

Functional Analysis and Over-representation Analysis (ORA)

- Functional analysis good because ...?
- Pattern matching : two questions
- Over-representation Analysis (ORA) revealed
- Starting from a specific experiment

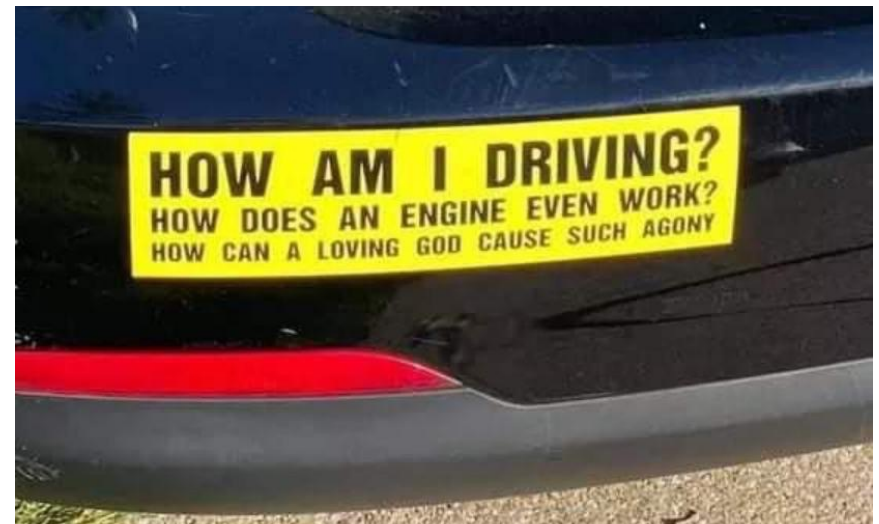
Why do we do functional analysis?

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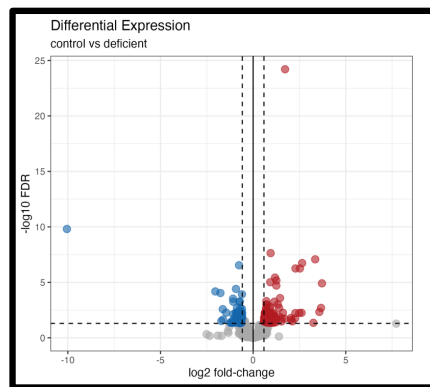
- Well, why do we do differential expression analysis?

~~Why do we do functional analysis?~~

- ~~• Well, why do we do differential expression analysis?~~
 - Wait - why did we run the experiment in the first place?



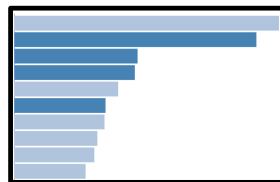
Why do we do functional analysis?



Matches observed DE patterns with biological phenomena

- 1) Connects results to the research question
- 2) Simplifies interpretation
- 3) Reveals coordinated changes across genes
- 4) Enables comparison across DE experiments

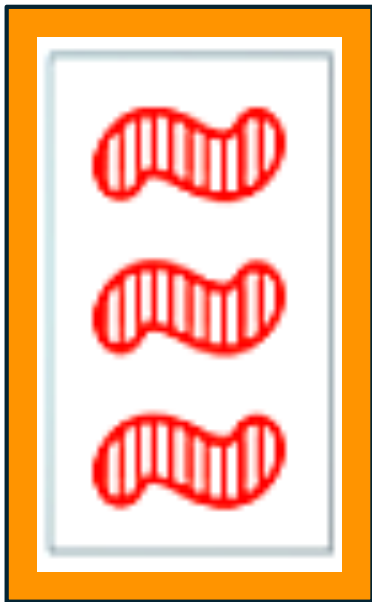
Biological gene set	Enrichment Ratio	P value
DNA mismatch repair	1	1
Aerobic respiration	0.2	0.021
Anaerobic respiration	1.6	0.093
Glycolytic process	3.6	2.51e-12
...		



Functional Analysis matches observed DE patterns with biological phenomena

- Let's do some pattern matching

Pattern matching (1)



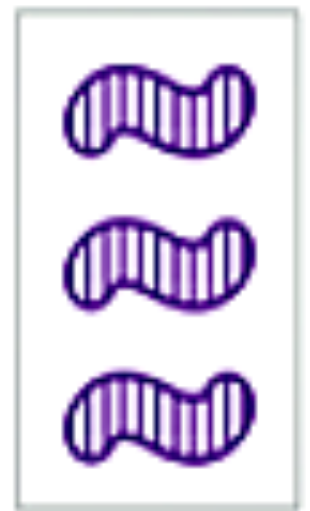
Is my card of interest
related to the other cards?



A

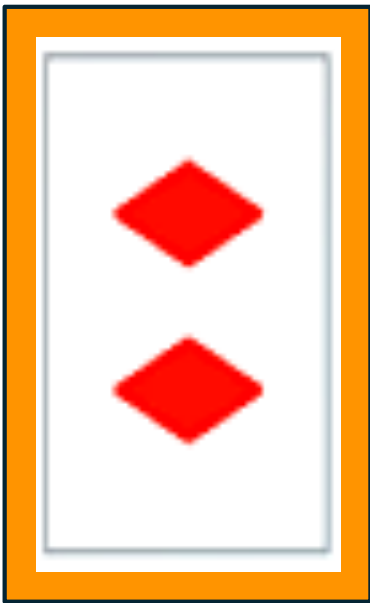


B



C

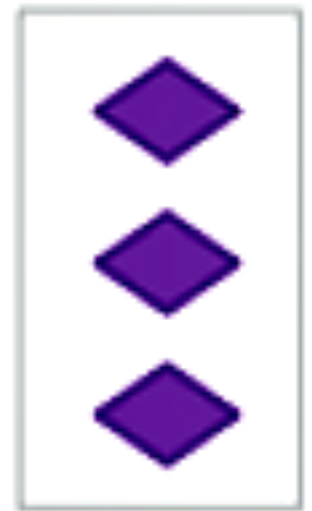
Pattern matching (2)



A

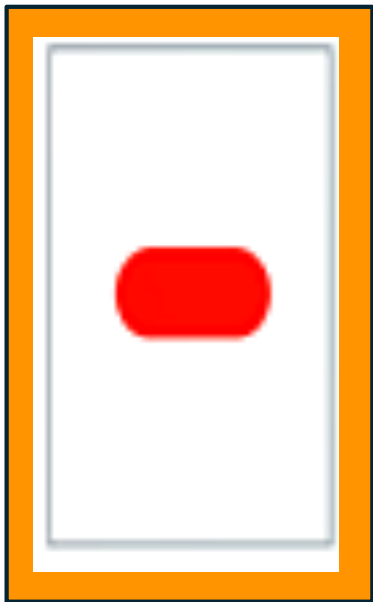


B



C

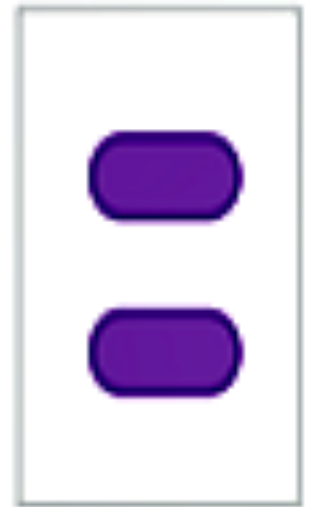
Pattern matching (3)



