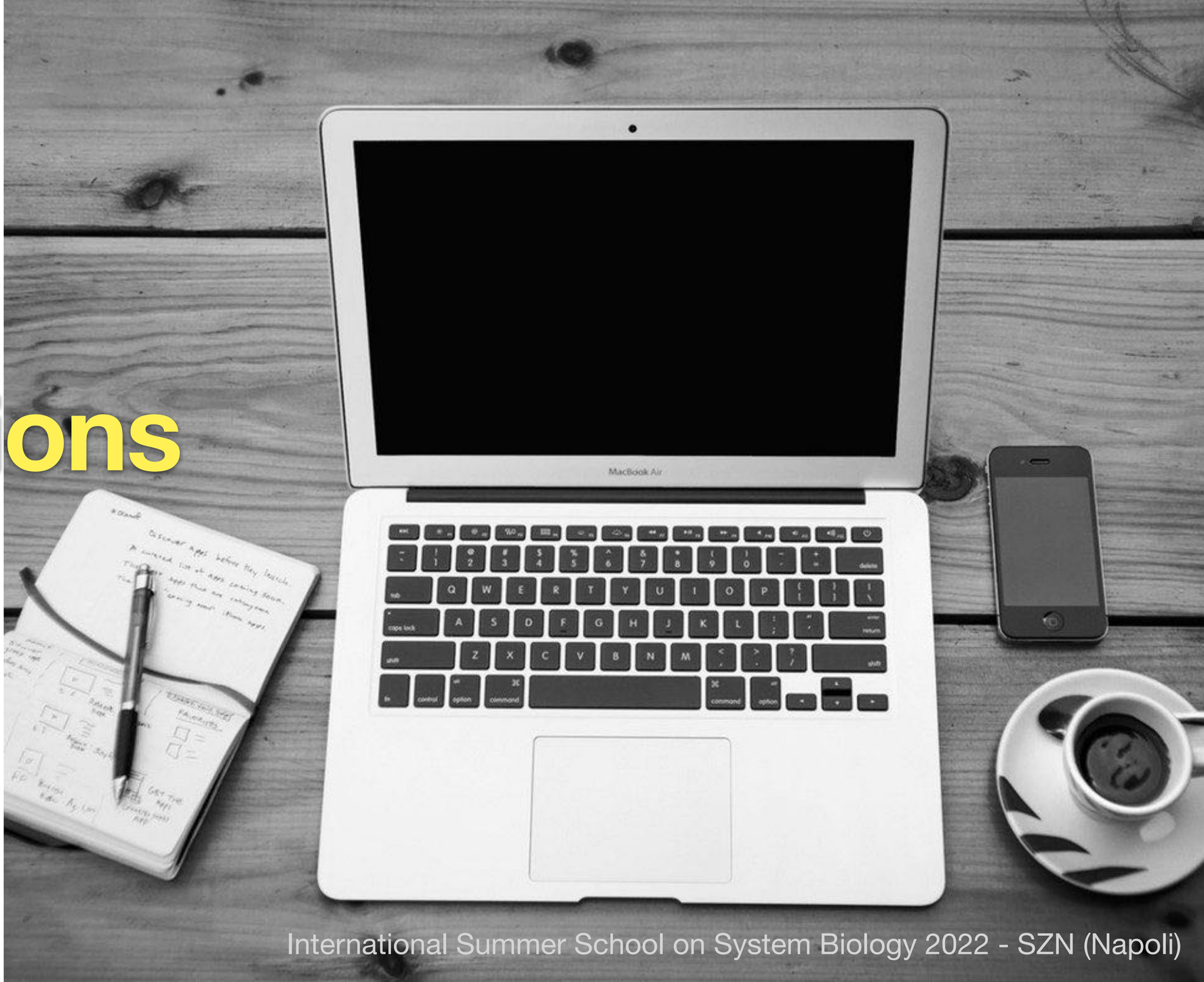
UNIVERSITÀ DEGLI STUDI
DEL SANNIO Benevento
DST
DIPARTIMENTO DI
SCIENZE E TECNOLOGIE

Lab sessions

Applications

- **Differential expression**
- **Promoter analysis**
- **Master Regulator**



Research involving in-silico analysis

Classical workflows

Biological Hypothesis supported by in-silico analyses

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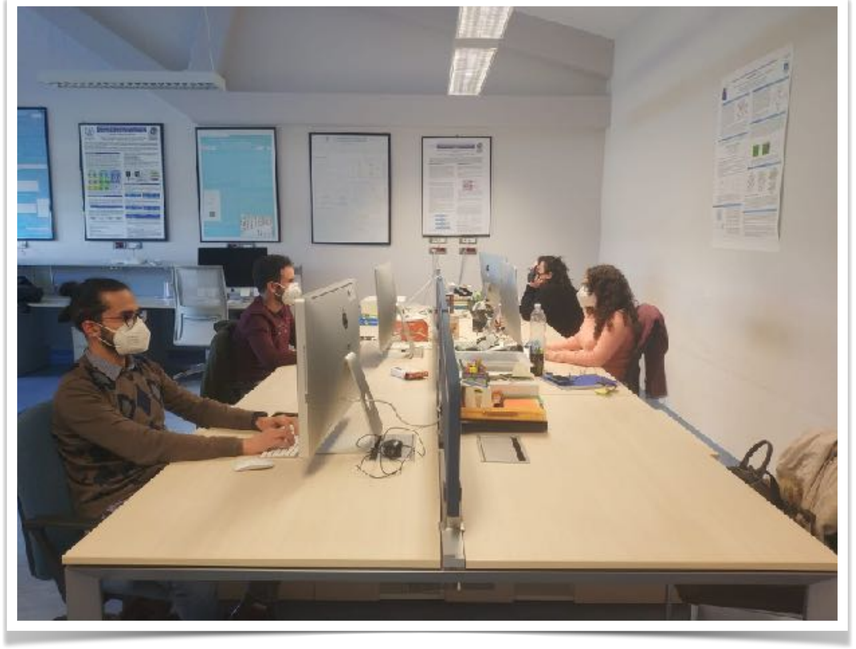

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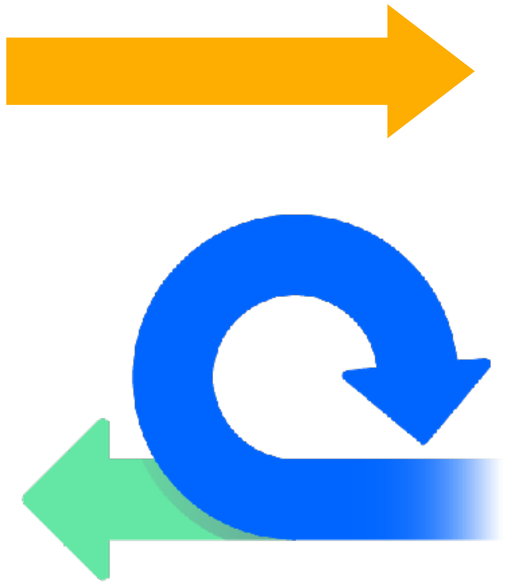
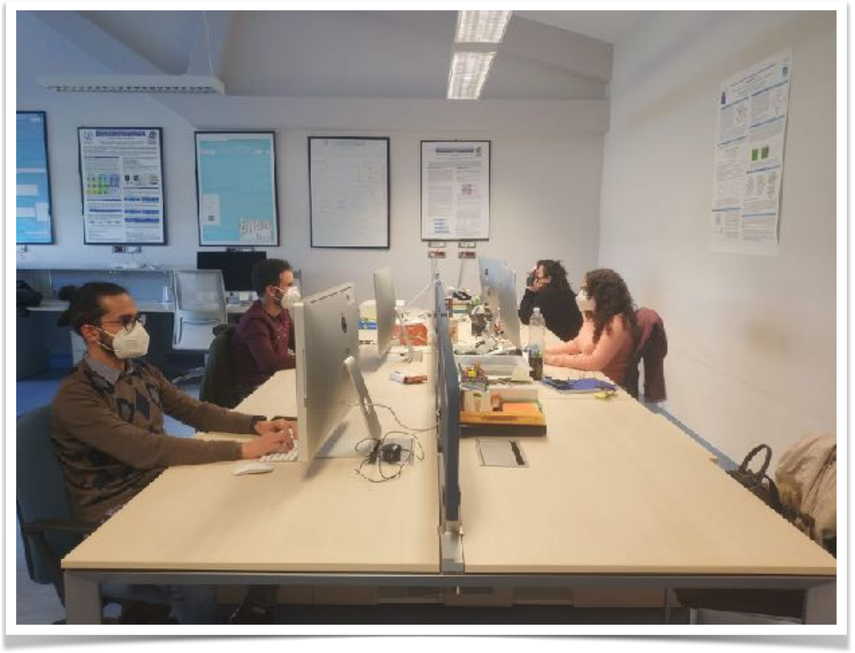
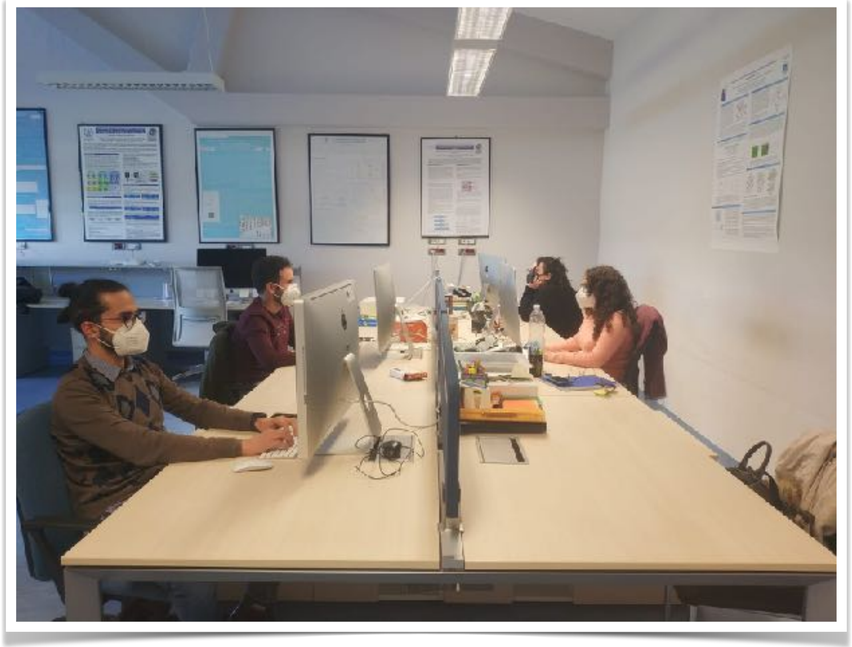




Research involving in-silico analysis

Classical workflows

In-silico Hypothesis tested in wet Lab



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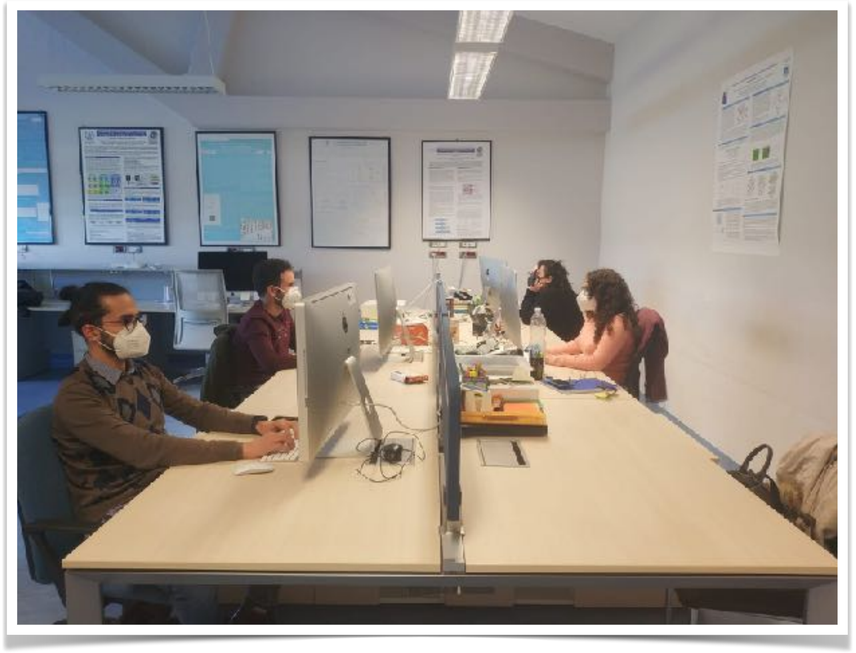

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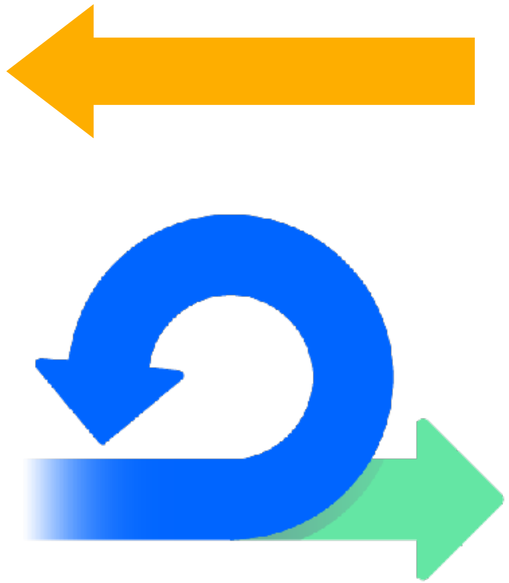
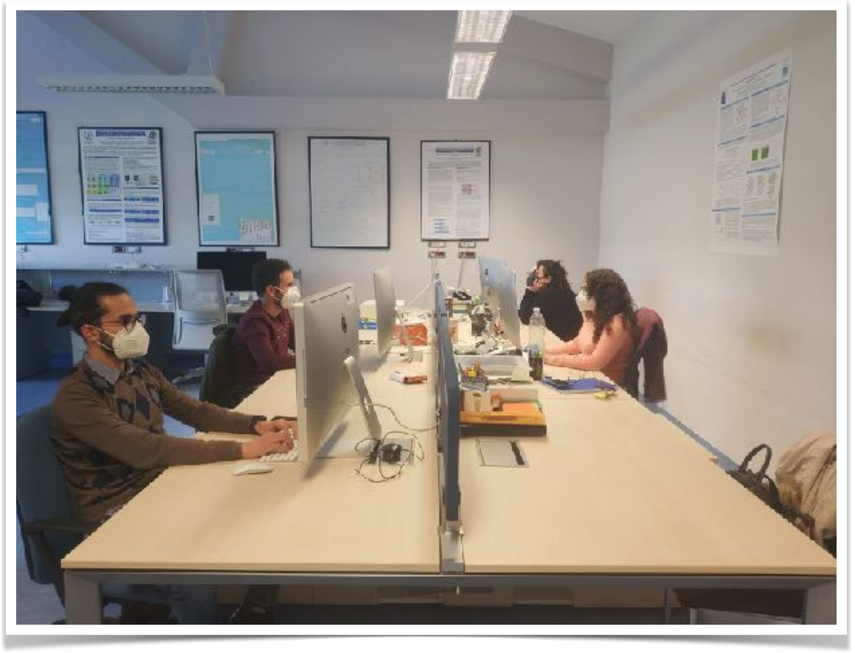


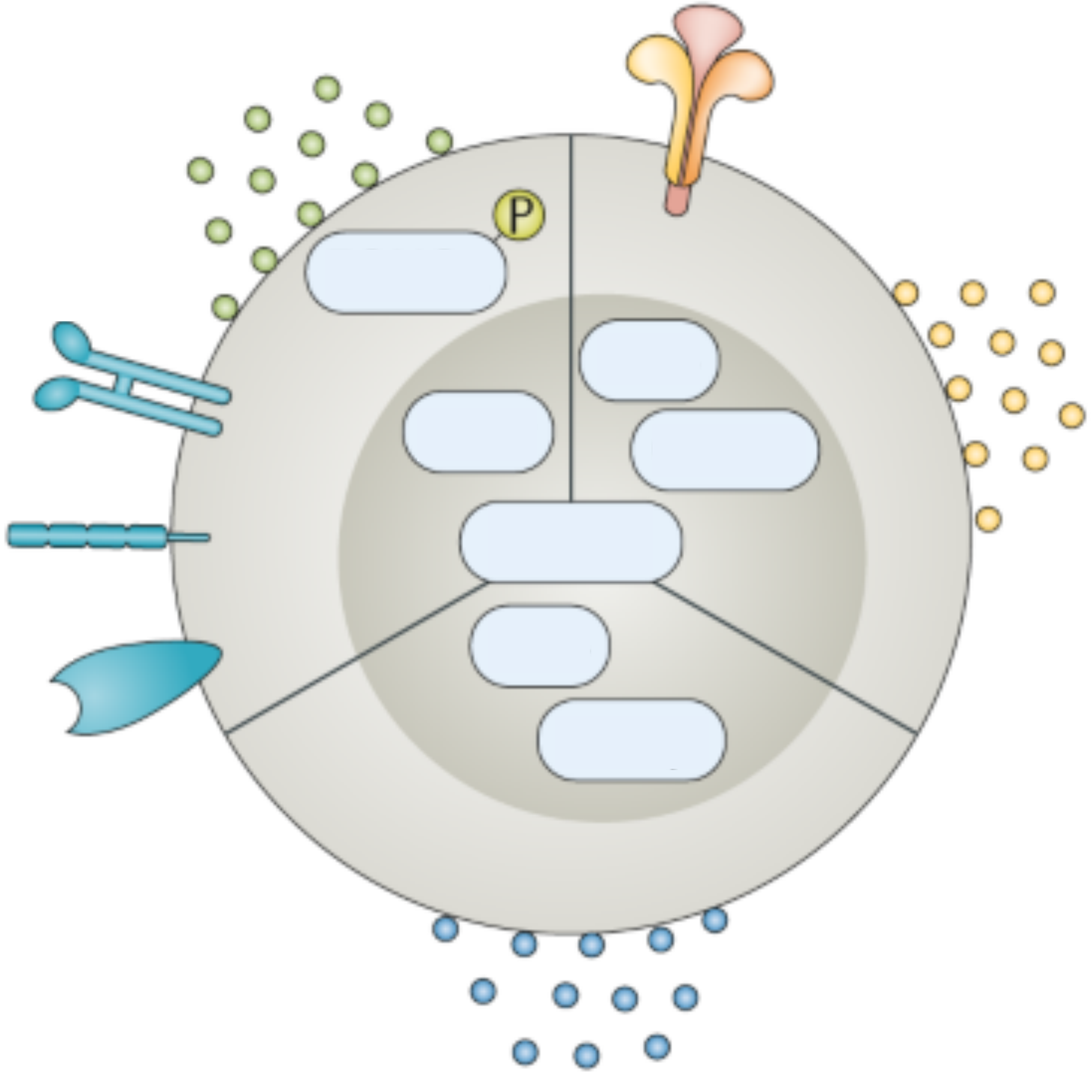


Research involving in-silico analysis

Integrating wet and dry labs

Dissect unknown molecular mechanisms

Typical workflow



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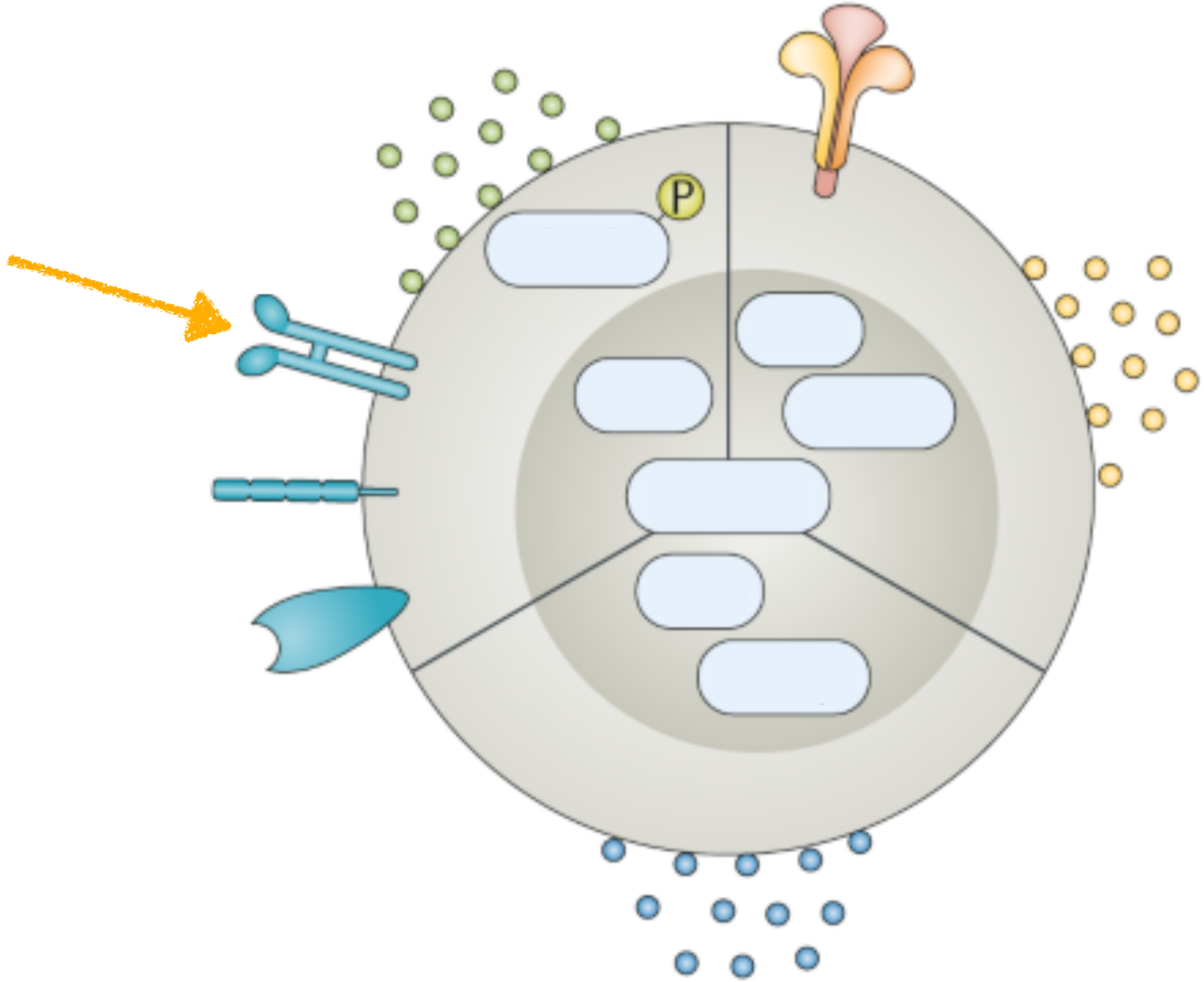

