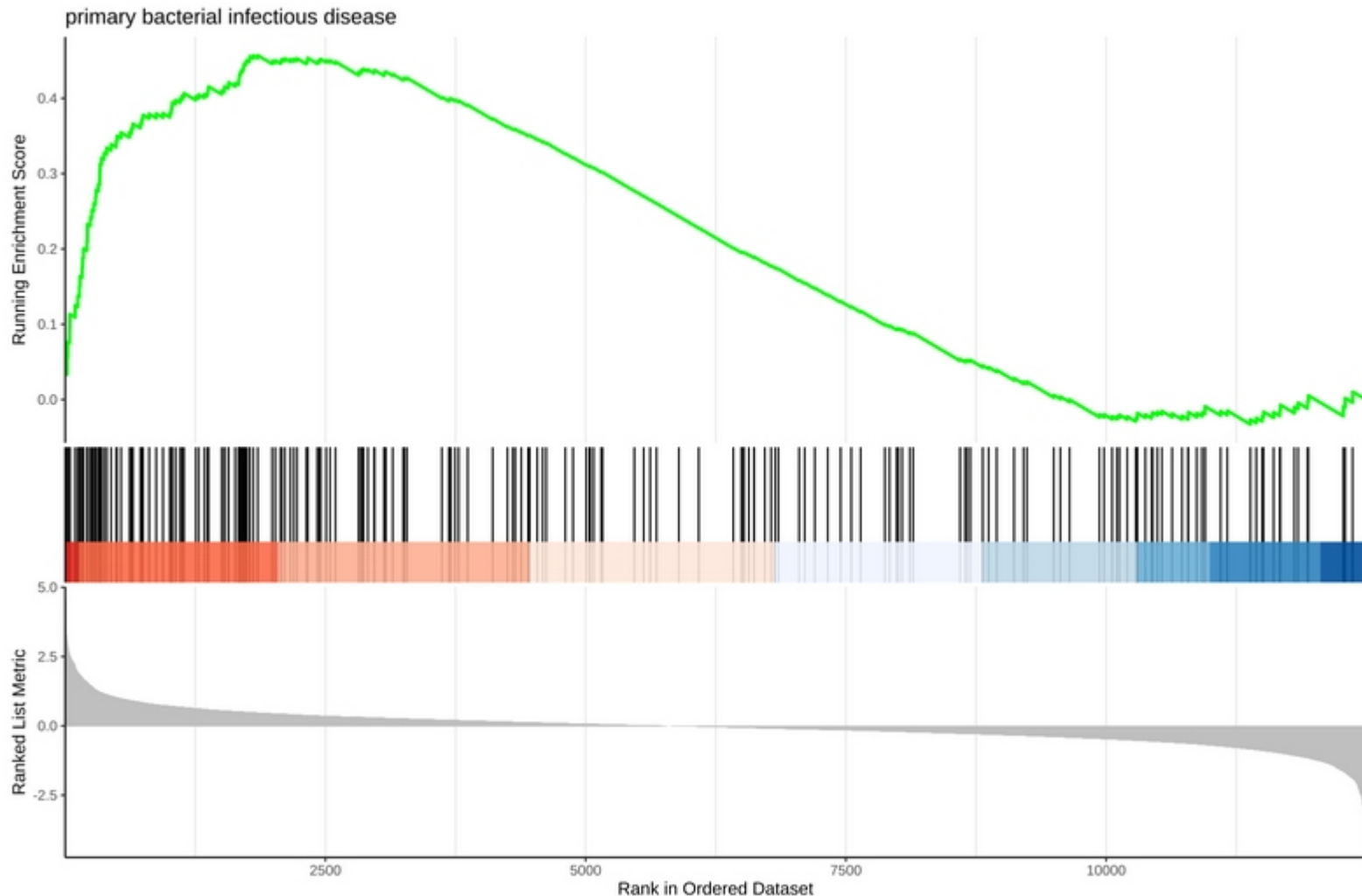
$n = A+C$ # DE genes
 $k = A$ # DE genes in set

$$p = 1 - \sum_{i=0}^{k-1} \frac{\binom{M}{i} \binom{N-M}{n-i}}{\binom{N}{n}}$$

Enrichment analysis – computing enrichment

- **2 possible approaches (among many!)**
- **Gene Set Enrichment Analysis**
 - **Do not rely on 0/1 DE status, but on a continuous measurement (eg. log2FC)**
 - **Computes Enrichment Score from list of ranked genes**
 - **Estimates significance using permutations**