A

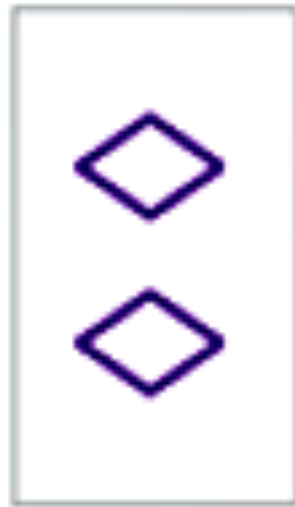


B



C

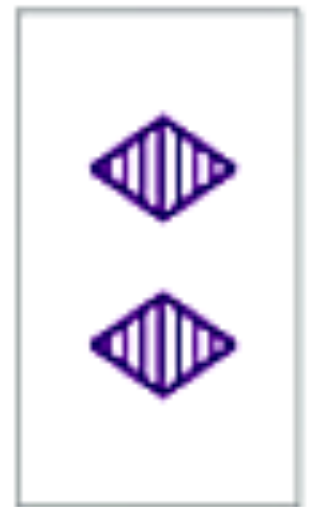
Pattern matching (4)



A

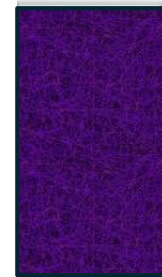
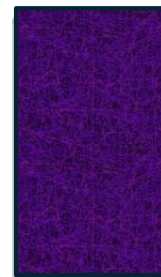
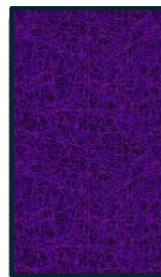
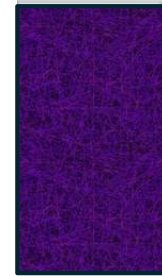
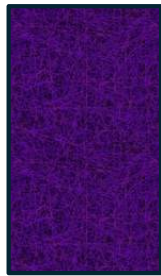
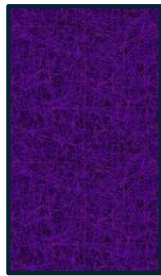
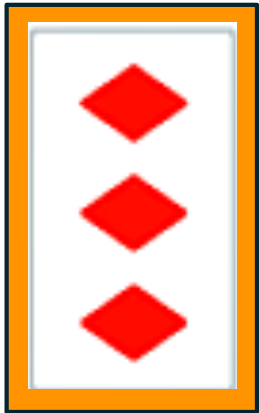