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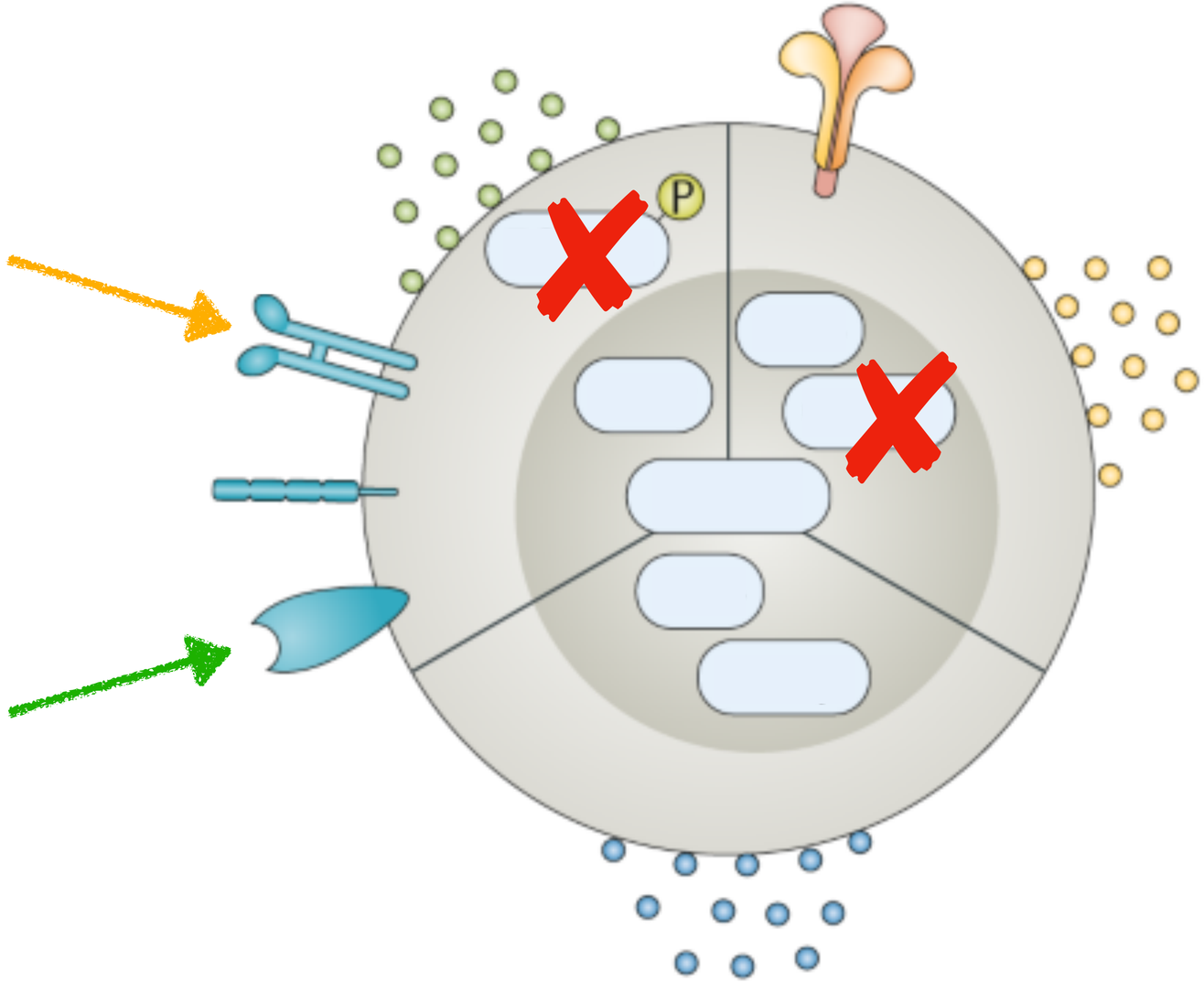

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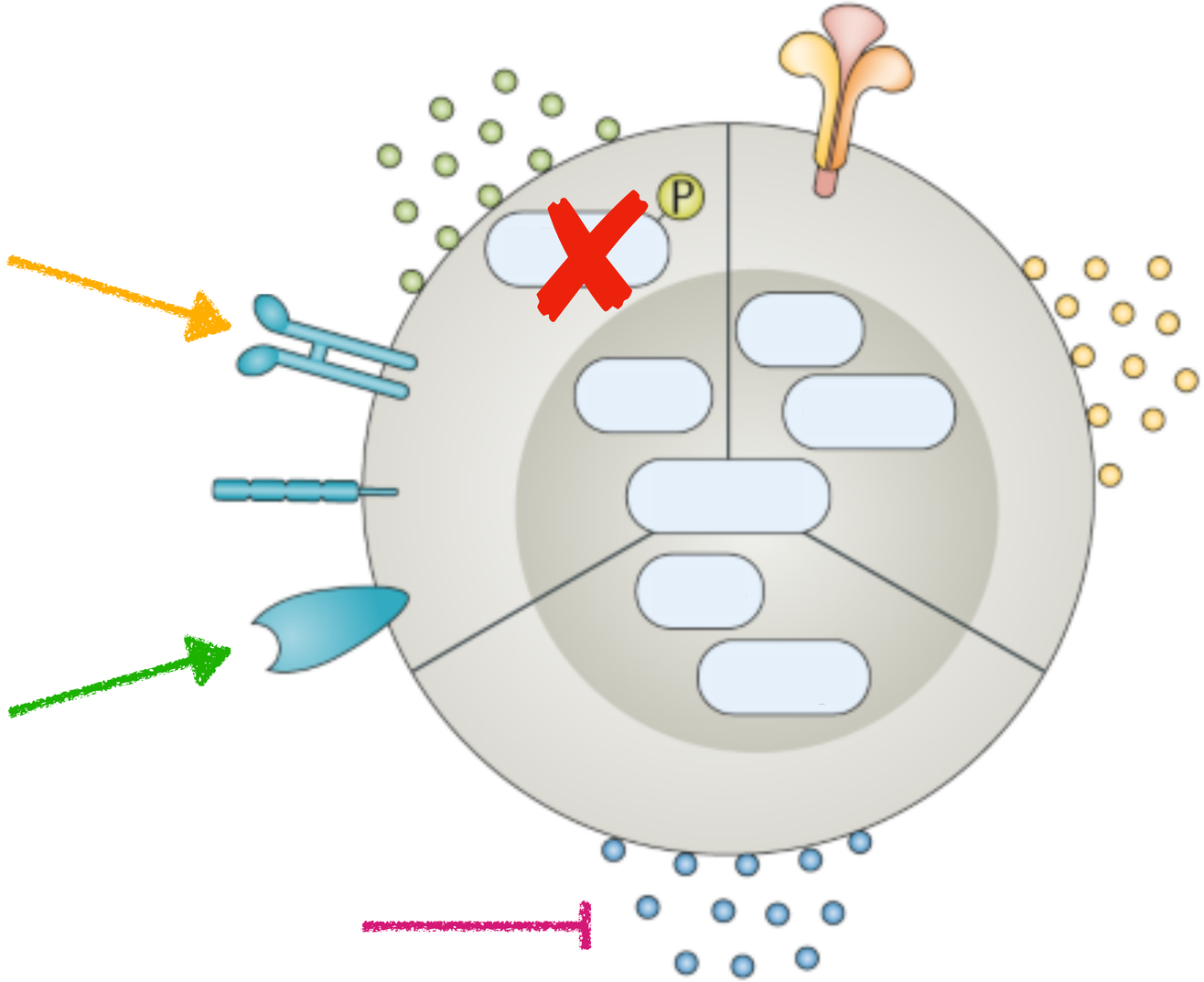

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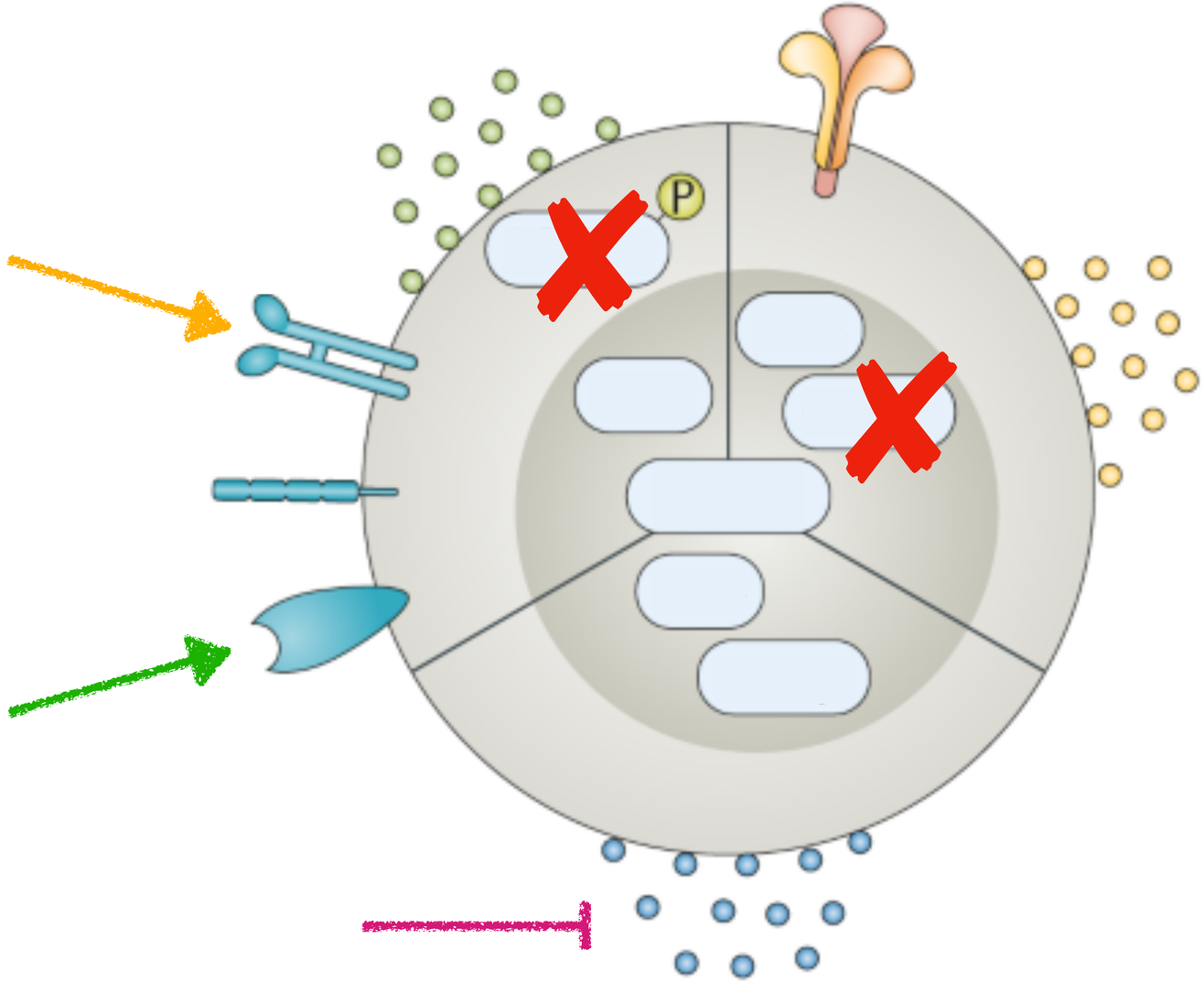

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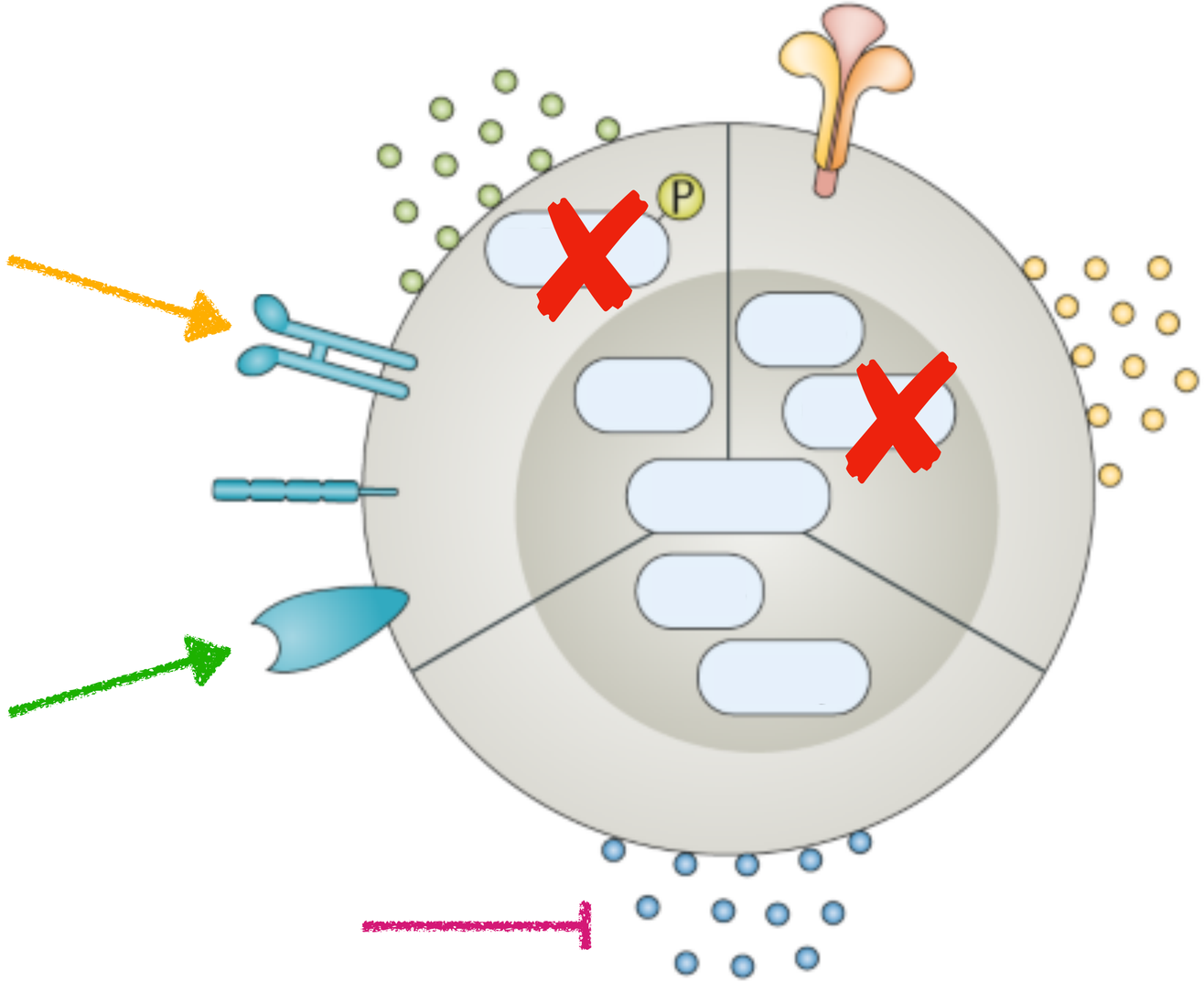