Enrichment analysis – computing enrichment



Enrichment Score visualized using functions from the R package enrichplot

<http://www.bioconductor.org/packages/release/bioc/html/enrichplot.html>

Enrichment analysis – computing enrichment

- **Many more methods or implementations:**

- **Signaling Pathway Impact Analysis**

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

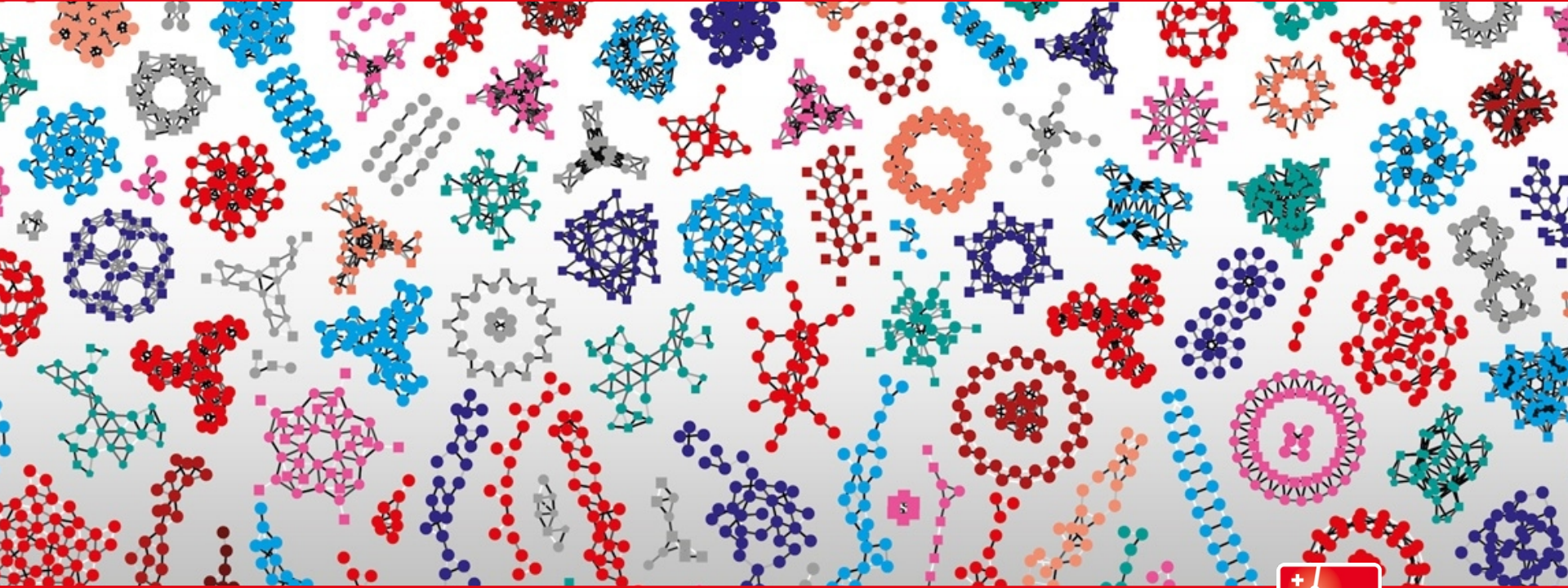
- **ISMARA**

- <https://ismara.unibas.ch/mara/>

- ...

Practical

- **Go to the website and follow the Enrichment practical**



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