B

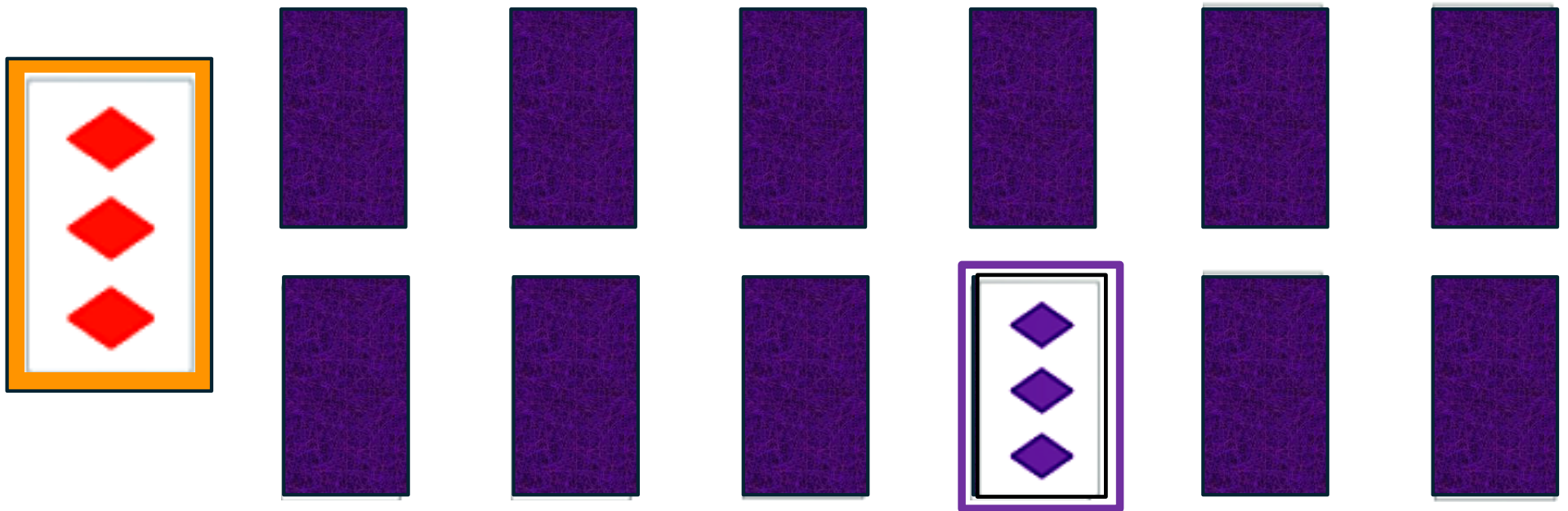


C

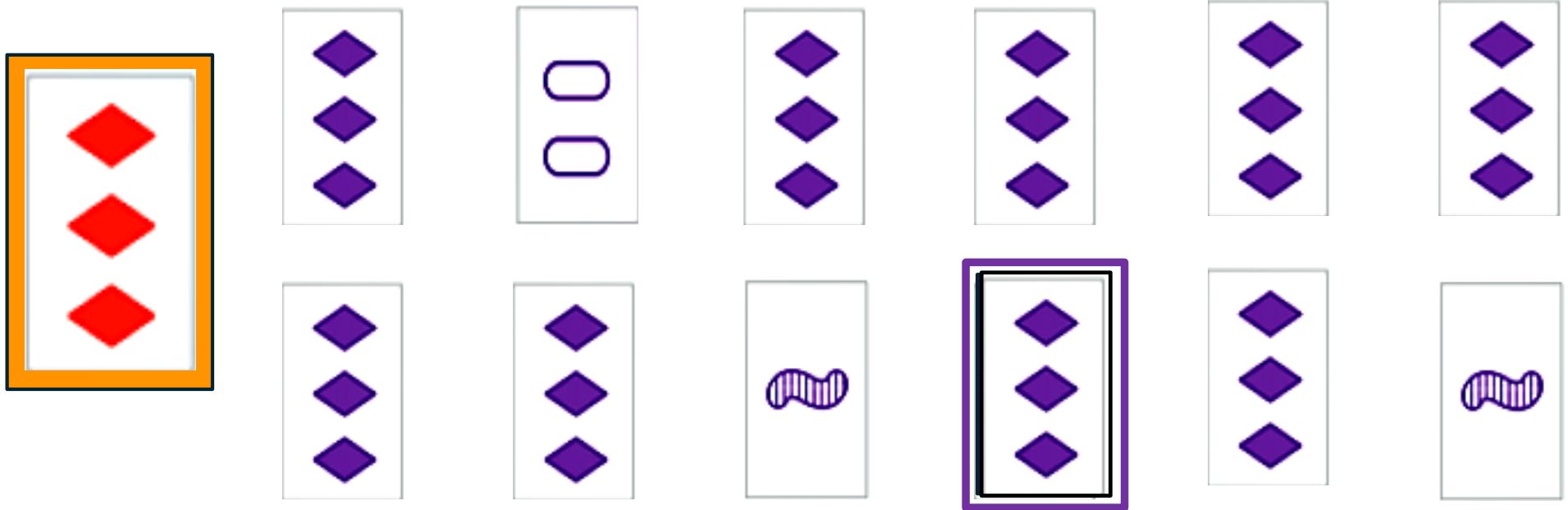
Pattern matching (5)



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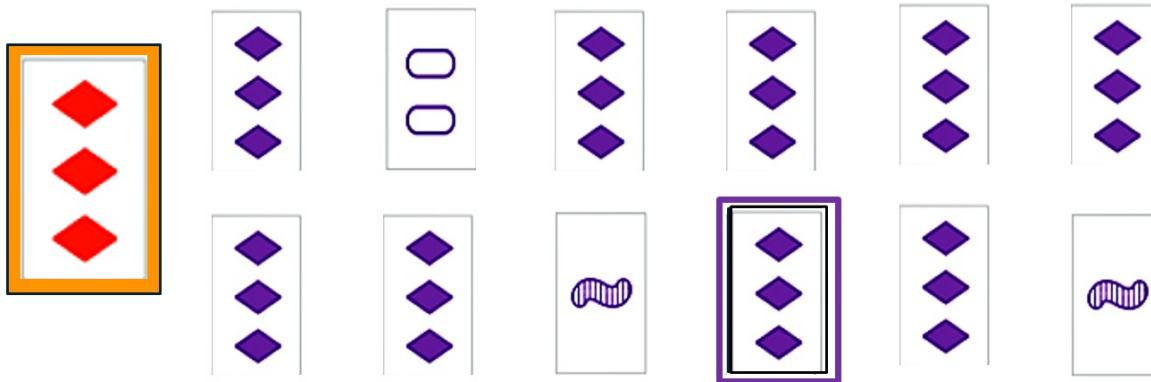


Pattern matching (5)



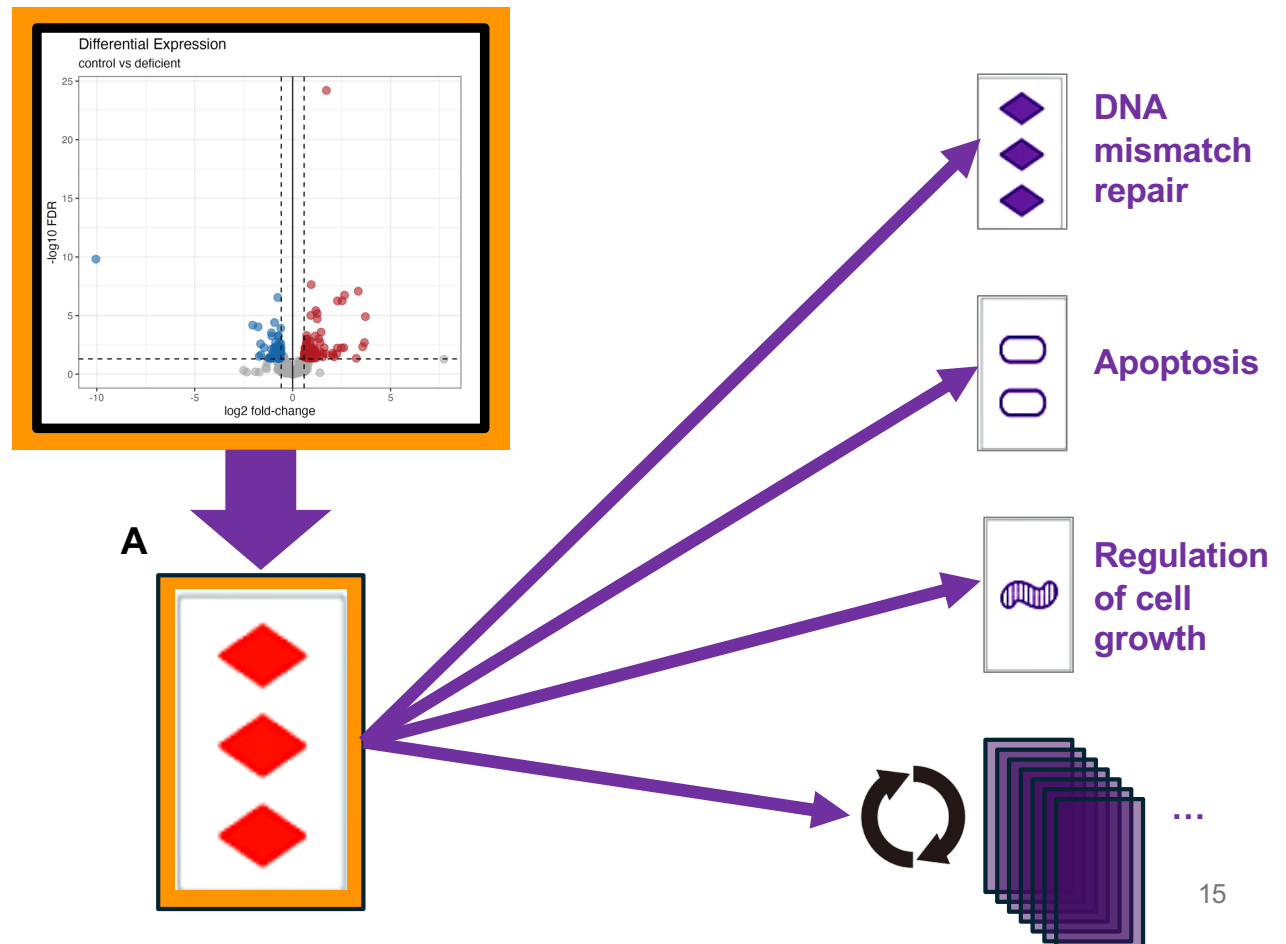
Pattern matching: Two questions

- 1) Is my card of interest related to the other cards?
- 2) How surprising is that relationship?