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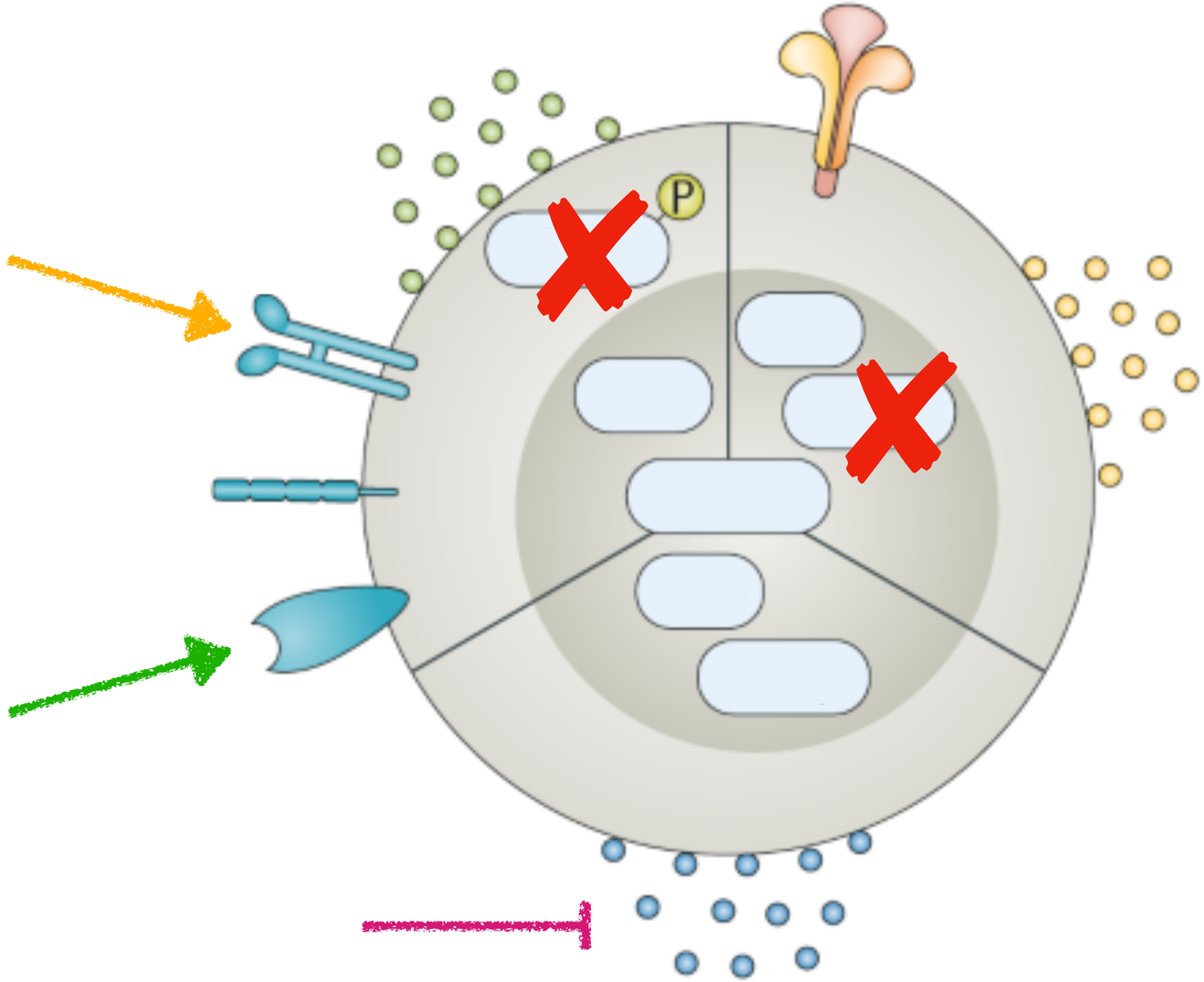
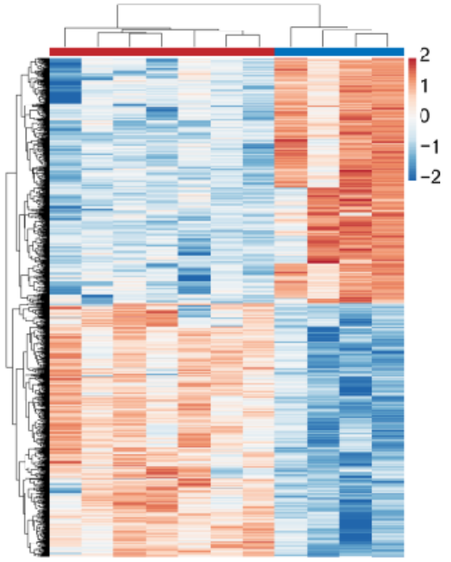
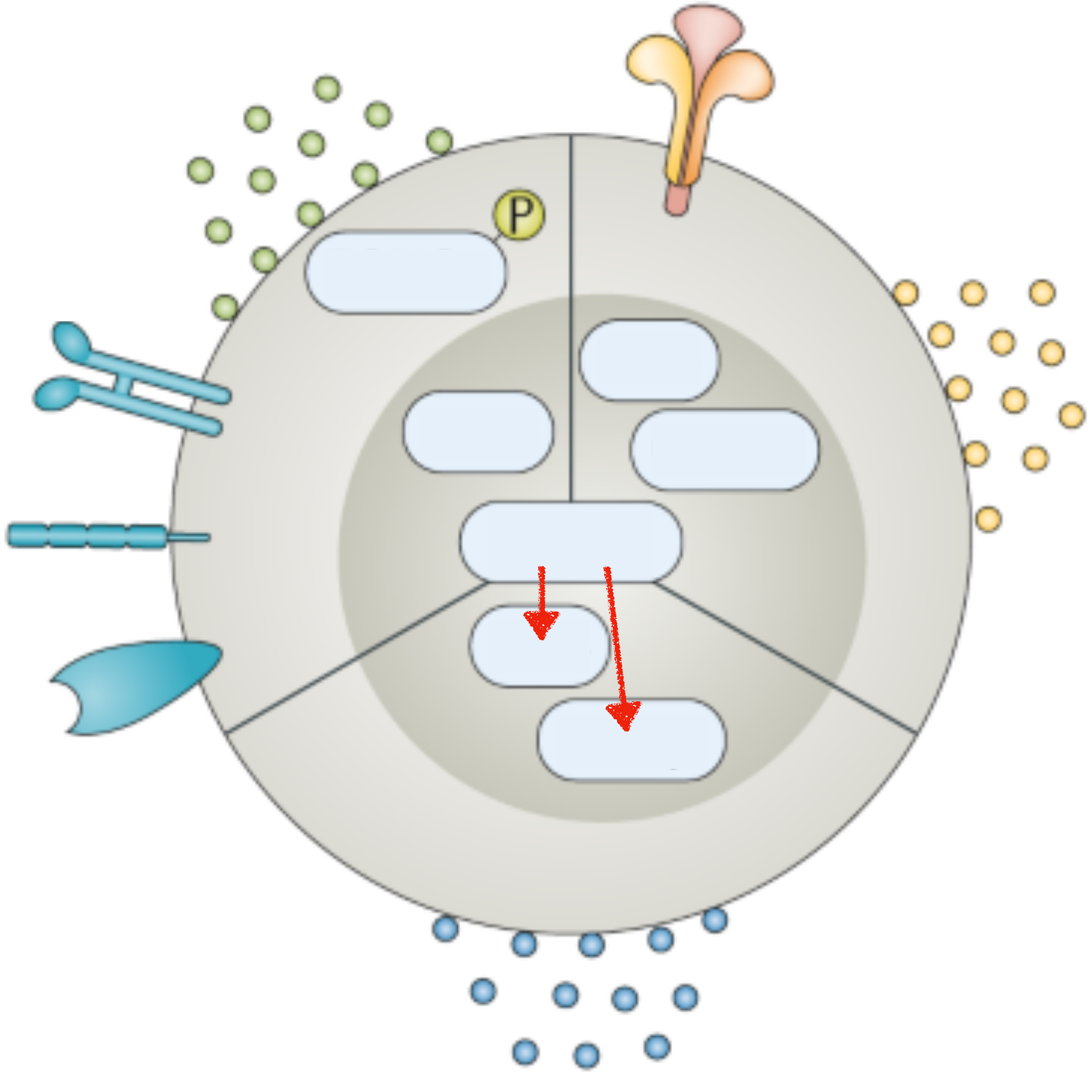


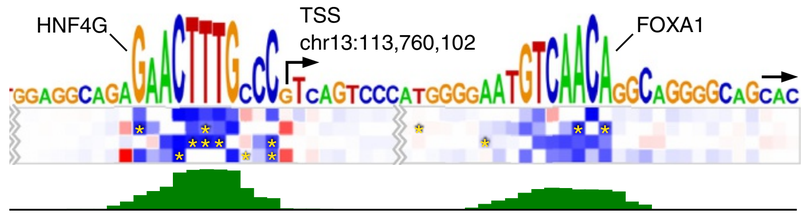


Differential expression Analysis

Dissect unknown molecular mechanisms

Typical workflow





Promoter Analysis

Dissect unknown molecular mechanisms

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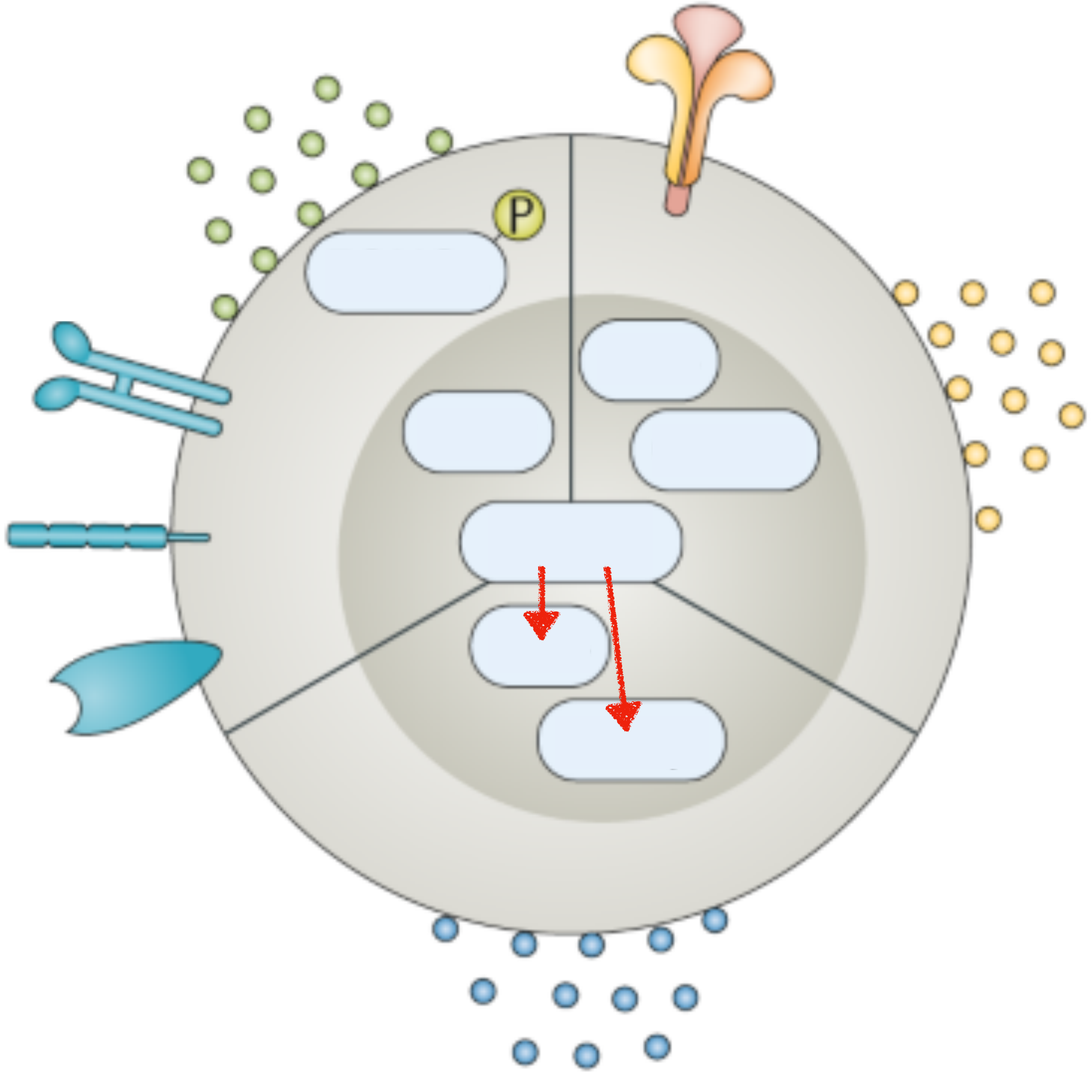
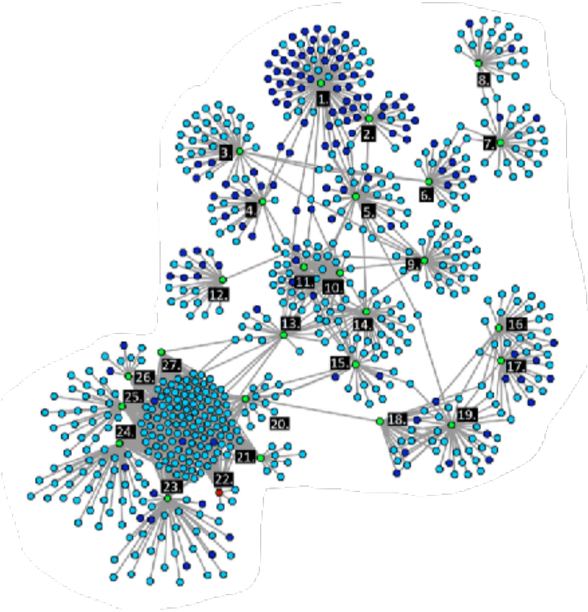
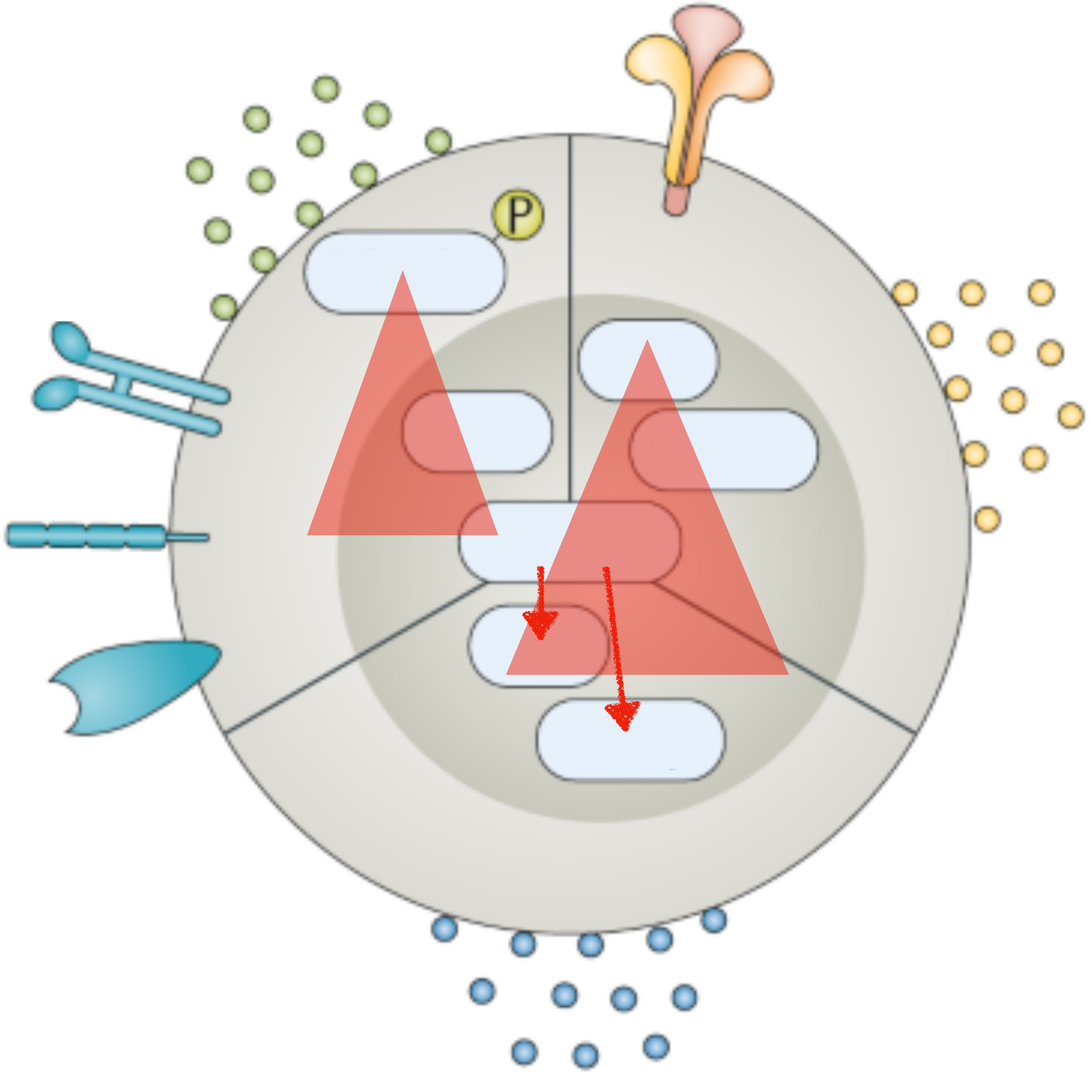


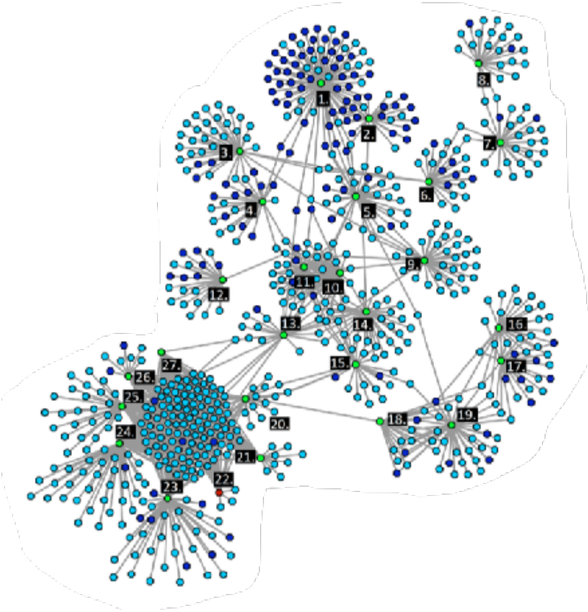


Master Regulator Analysis

Dissect unknown molecular mechanisms

Typical workflow





Master Regulator Analysis

Dissect unknown molecular mechanisms

Master regulator analysis

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Master regulator analysis

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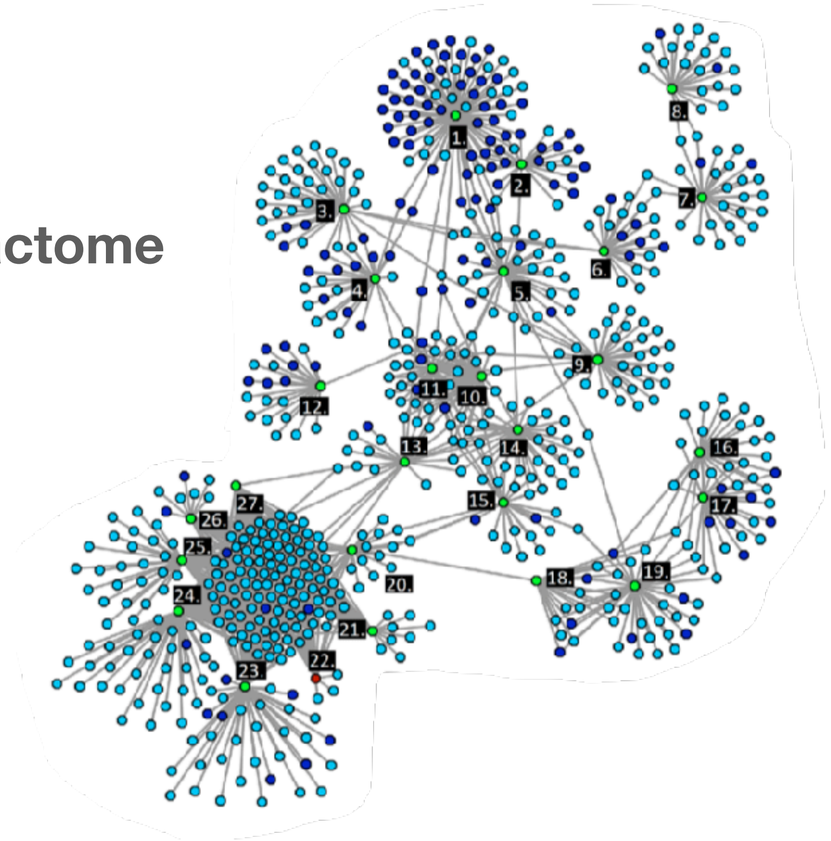
Interactome



Dissect unknown molecular mechanisms

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Or adopt a known static network (e.g. from STRING)

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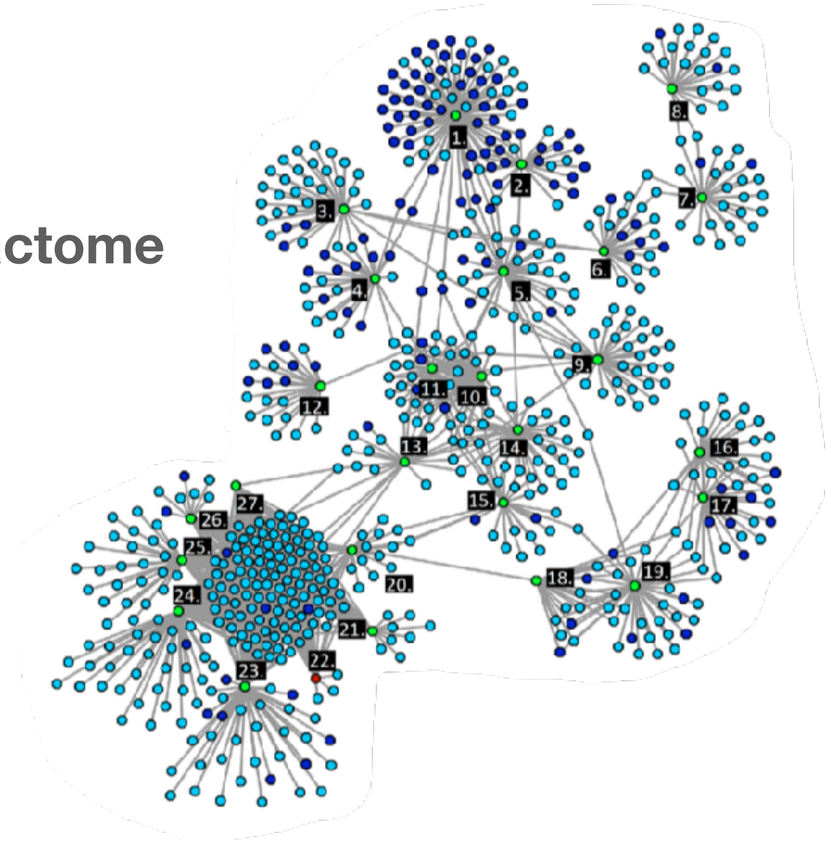

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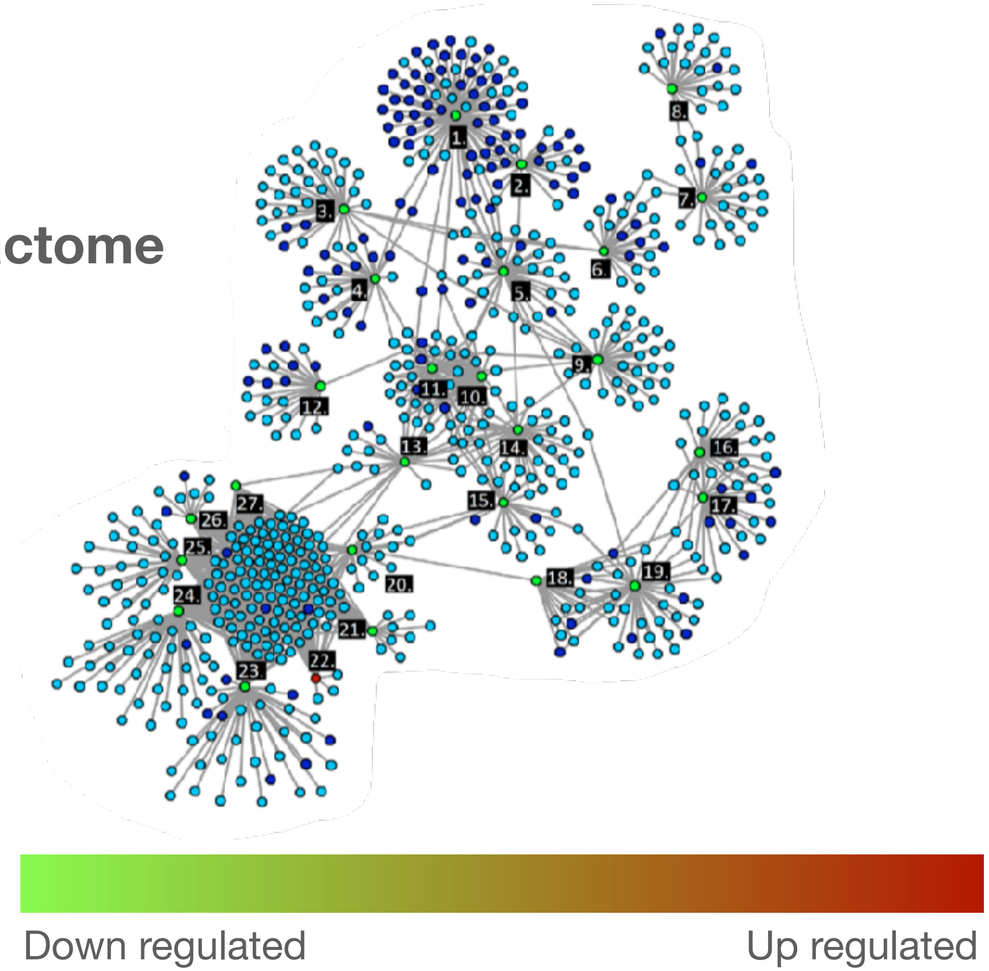

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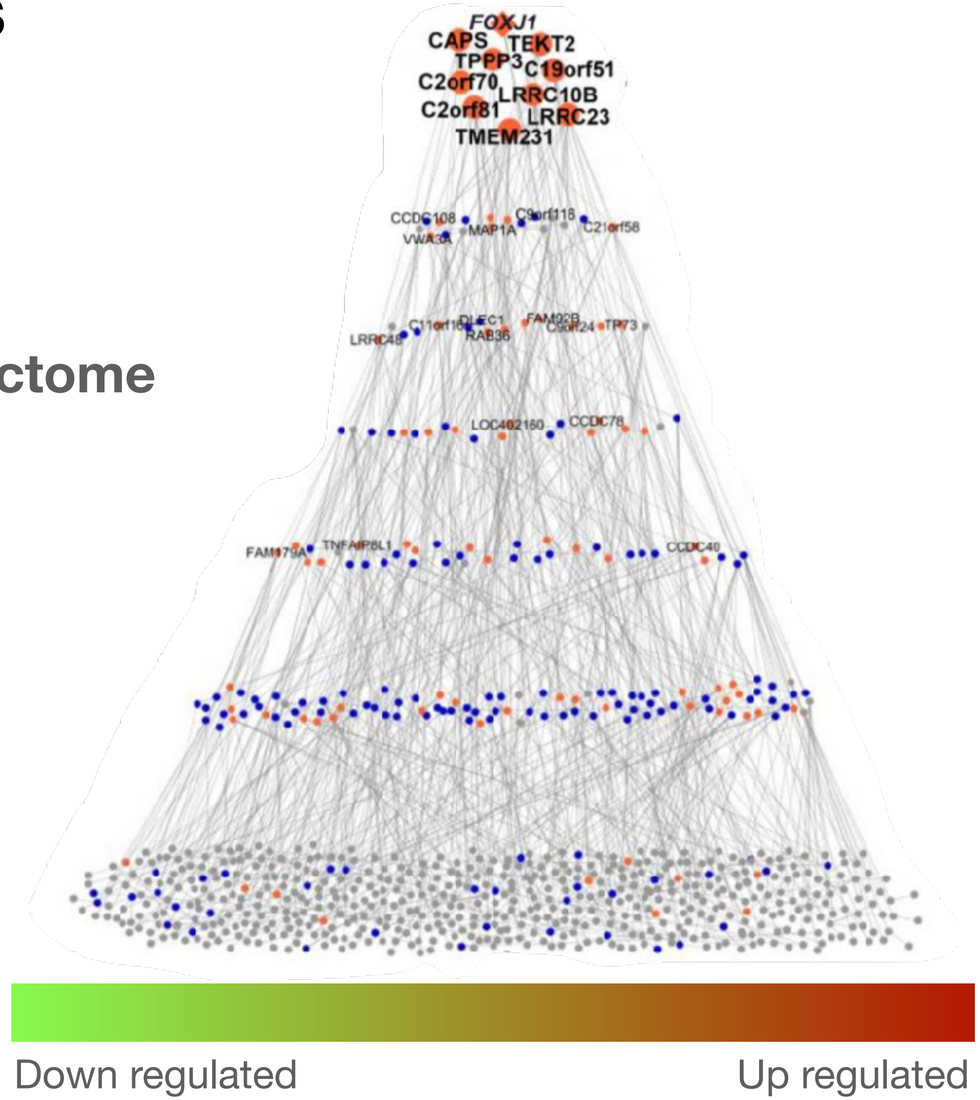

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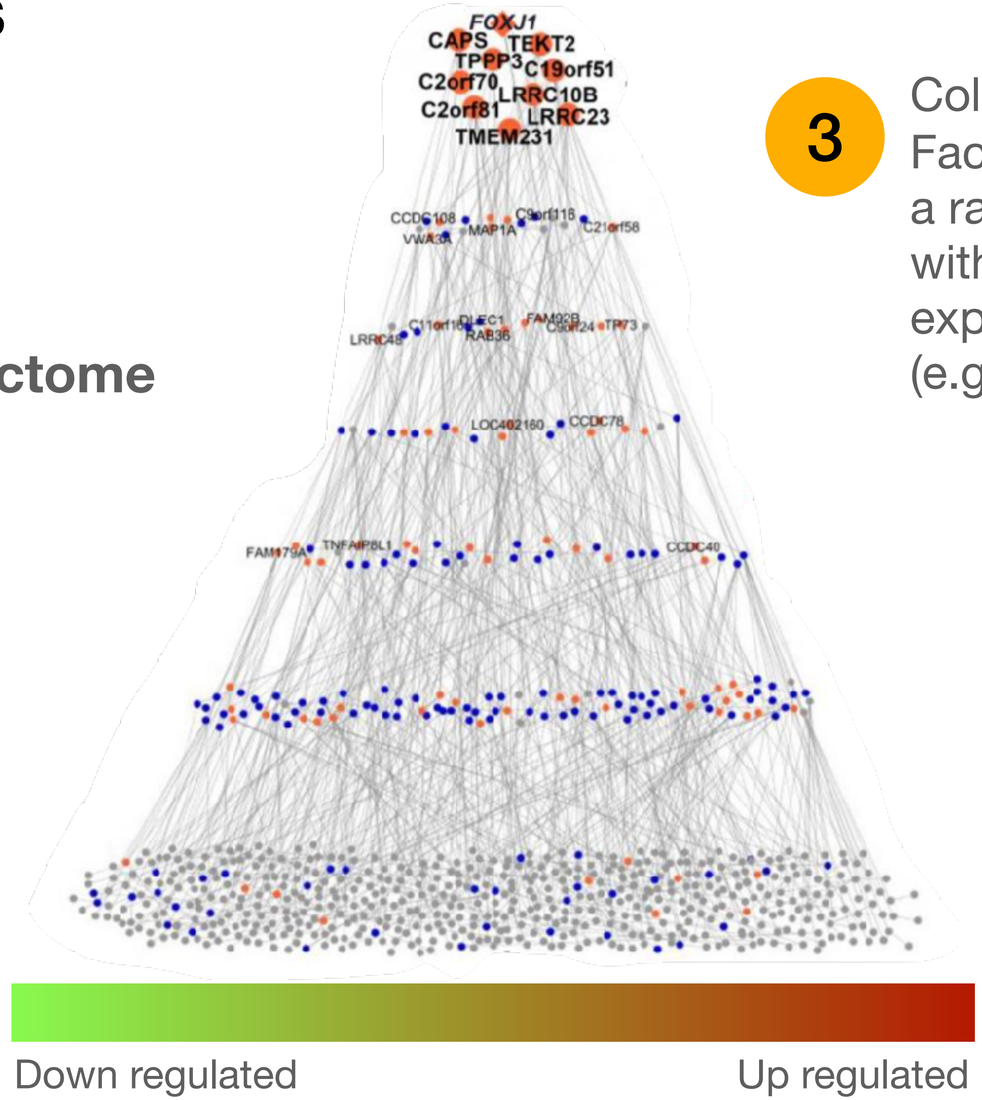

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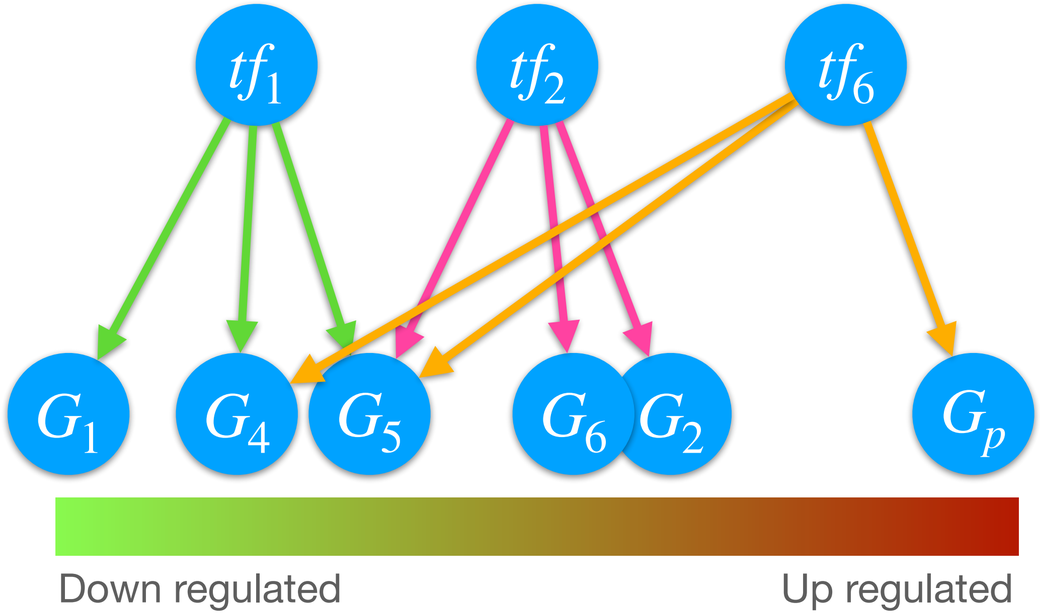

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http://www.massivegenesetstest.org/

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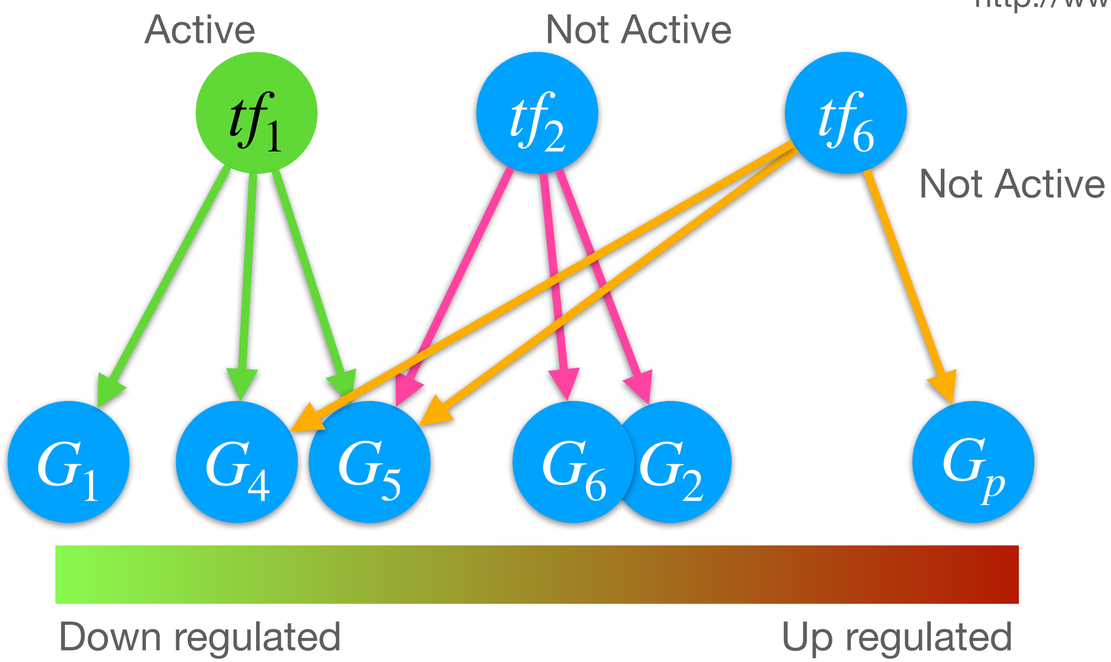
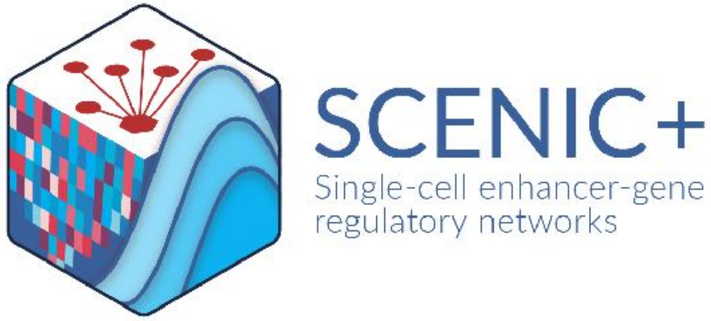


Reverse engineering of gene regulatory nets

SCENIC

SCENIC is a suite of tools to study and decipher gene regulation (with GENIE3) to infer transcription factors, gene regulatory networks, and cell types from single-cell RNA-seq data or the combination of single-cell RNA-seq and single-cell ATAC-seq data.



Reverse engineering of gene regulatory nets

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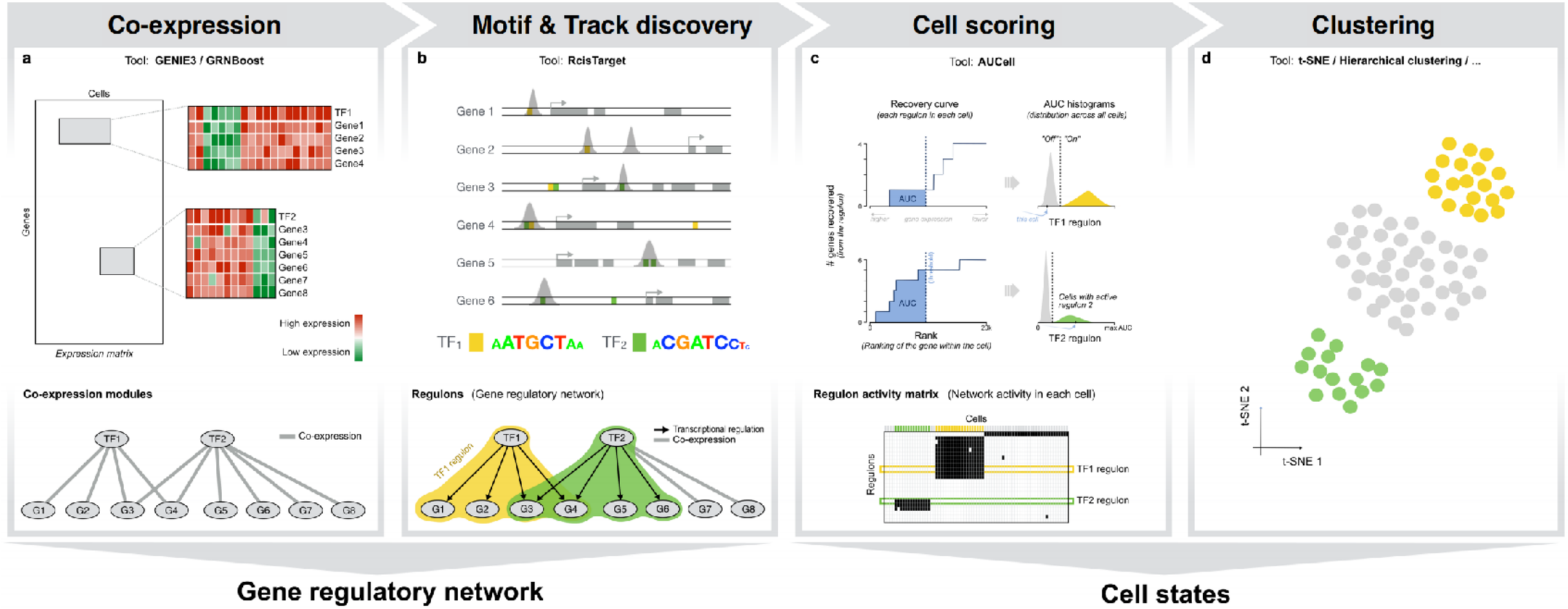