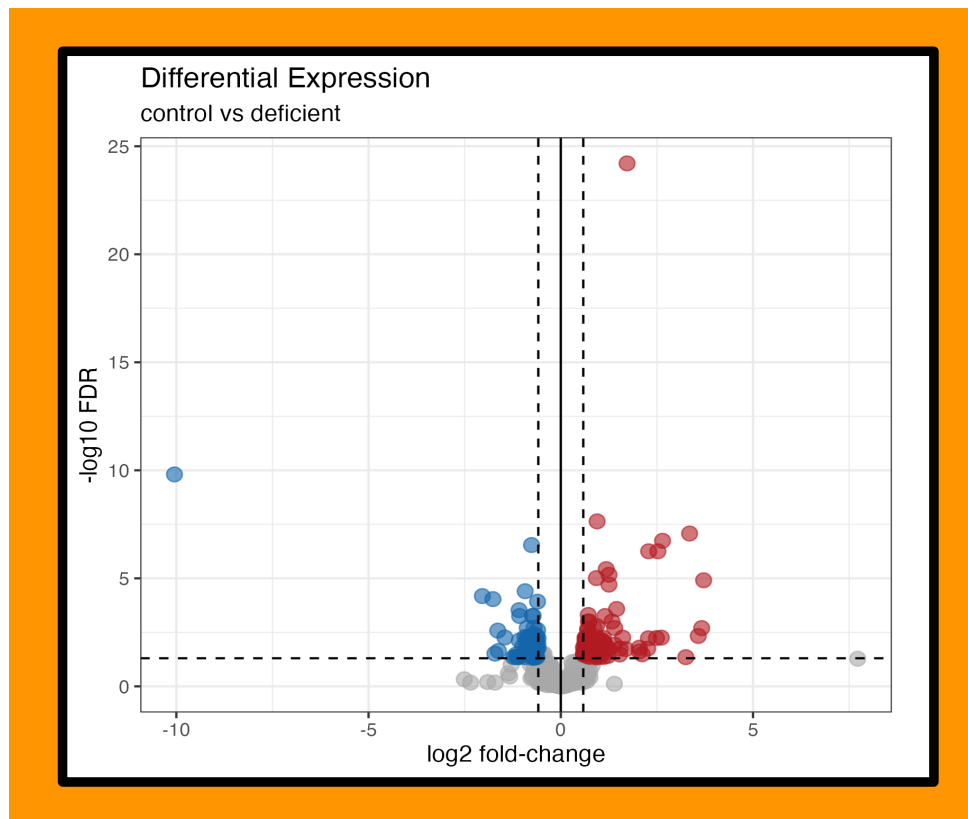
Functional Analysis is pattern matching

- 1) Are my **DE genes of interest** related to the other **biological gene sets**?
- 2) How surprising is that relationship?



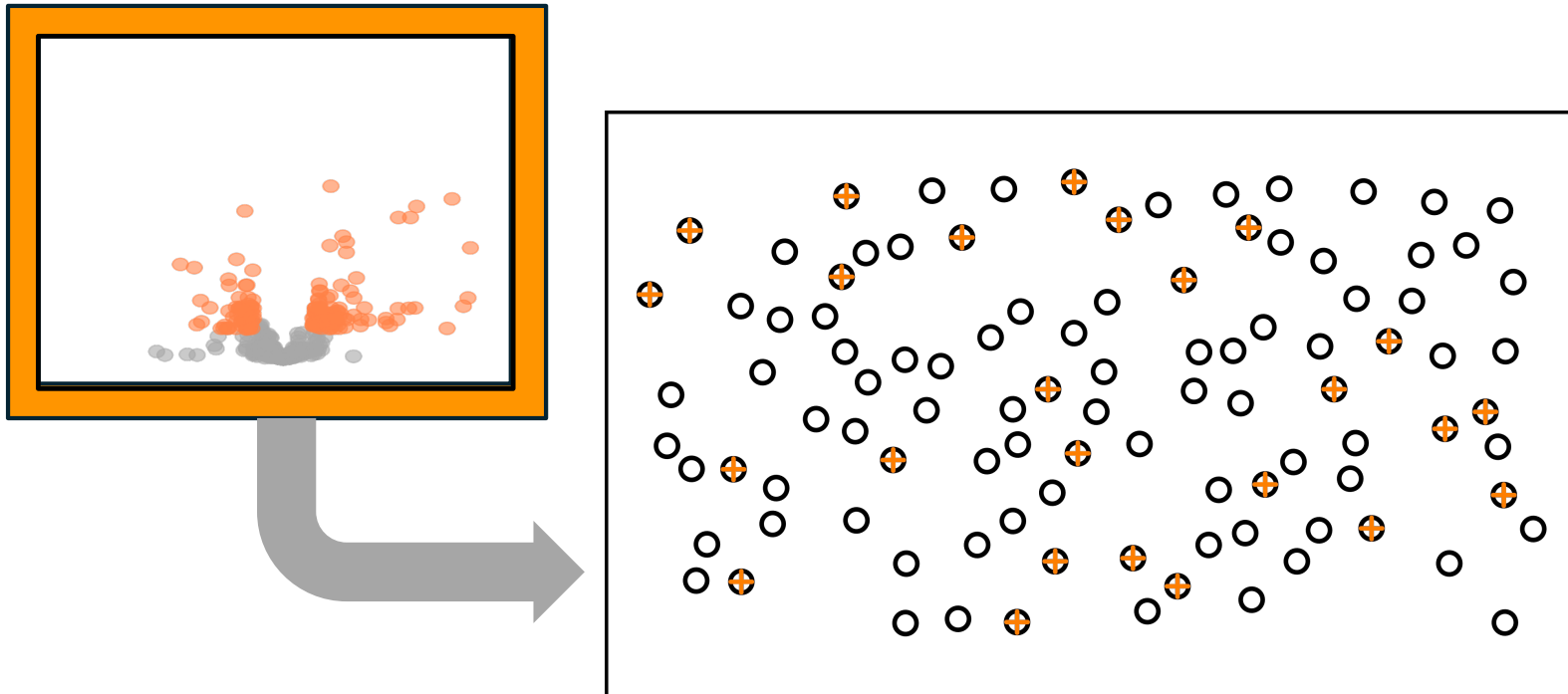
Over-representation Analysis (ORA)