Aibar et al., Nature Methods, 2017

Reverse engineering of gene regulatory nets

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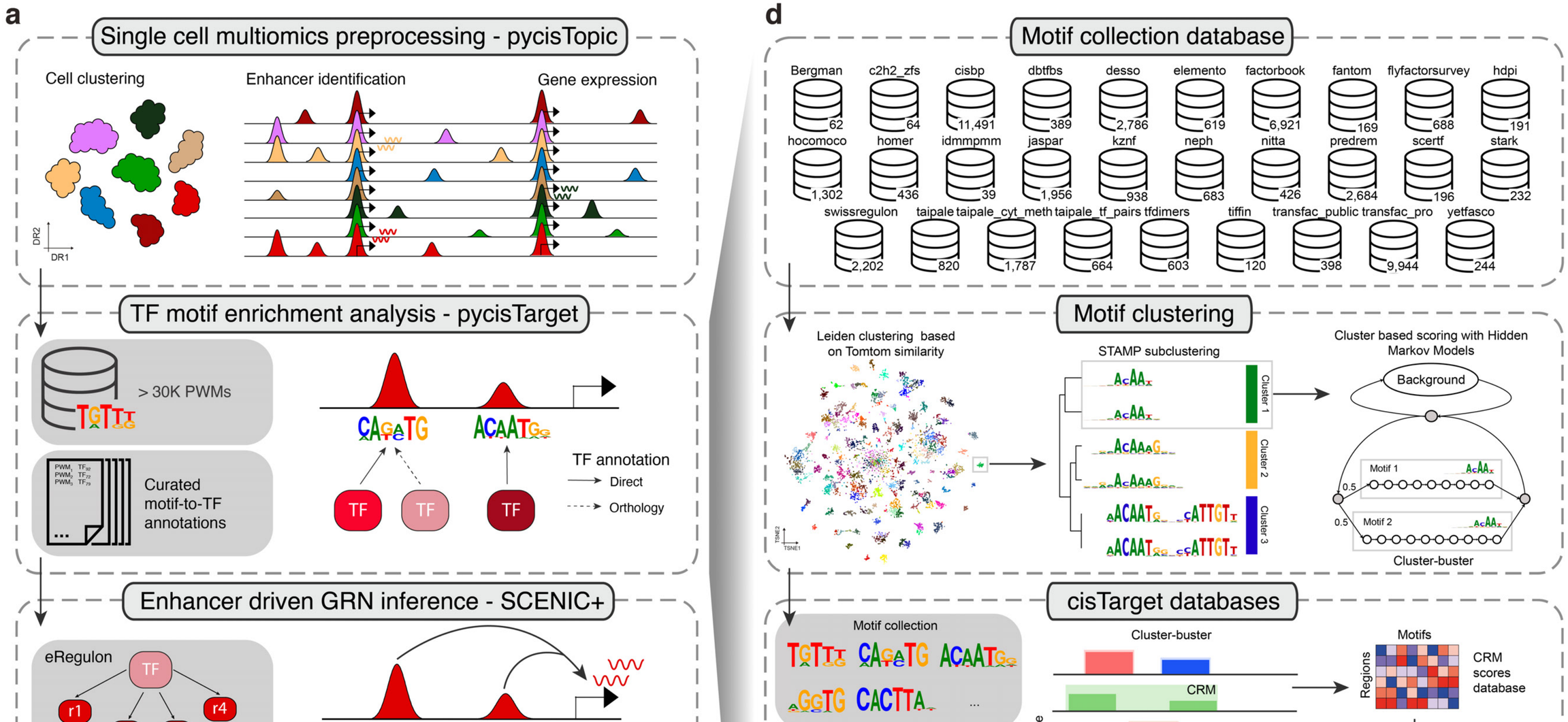
SCENIC+ Bravo González-Blas et al., preprint bioxiv, 2021



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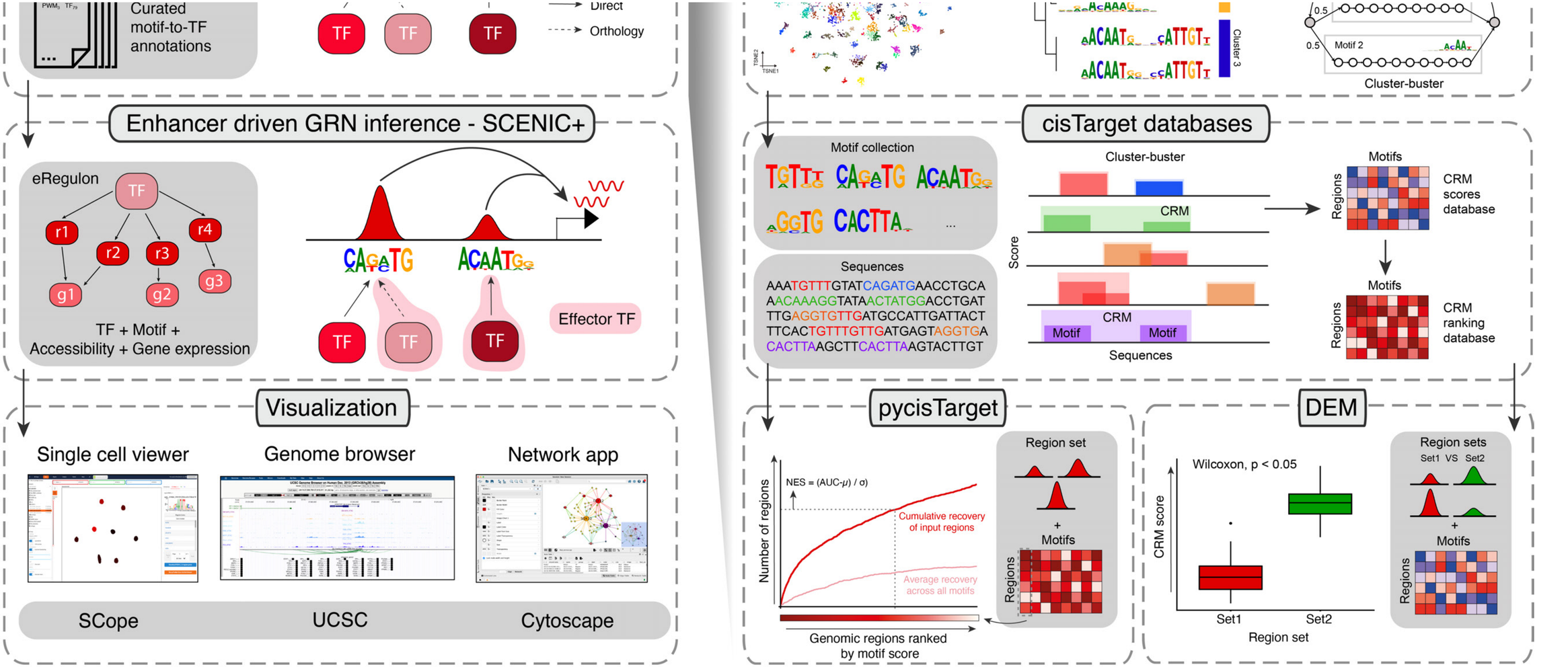

Functional genomics

Zscan regulation in Embrionic Stem Cells

OPEN ACCESS Freely available online

PLOS ONE

Identification of a Novel Gene Signature of ES Cells Self-Renewal Fluctuation through System-Wide Analysis

Luigi Cerulo[1,2☯], Daniela Tagliaferri[1,2☯], Pina Marotta[1], Pietro Zoppoli[1¤], Filomena Russo[1], Claudia Mazio[1], Mario DeFelice[1,3], Michele Ceccarelli[1,2*], Geppino Falco[1,2*]

1 Department of Stem Cell and Development, Istituto di Ricerche Genetiche Gaetano Salvatore Biogem scarl, Ariano Irpino, Italy, **2** Department of Science, Università degli Studi del Sannio, Benevento, Italy, **3** Department of Medicina Molecolare e Biotecnologie mediche, Università di Napoli Federico II, Naples, Italy

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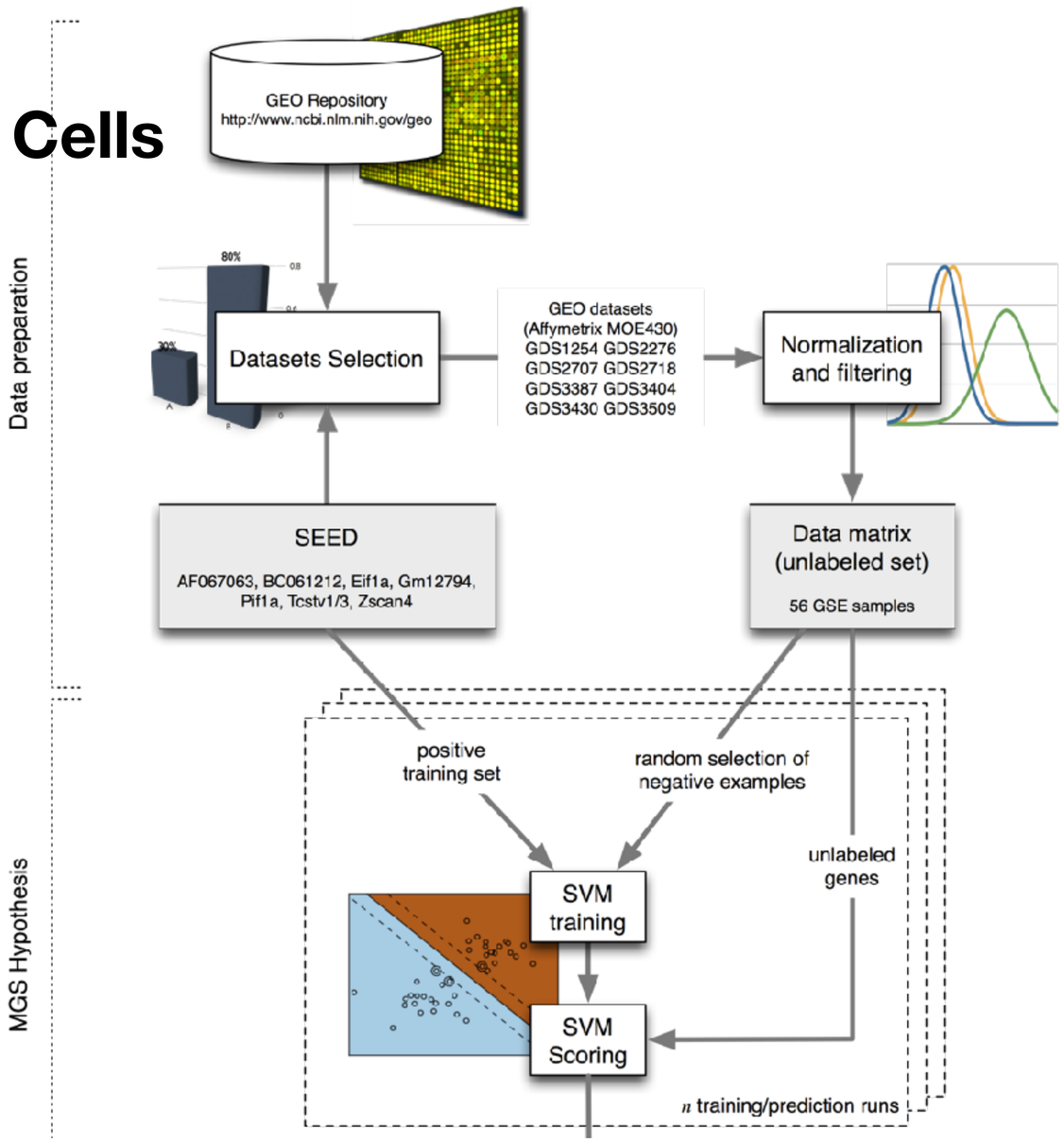

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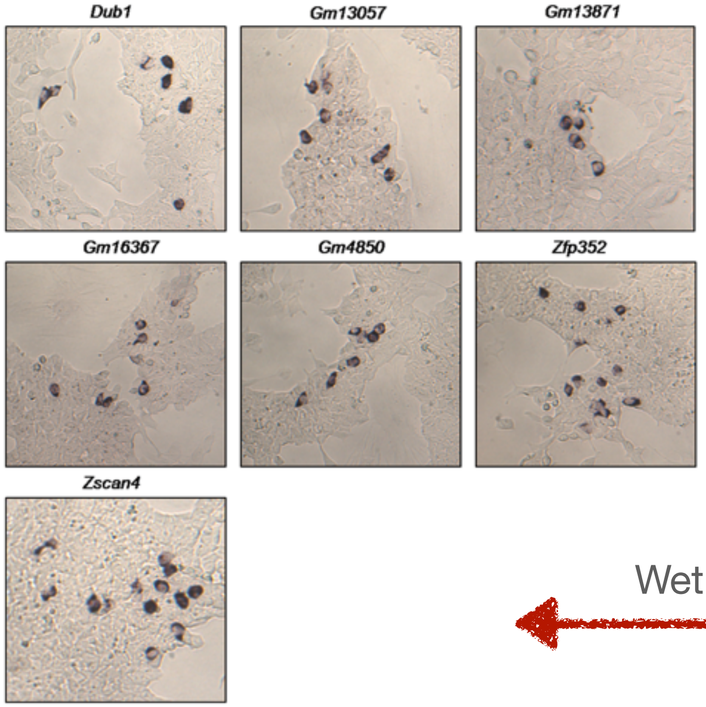
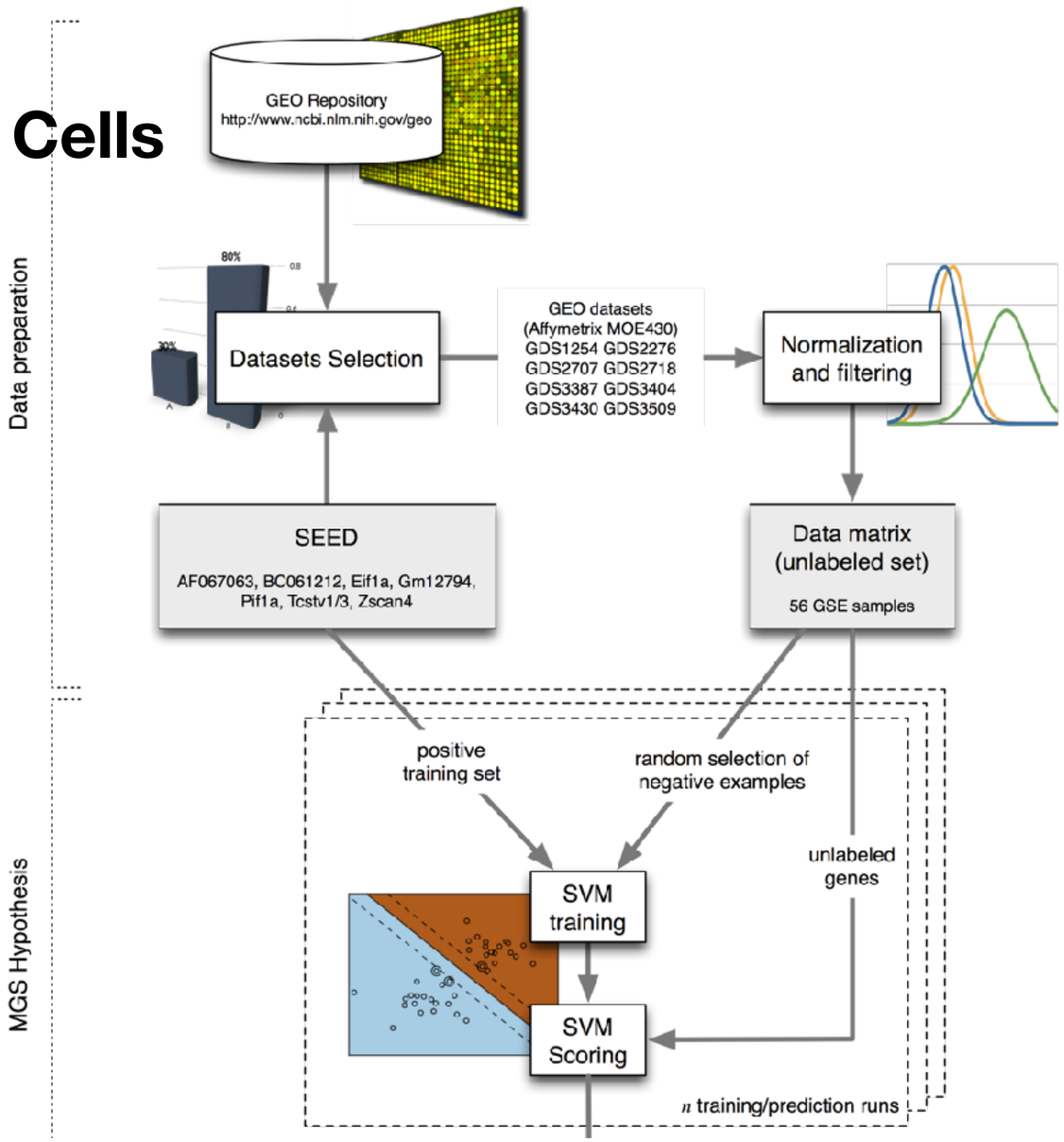


Wet Lab validation



Functional genomics

Zscan regulation in Embrionic Stem Cells

frontiers
in Cell and Developmental Biology

Retinoic Acid Induces Embryonic Stem Cells (ESCs) Transition to 2 Cell-Like State Through a Coordinated Expression of *Dux* and *Duxbl1*

OPEN ACCESS

Edited by:
William L. Stanford,

Daniela Tagliaferri[1†], Pellegrino Mazzone[1†], Teresa M. R. Noviello[1,2†], Martina Addeo[1,3], Tiziana Angrisano[3], Luigi Del Vecchio[4,5], Feliciano Visconte[5], Vitalba Ruggieri[6], Sabino Russi[6], Antonella Caivano[6], Irene Cantone[4], Mario De Felice[4,7], Michele Ceccarelli[1,2], Luigi Cerulo[1,2] and Geppino Falco[1,2,6,7]*

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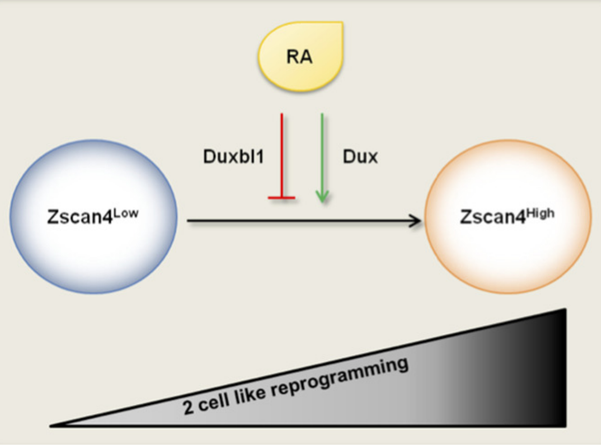

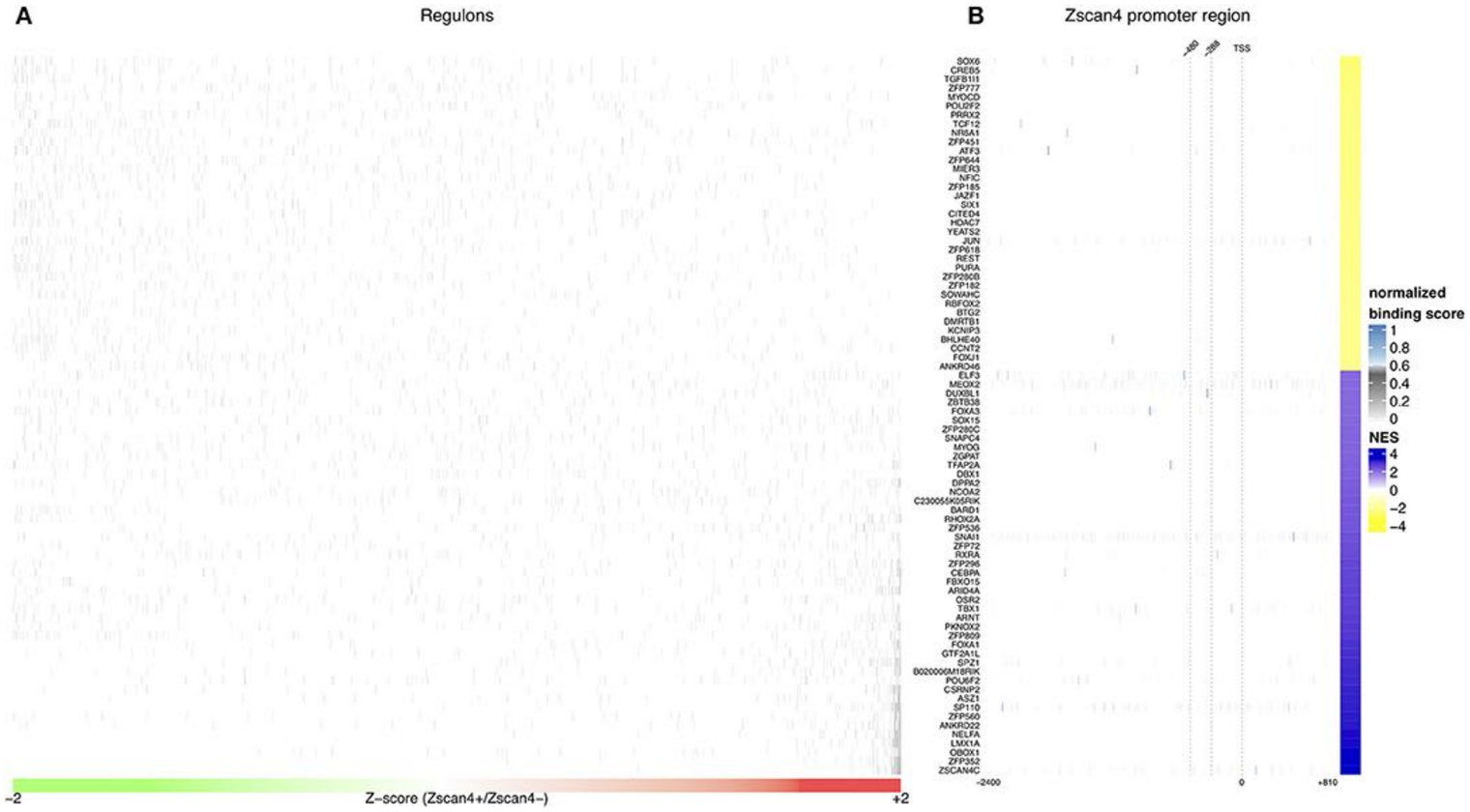

Applications

De novo Motif discovery

A motif is an approximate sequence pattern with no gaps that occurs repeatedly in a group of related sequences.

A motifs can be modelled as position-dependent letter-probability matrices that describe the probability of each possible letter at each position in the pattern.

The input is a group of sequences and the outputs are the most significant motifs occurring in all sequences.

Applications

MEME suite

Discovered Motifs

	Logo	E-value	Sites	Width	More	Submit/Download
1.		3.7e-033	14	18		
2.		7.1e-003	4	45		
3.		7.4e+000	6	40		

Stopped because requested number of motifs (3) found.

Motif Locations

Only Motif Sites | Motif Sites+Scanned Sites | All Sequences | Download PDF | Download SVG

	Name	*p*-value	Motif Locations
1.	cloacin-df13	2.14e-15	
2.	colicin-e1	1.31e-5	
3.	colicin-ia	3.11e-41	
4.	colicin-ib	1.14e-38	
5.	reca	1.43e-17	
6.	recn	1.28e-6	
7.	sula	4.56e-12	
8.	umu-operon	4.95e-6	
9.	uvra	3.02e-12	

Applications

Motif scanning

Motif scanners scan sequences (e.g. promoters) to match known motif represented as position-dependent letter-probability matrices that describe the probability of each possible letter at each position in the pattern.

The input is a group of sequences and a grioput of known motifs
the outputs are the most significant motifs found in all sequences.

Applications

FIMO motif scanner

DATABASE AND MOTIFS

```
DATABASE mm9_tss_500bp_sampled_1000.fna
Database contains 1000 sequences, 500000 residues

MOTIFS some_vertebrates.meme (DNA)

   MOTIF     WIDTH  BEST POSSIBLE MATCH
  MA0108.1      15  GTATAAAAGGCGGGG
 UP00093_1      16  TCGACCCCGCCCCTAT
 UP00020_1      16  ACGATGACGTCATCGA
 UP00002_2      15  CAAAGGCGTGGCCAG
  MA0060.1      16  CTCAGCCAATCAGCGC

Random model letter frequencies (--nrdb--):
A 0.275 C 0.225 G 0.225 T 0.275
```

Motif ID	Alt ID	Sequence Name	Strand	Start	End	p-value	q-value	Matched Sequence
MA0060.1	NFYA	chr2	-	60221163	60221178	3.36e-09	0.00195	CTCGGCCAATCAGAGC
MA0060.1	NFYA	chr3	-	54858838	54858853	4.77e-09	0.00195	ATCAGCCAATCAGCGG
UP00093_1	Klf7_primary	chr2	+	172266018	172266033	1.06e-08	0.00496	GCGACCCCGCCCCTTT
UP00093_1	Klf7_primary	chr11	+	65981465	65981480	1.31e-08	0.00496	TTGACCCCGCCCCTCA
UP00020_1	Atf1_primary	chr3	+	65470135	65470150	2.63e-08	0.0222	GCTGTGACGTCACCGC
MA0060.1	NFYA	chrX	+	51925276	51925291	3.55e-08	0.00584	TTCAGCCAATCAGCGC
MA0060.1	NFYA	chrX	+	52016291	52016306	3.55e-08	0.00584	TTCAGCCAATCAGCGC
UP00093_1	Klf7_primary	chr1	+	93302476	93302491	3.87e-08	0.00898	TCGGCCCCGCCCCTCC

Applications

Exercise 1 - motif scanning

We would like to test whether Mitochondrial genes in Mouse have TBP binding sequences in their promoter regions (500 bp flank-coding upstream region)

1. With Jaspar (https://jaspar.uio.no) search for TBP PWM matrix and download it in MEME format
2. With Biomart (https://www.ensembl.org/biomart/martview) download promoter sequences of all genes located in Mouse Mitochondrial chromosome
3. With FIMO (https://meme-suite.org/meme/tools/fimo) search TBP binding regions using previous downloaded data

Applications

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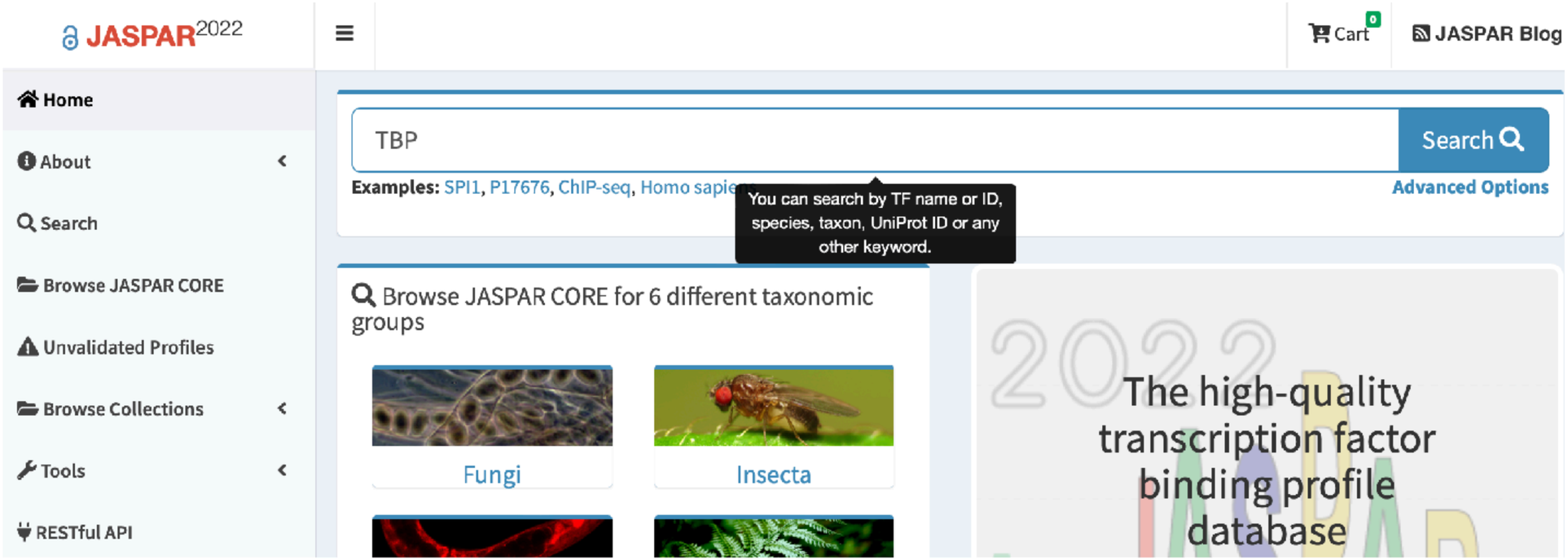

Applications

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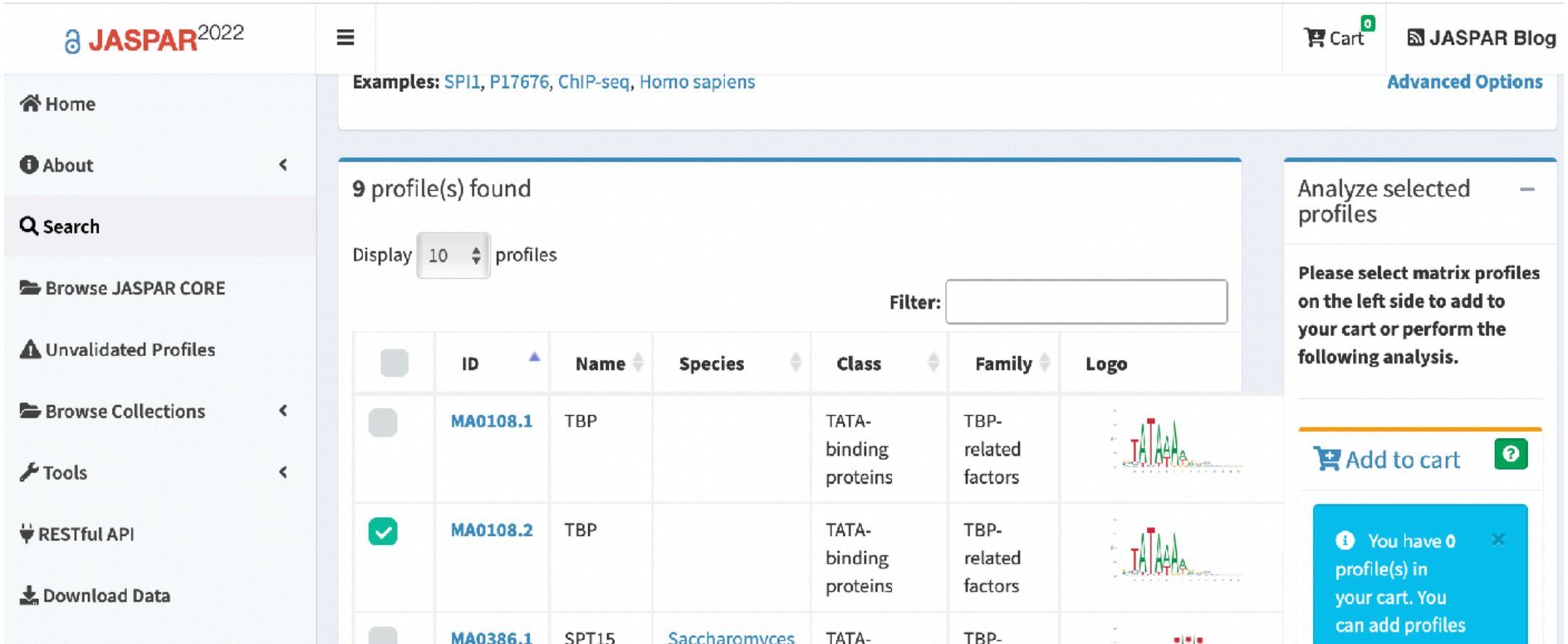

Applications

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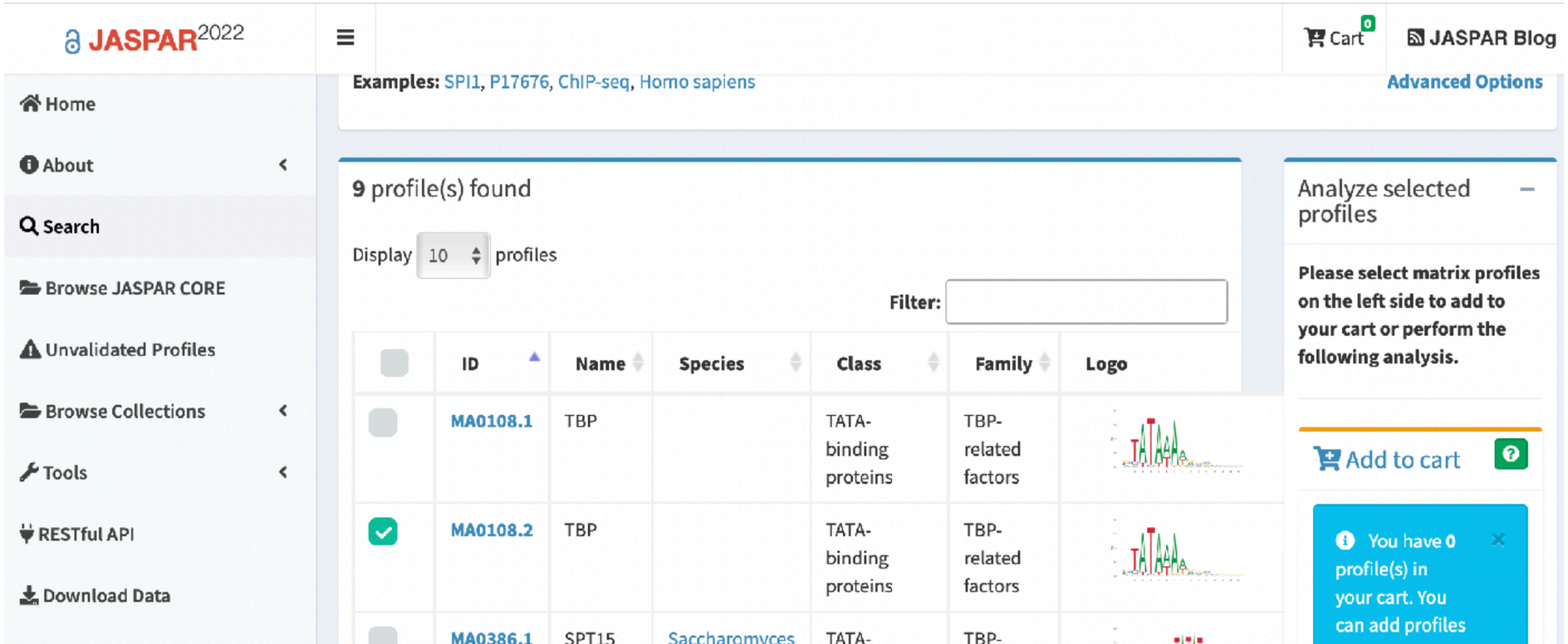

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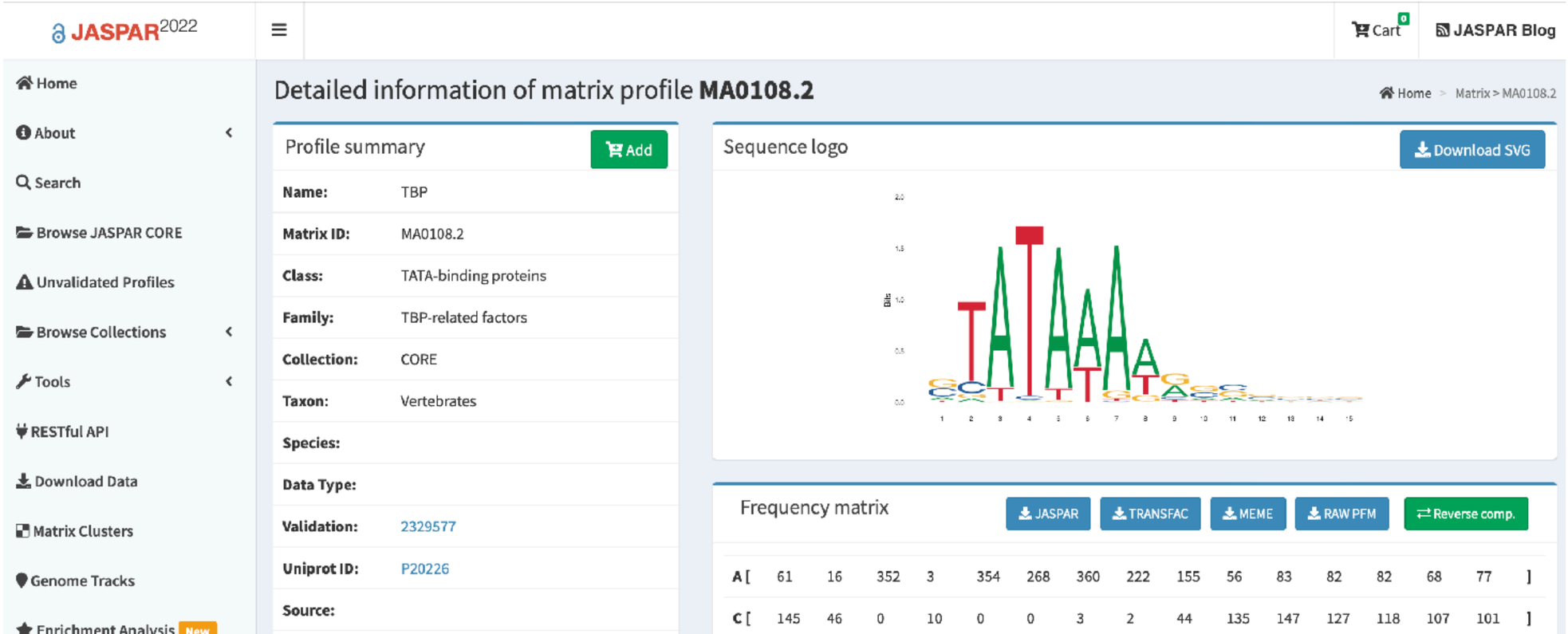
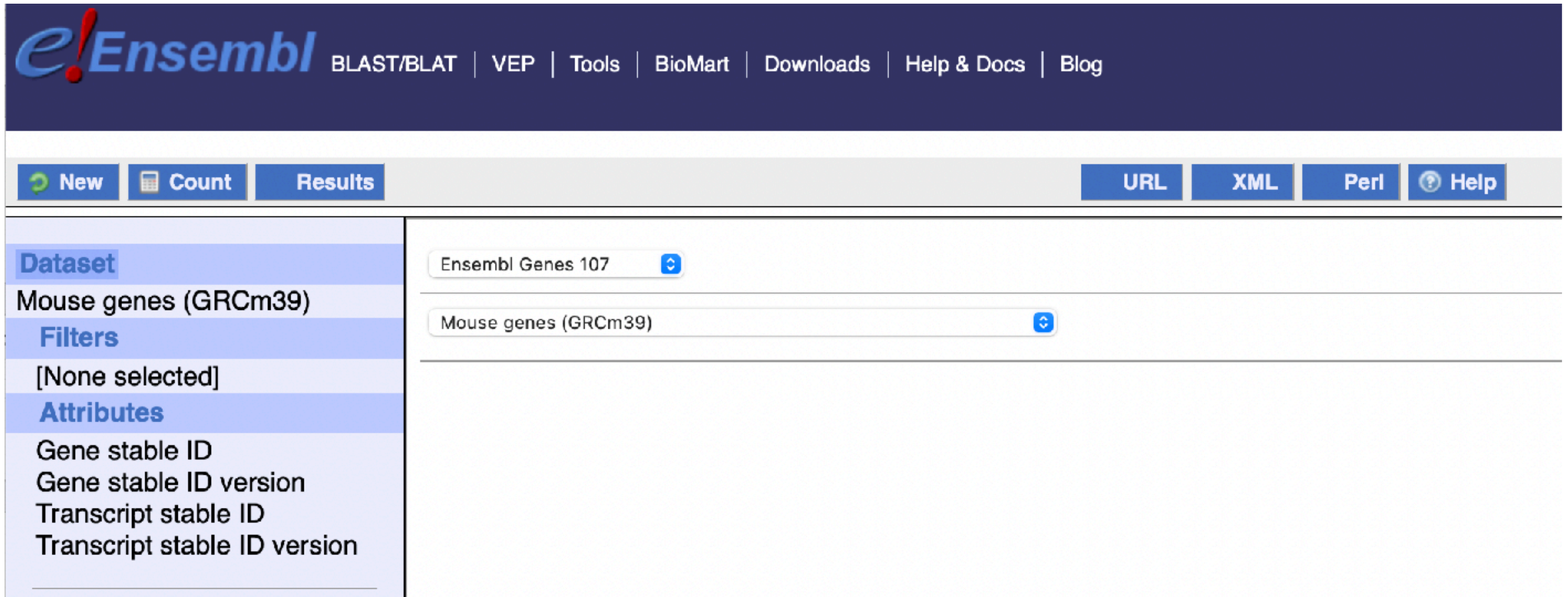