Step 1: Transform observed DE pattern

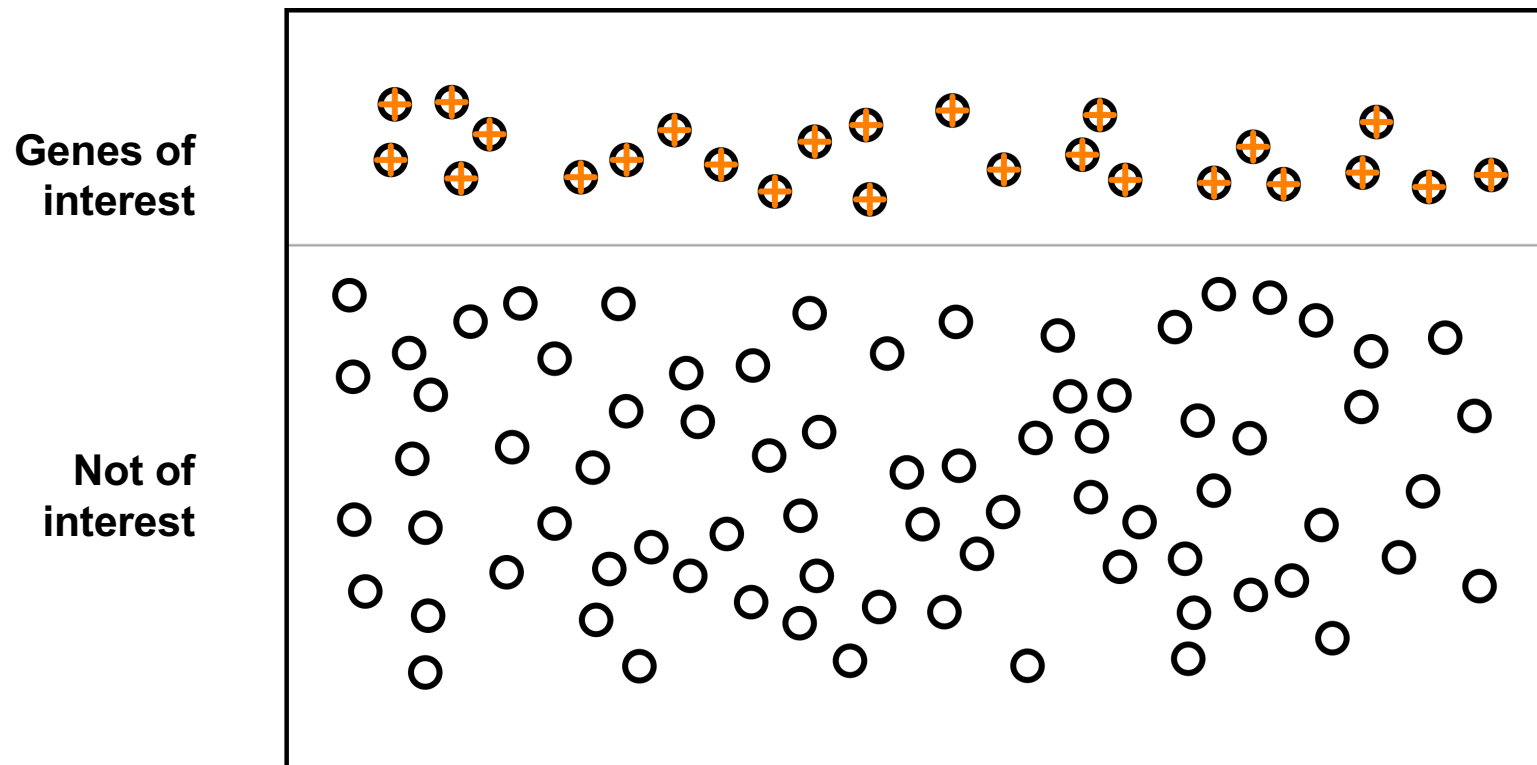


ORA: Transform observed DE pattern

- A) Mark DE genes (aka “interesting genes”).
- B) Dump all genes in a box



Float genes of interest to the top

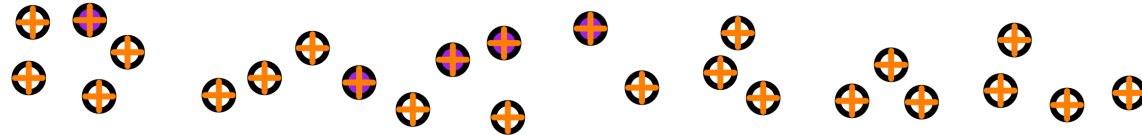


DNA mismatch
repair

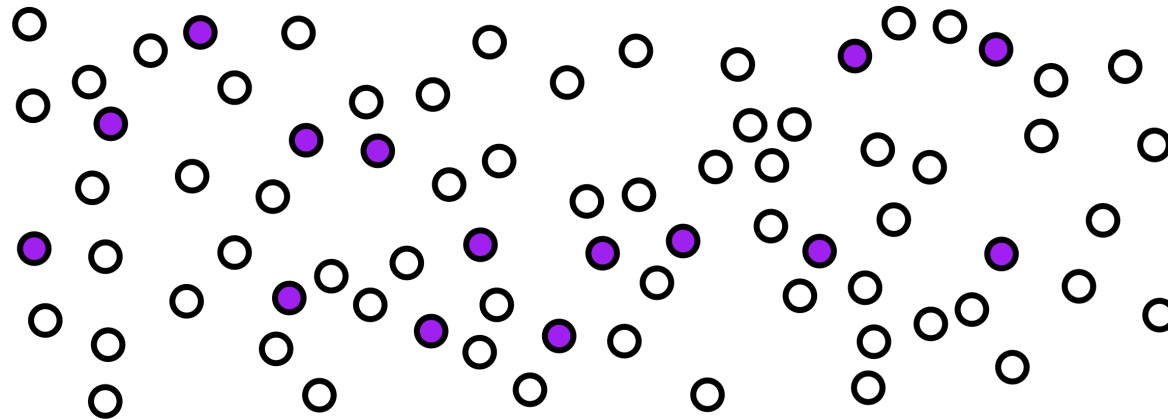