Transcription Factor promoter analysis

Exercise 1 - motif scanning

2. With Biomart (https://www.ensembl.org/biomart/martview) download promoter sequences of all genes located in Mouse Mitochondrial chromosome



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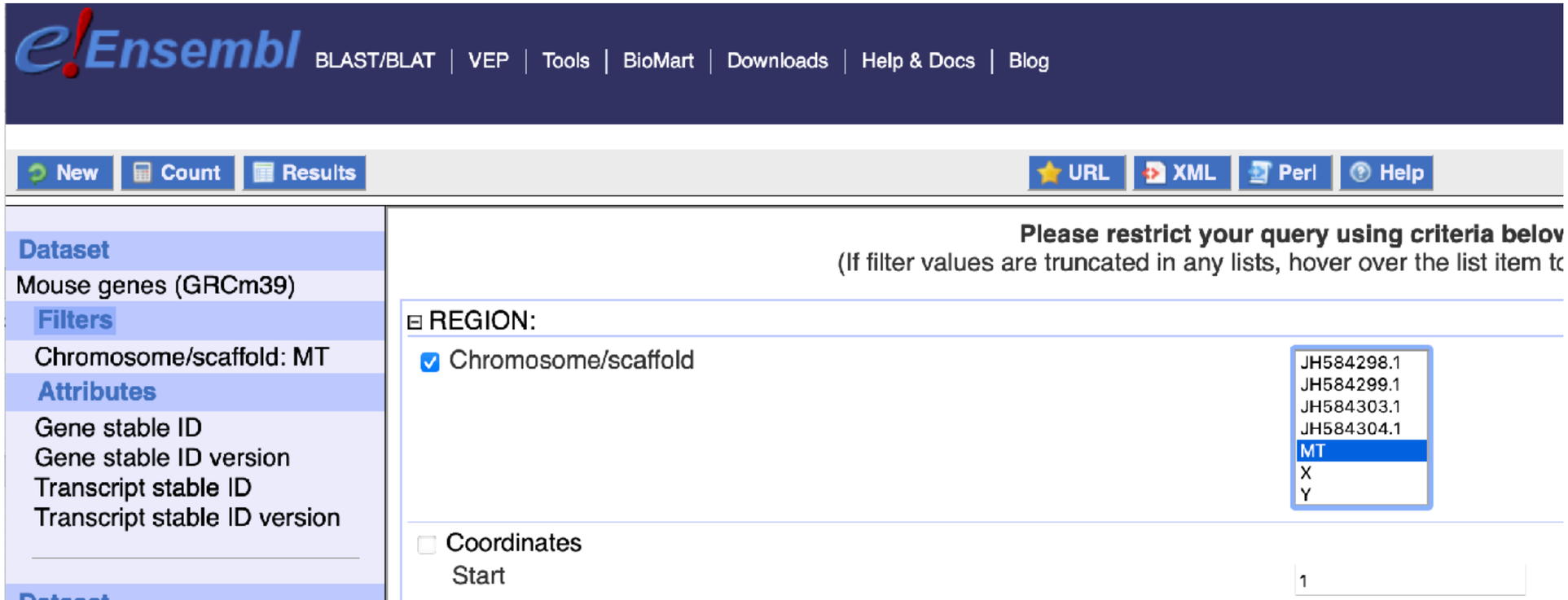

Transcription Factor promoter analysis

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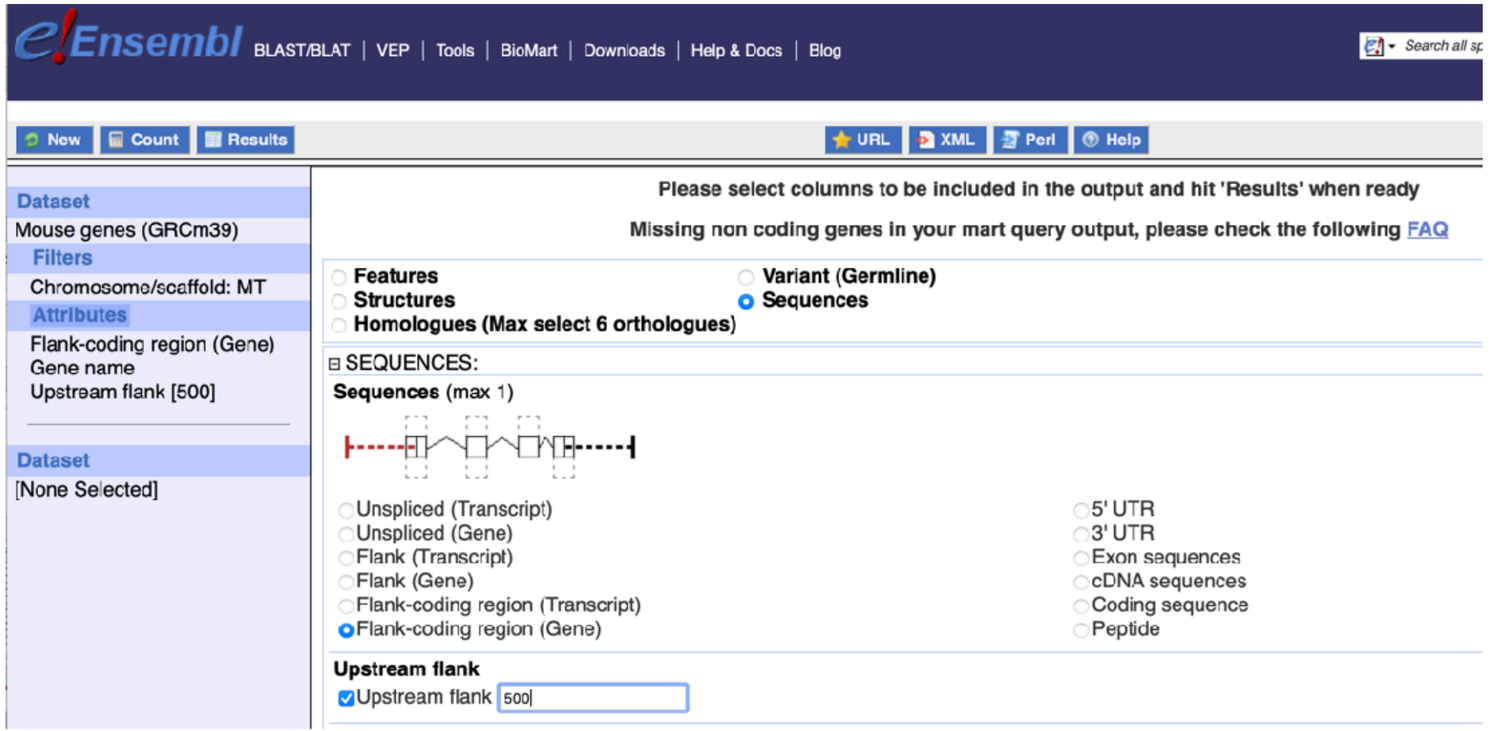

Transcription Factor promoter analysis

Exercise 1 - motif scanning

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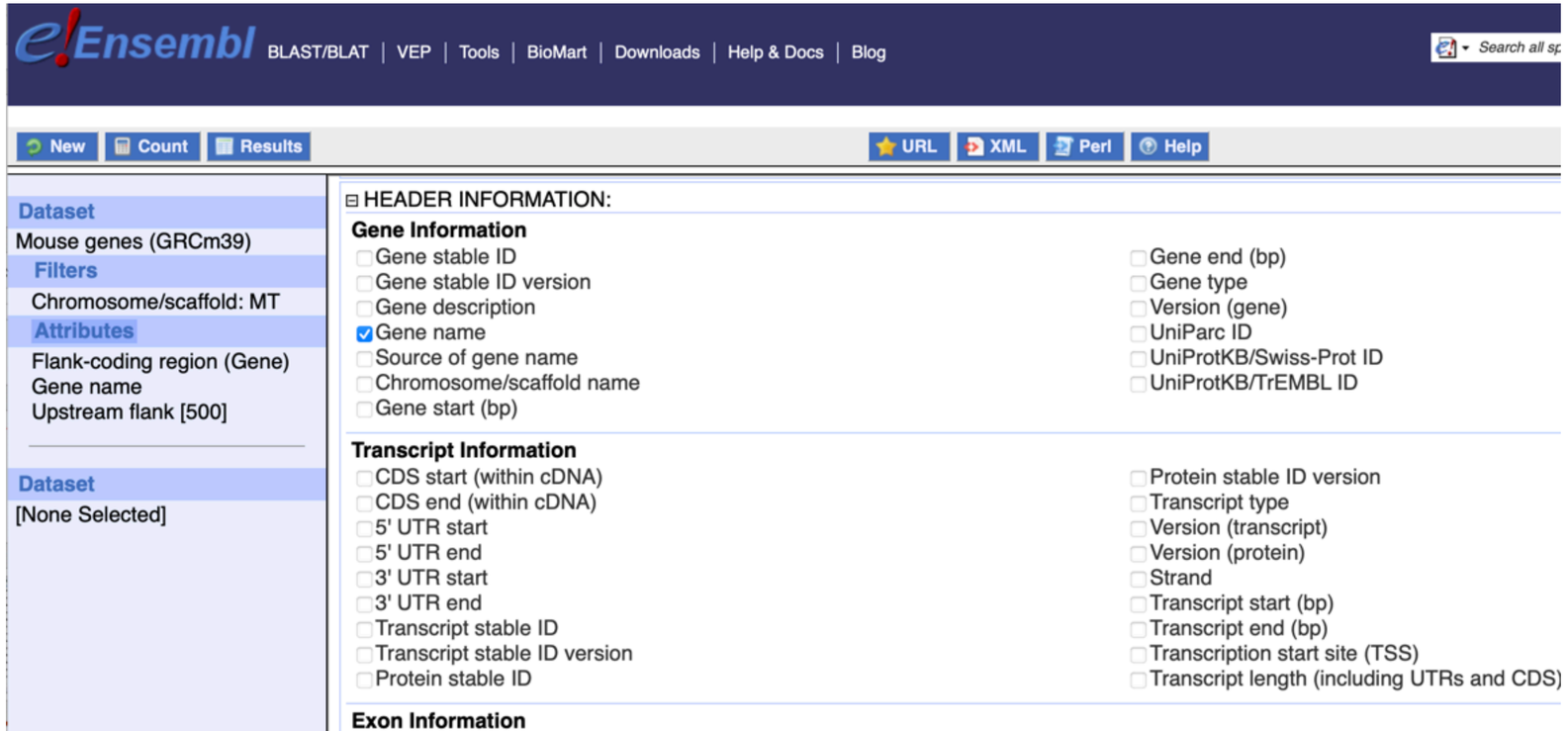

Transcription Factor promoter analysis

Exercise 1 - motif scanning

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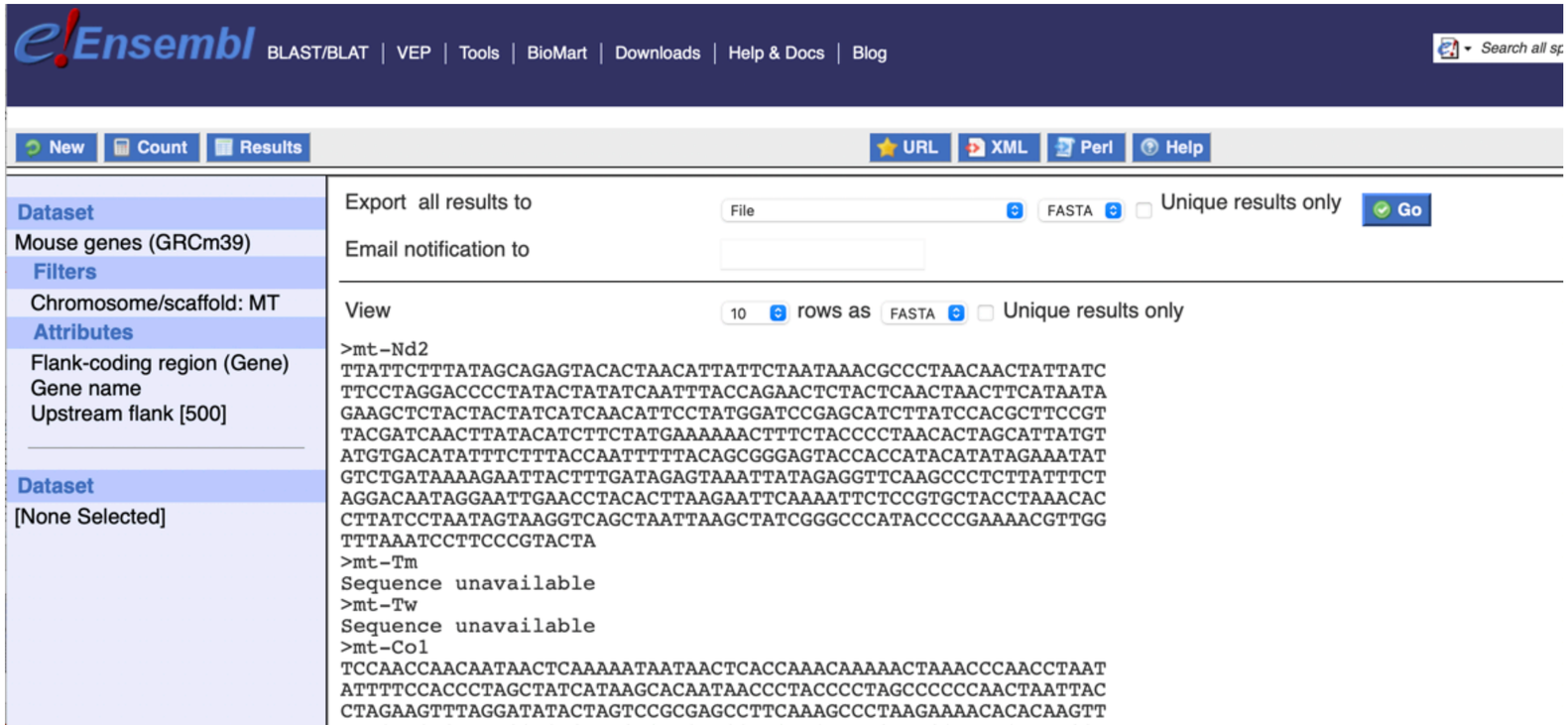
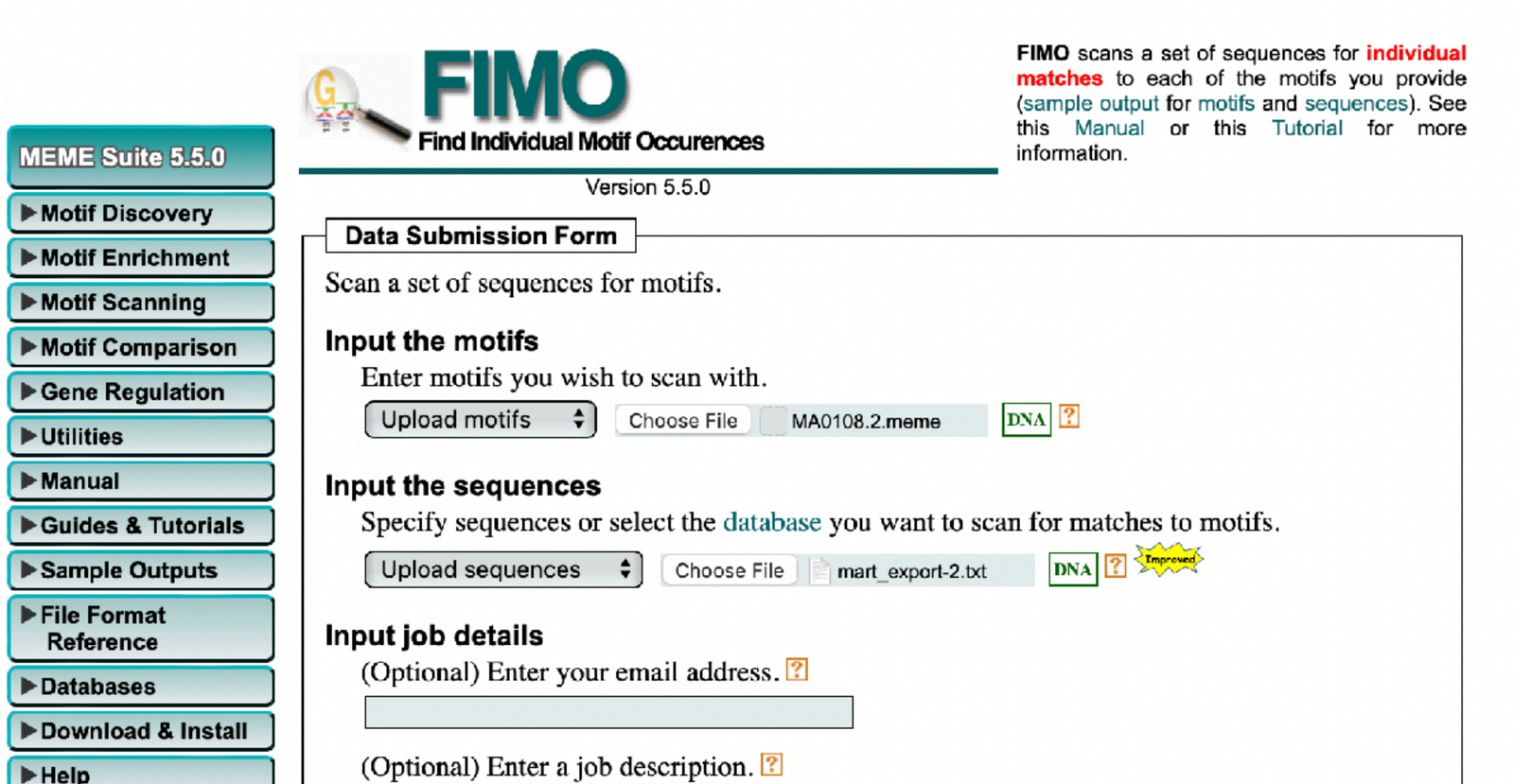