Mark a **biological gene set**

Genes of
interest



Not of
interest



DNA mismatch
repair



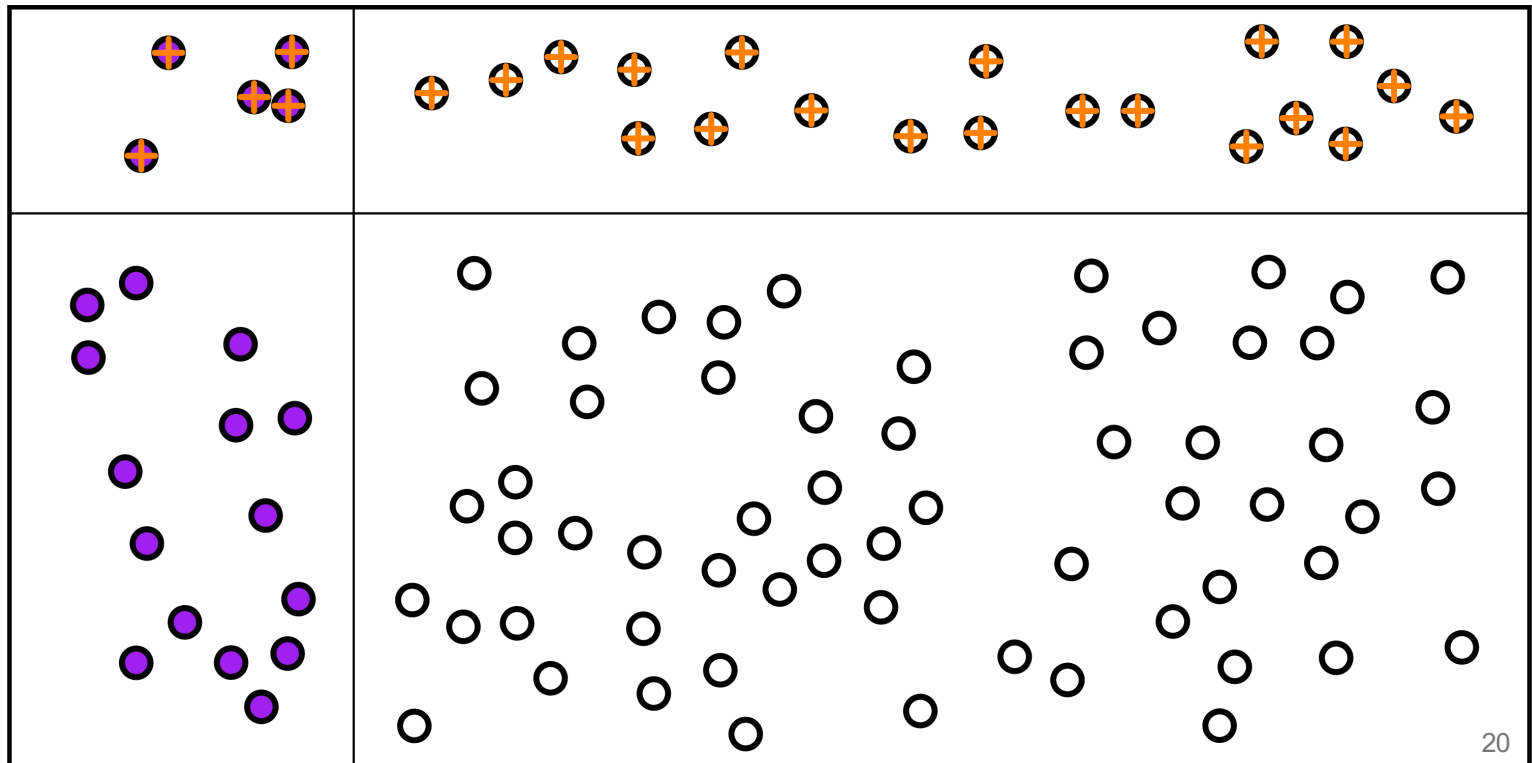
Slide bio gene set left

In biological
gene set

Not in biological
gene set

Gene set
of interest

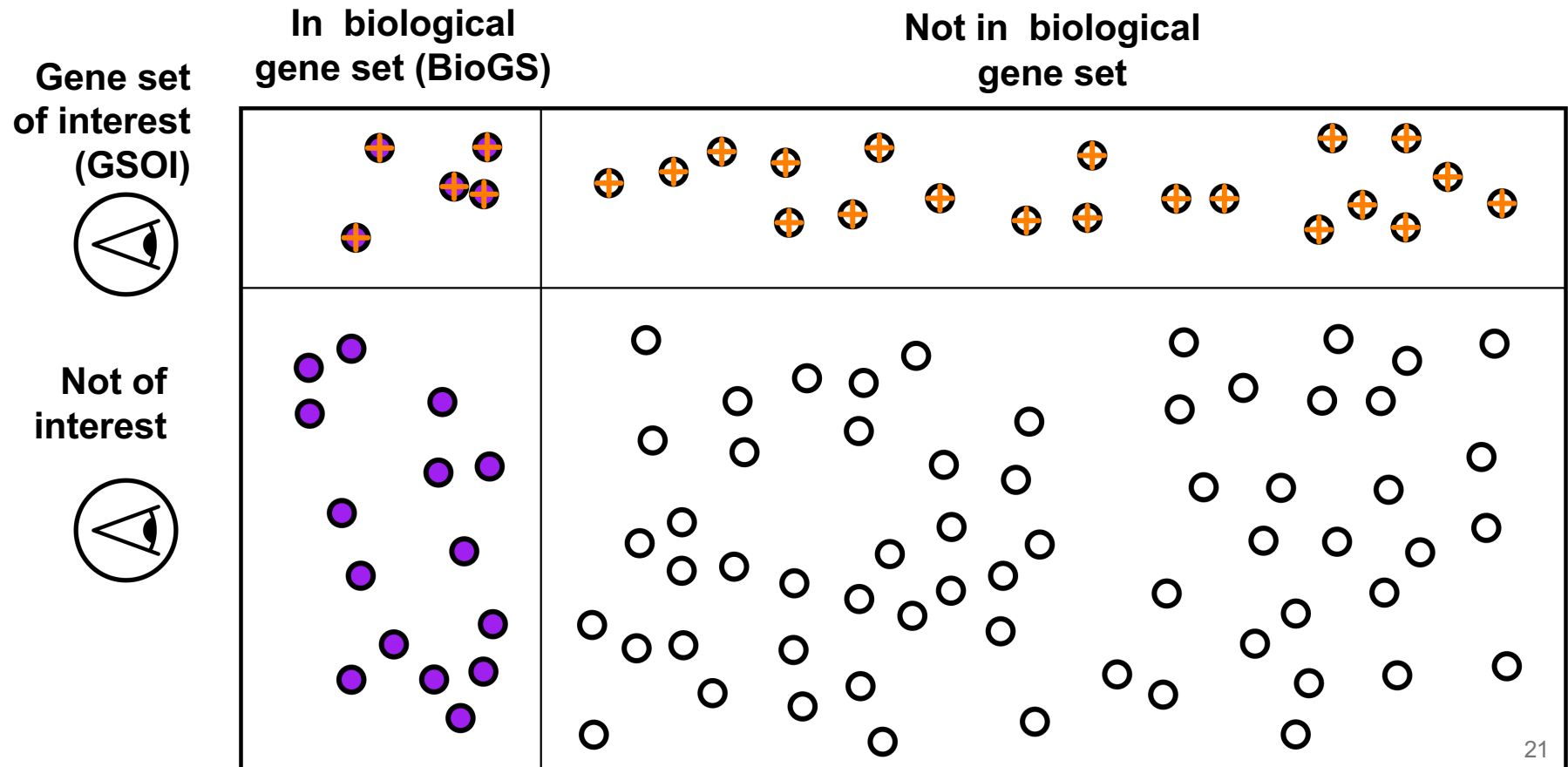
Not of
interest



DNA mismatch
repair



GSOI related to Bio GS? (1)



Glycolytic
process

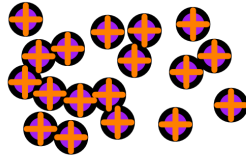


GSOI related to Bio GS? (2)

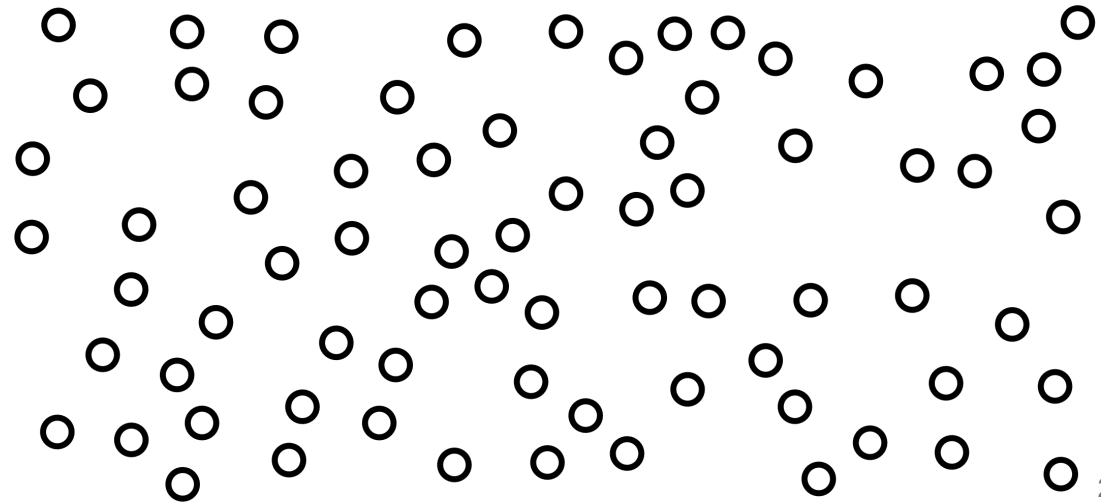
In biological
gene set

Not in biological
gene set

Gene set
of interest



Not of
interest



Aerobic
respiration



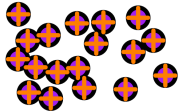


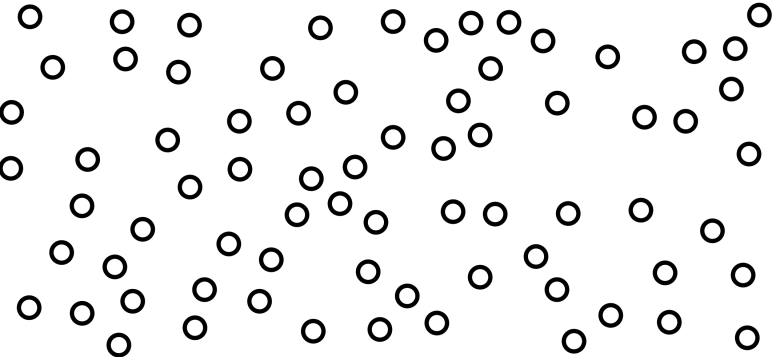
GSOI related to Bio GS? (3)

	In biological gene set	Not in biological gene set
Gene set of interest		
Not of interest		

ORA is based on 4 numbers

Glycolytic process



	18 In biological gene set	Not in biological gene set	7
Gene set of interest			
Other genes			
	2		73

4 numbers (aka “Contingency table”)

Glycolytic process			
	In biological gene set	Not in biological gene set	Total
Genes of interest	18	7	25
Not of interest	2	73	75
Total	20	80	100

What's the expected proportion?



Glycolytic process			
	In biological gene set	Not in biological gene set	Total
Genes of interest	18	7	25
Not of interest	2	73	75
Total	20	80	100

	Proportion	Count
Expected	$20 / 100 = 0.20$	$0.20 * 25 = 5$

What's the observed proportion?



Glycolytic process			
	In biological gene set	Not in biological gene set	Total
Genes of interest	18	7	25
Not of interest	2	73	75
Total	20	80	100

	Proportion	Count
Expected	$20 / 100 = 0.20$	$0.2 * 25 = 5$
Observed	$18 / 25 = 0.72$	18

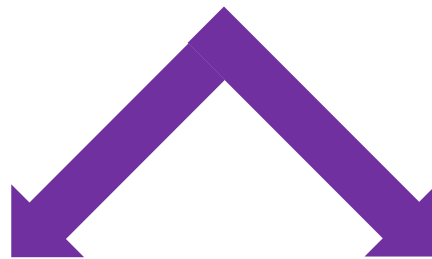
Enrichment Ratio = Observed/Expected

Glycolytic process			
	In biological gene set	Not in biological gene set	Total
Genes of interest	18	7	25
Not of interest	2	73	75
Total	20	80	100

	Proportion	Count
Expected	$20 / 100 = 0.20$	$0.2 * 25 = 5$
Observed	$18 / 25 = 0.72$	18
Enrichment Ratio	$0.72 / 0.20 = 3.6$	

Enrichment Ratio and p value

Glycolytic process			
	In biological gene set	Not in biological gene set	Total
Genes of interest	18 a	7 b	25
Not of interest	2 c	73 d	75
Total	20	80	100 n



Fisher's exact test

$$p = \frac{\binom{a+b}{a} \binom{c+d}{c}}{\binom{n}{a+c}}$$

Enrichment Ratio = 3.6

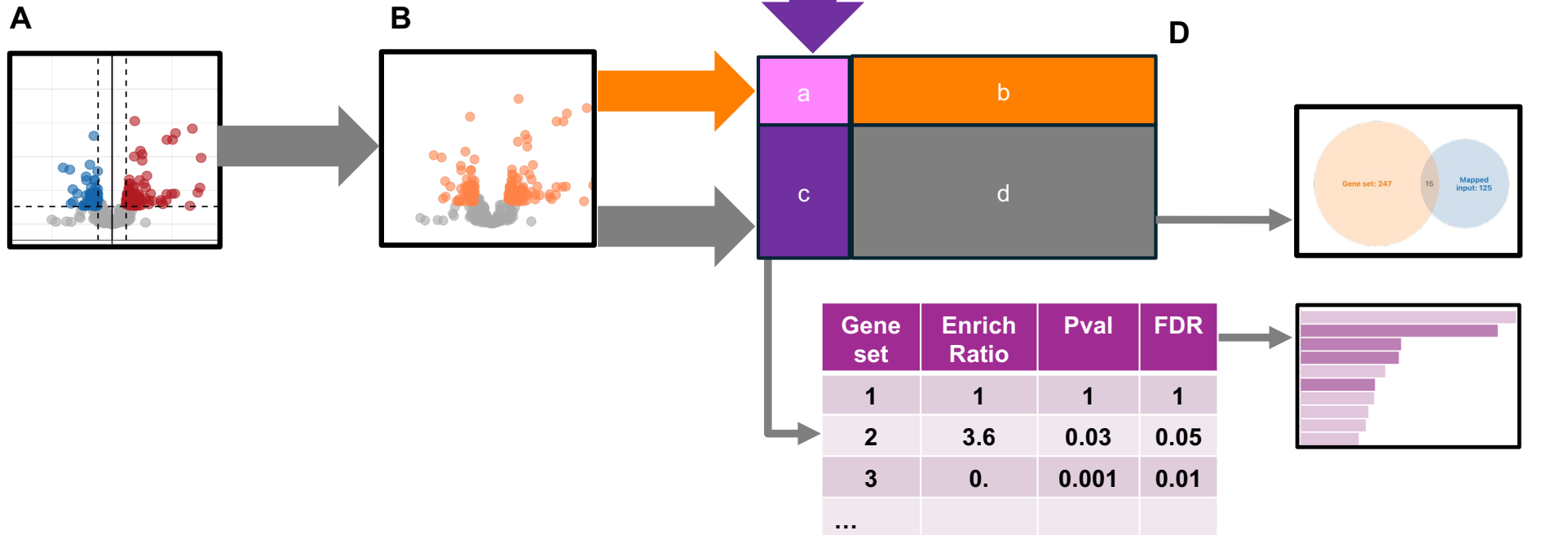
Are my genes of interest related to another other biological gene set?

p value = 2.51e-12

How surprising is that relationship?

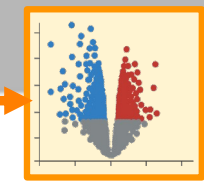
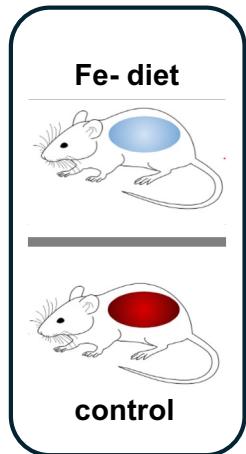
ORA Overview

- 1) Are my genes of interest related to the other biological gene sets?
- 2) How surprising is that relationship?

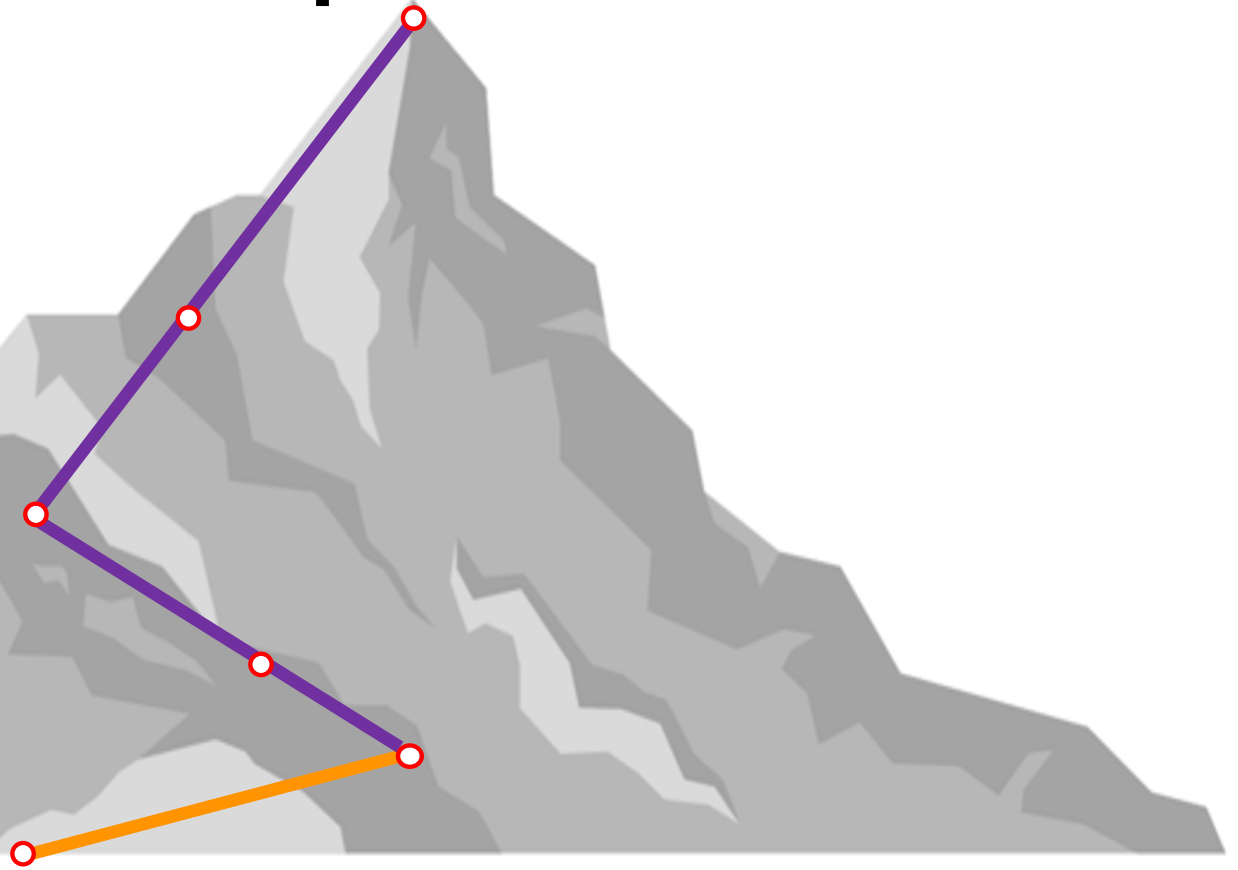


Consider a specific experiment

Over-representation Analysis (ORA)



Bulk RNA-Seq



Summary

Over-representation Analysis (ORA)



Functional analysis connects your expression patterns with known biological phenomena.

Over-representation Analysis (ORA)

1) Are my DE genes of interest related to the other biological gene sets?

2) How surprising is that relationship?

We will start from a bulk-RNA Seq using ORA on WebGestalt.