Transcription Factor promoter analysis

Exercise 1 - motif scanning

3. With FIMO (https://meme-suite.org/meme/tools/fimo) search TBP binding regions using previous downloaded data



Transcription Factor promoter analysis

Exercise 1 - motif scanning

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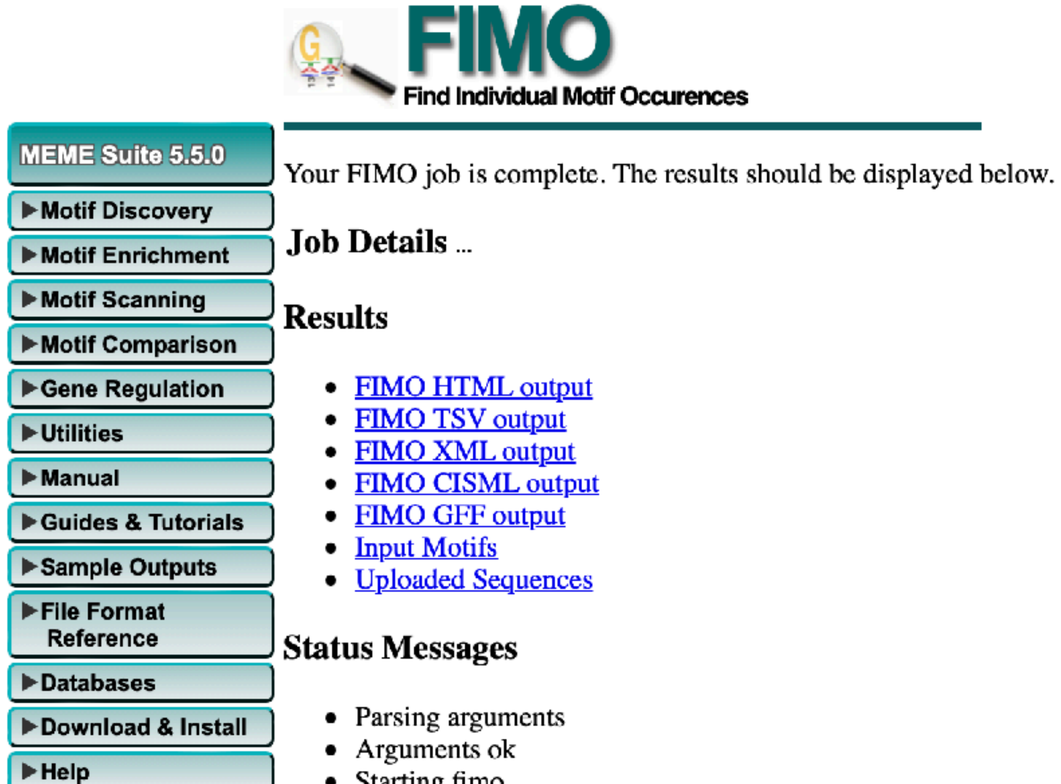


Transcription Factor promoter analysis

Exercise 1 - motif scanning

3. With FIMO (https://meme-suite.org/meme/tools/fimo) search TBP binding regions using previous downloaded data

DATABASE AND MOTIFS

```
DATABASE mart_export-2.txt
Database contains 13 sequences, 6500 residues

MOTIFS MA0108.2.meme (DNA)

  MOTIF     WIDTH   BEST POSSIBLE MATCH
 MA0108.2      15   GTATAAAAGGCGGGG

Random model letter frequencies (--nrdb--):
A 0.275 C 0.225 G 0.225 T 0.275
```

SECTION I: HIGH-SCORING MOTIF OCCURENCES

- There were 1 motif occurences with a p-value less than 0.0001. The full set of motif occurences can be seen in the TSV (tab-delimited values) output file fimo.tsv, the GFF3 file fimo.gff which may be suitable for uploading to the UCSC Genome Table Browser (assuming the FASTA input sequences included genomic coordinates in UCSC or Galaxy format), or the XML file fimo.xml.
- The *p*-value of a motif occurrence is defined as the probability of a random sequence of the same length as the motif matching that position of the sequence with as good or better a score.
- The score for the match of a position in a sequence to a motif is computed by summing the appropriate entries from each column of the position-dependent scoring matrix that represents the motif.
- The q-value of a motif occurrence is defined as the false discovery rate if the occurrence is accepted as significant.
- The table is sorted by increasing *p*-value.

Motif ID	Alt ID	Sequence Name	Strand	Start	End	p-value	q-value	Matched Sequence
MA0108.2	TBP	mt-Nd6	+	39	53	4.73e-05	0.485	CTATAAATGCTGTGG

Transcription Factor promoter analysis

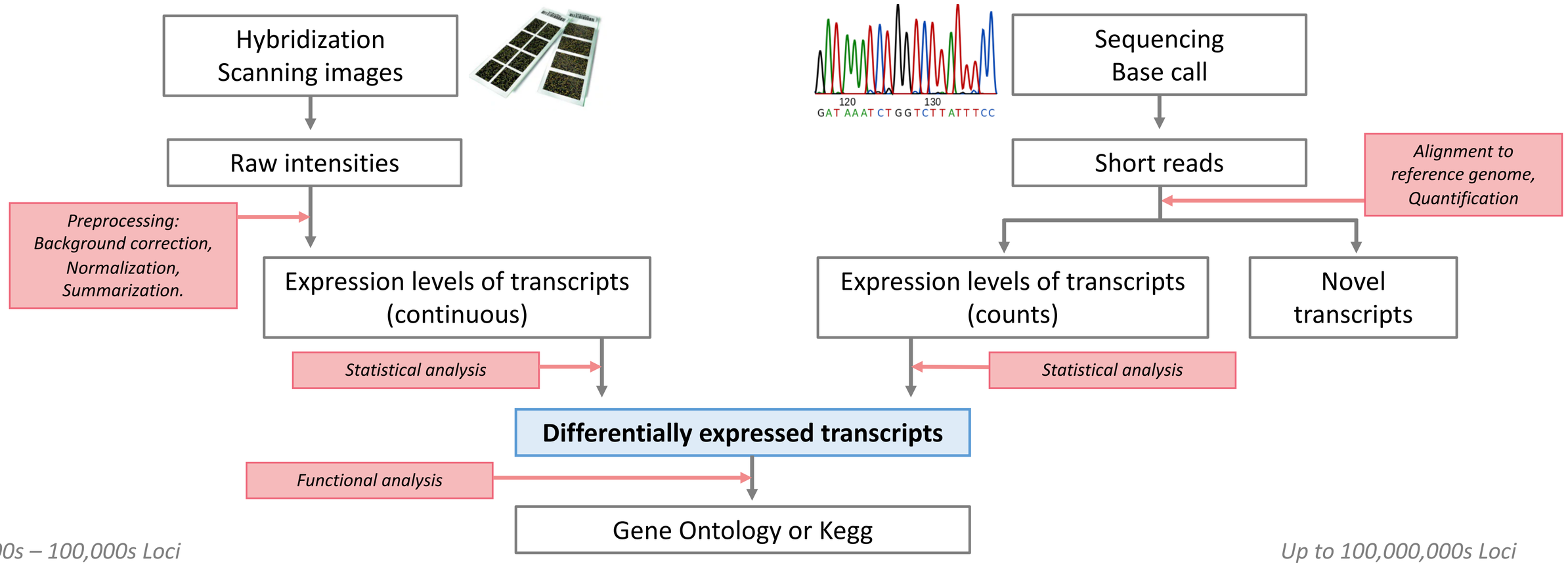
Exercise 2 - motif scanning

Some studies revealed that DAL1, DAL2, DAL4, DAL5, DAL7, DAL80, and GAP1 are strongly co-expressed in S.Cerevisiae in more than 200 different conditions (Allocco et al., 2004). It could be the case that those genes are regulated by a common Transcription Factor.

1. With Biomart download the upstream flank-coded sequences (1500 bp upstream) of those genes
2. With FIMO perform a promote analysis scanning all available motifs in S.Cerevisiae downloaded from Jaspar
3. Analyse results in Excel making convincing conclusions

Applications

Differential Expression Analysis



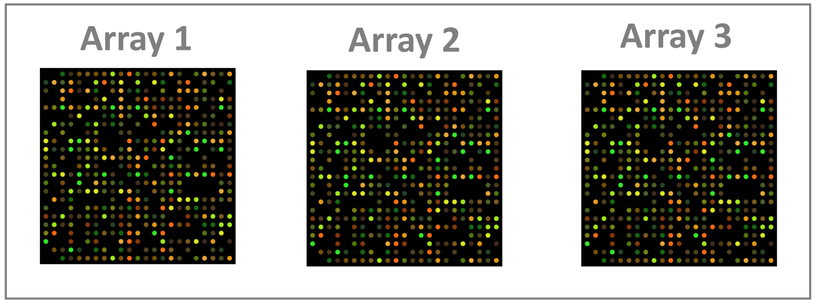
100s – 100,000s Loci
Limited to probes on Array

Up to 100,000,000s Loci
Limited by cost

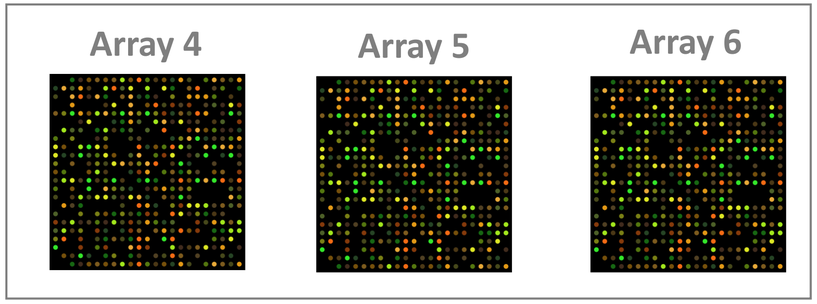
Applications

Differential Expression Analysis

Tumore



Controllo



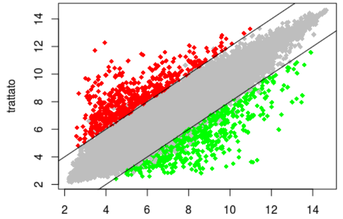
Ogni array rappresenta il profilo di espressione genica di un campione

1. Normalizzare i dati

geni

	Array1	Array2	Array3	Array4	Array5	Array6
1007_s_at	9.347249	9.568875	9.820663	11.066680	11.007247	10.792517
1053_at	8.700141	8.965633	8.847094	9.049528	9.064799	8.750276
117_at	5.800838	5.776382	5.795153	5.048881	5.246541	5.306622
121_at	7.214928	7.376463	7.379221	8.056964	8.018169	7.836705
1255_g_at	2.543790	2.637345	2.625955	2.614629	2.982887	2.584014
1294_at	6.099539	6.201490	6.424293	6.450105	6.318168	6.049103
1316_at	6.186417	6.114881	5.901316	6.172999	6.109812	5.739915
1320_at	4.334868	4.668779	4.650498	5.075092	5.192537	5.244987
1405_i_at	3.339094	3.189086	3.679687	8.734428	8.535258	7.914109

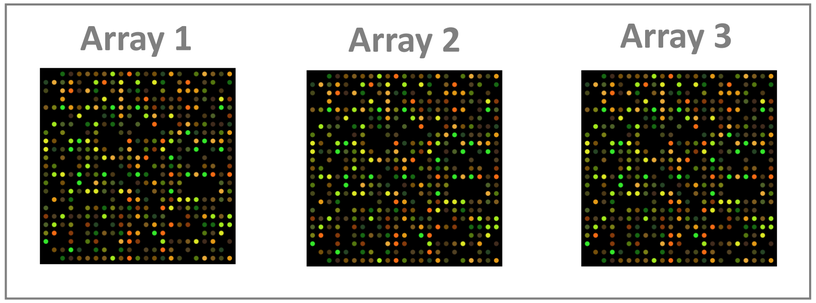
2. Quantificare la differenza di espressione di ciascun gene tra le diverse condizioni



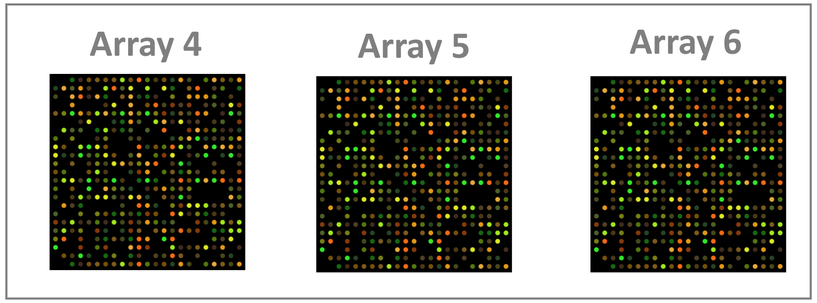
Applications

Differential Expression Analysis

Tumore



Controllo



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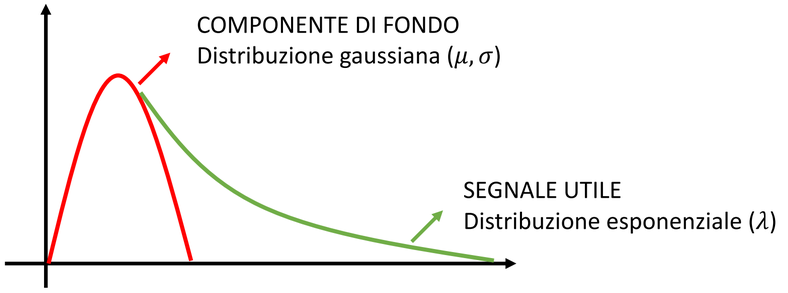

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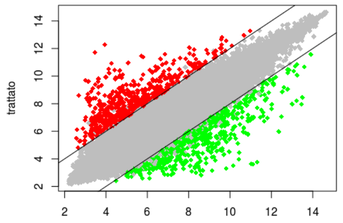

Applications

Differential Expression Analysis

$$FC = \frac{A}{B} = \frac{4}{2} = 2$$ *A è 2 volte B*

Tumore *Controllo*

geni

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1007_s_at	9.347249	9.568875	9.820663	11.066680	11.007247	10.792517
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1405_i_at	3.339094	3.189086	3.679687	8.734428	8.535258	7.914109

N.B. i valori sono in scala logaritmica

Per ciascun gene:

$$FC = \frac{media\ Condizione1}{media\ Condizione2} = \frac{media\ Tumore}{media\ Controllo}$$

$$logFC = (media\ Tumore) - (media\ Controllo)$$

logFC = (3.3 + 3.2 + 3.7)/3 – (8.7 + 8.5 + 7.9)/3 = 3.4 – 8.4 ≈ −5

Applications

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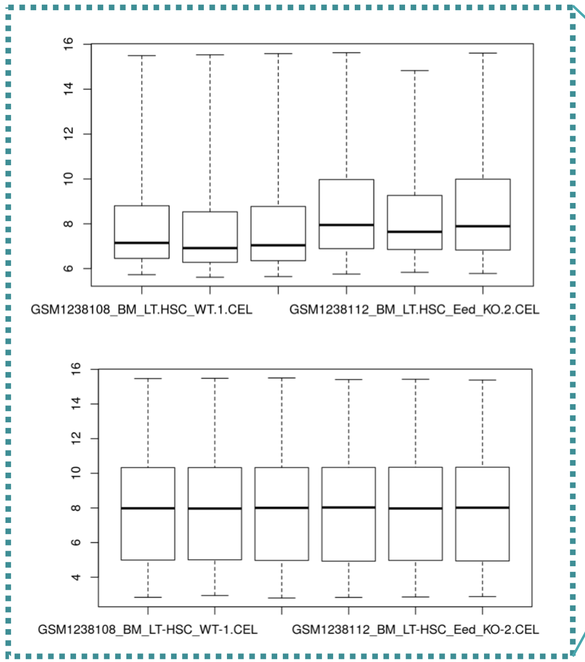
*logFC > 1 gene **up-regolato** nel Tumore*
*logFC < -1 gene **down-regolato** nel Tumore*

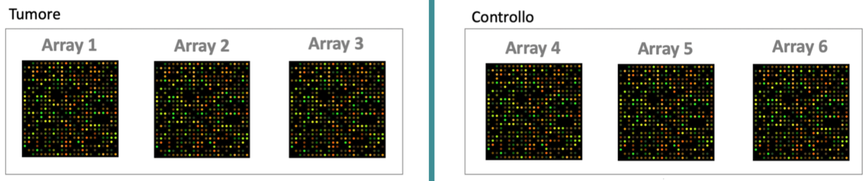
Applications

Differential Expression Analysis

Boxplot prima e dopo la normalizzazione



INPUT: file .CEL



1. Normalizzazione

Robust Multiarray Averaging (RMA):

- Background correction
- Normalization
- Summarization

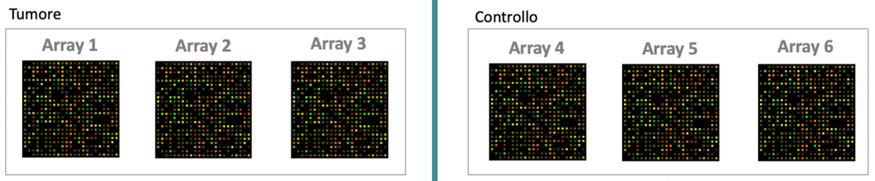
2. Quantificazione dei geni differenzialmente espressi tra due condizioni

Calcolo del Fold Change e del p-Value per identificare

Applications

Differential Expression Analysis

INPUT: file .CEL



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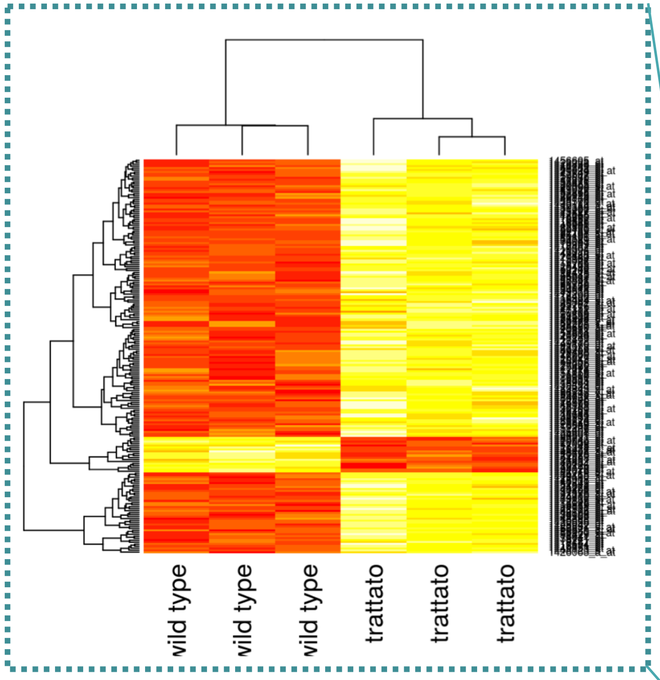
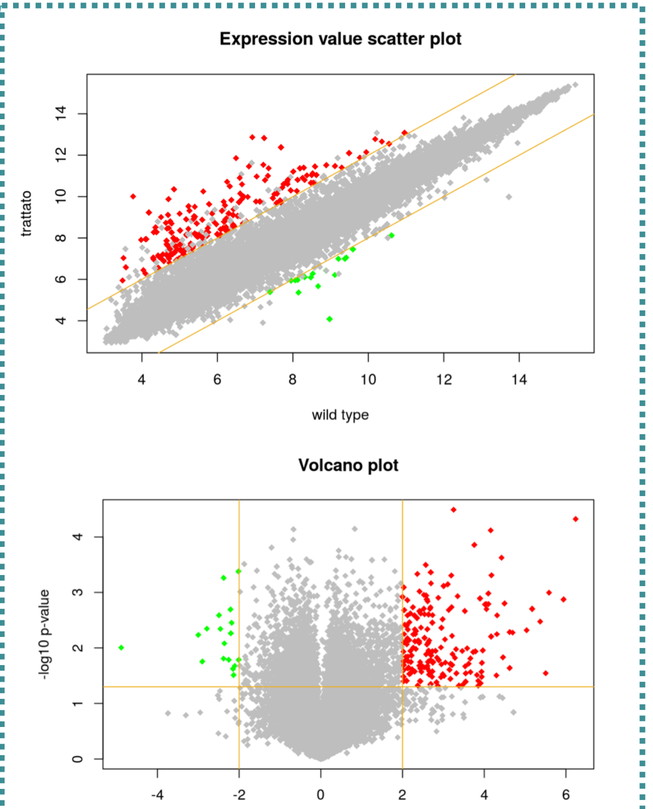
Heatmap



Scatter plot e volcano plot



Applications

Differential Expression Analysis

Visualizzazione dei risultati

	Array1	Array2	Array3	Array4	Array5	Array6
1007_s_at	9.347249	9.568875	9.820663	11.066680	11.007247	10.792517
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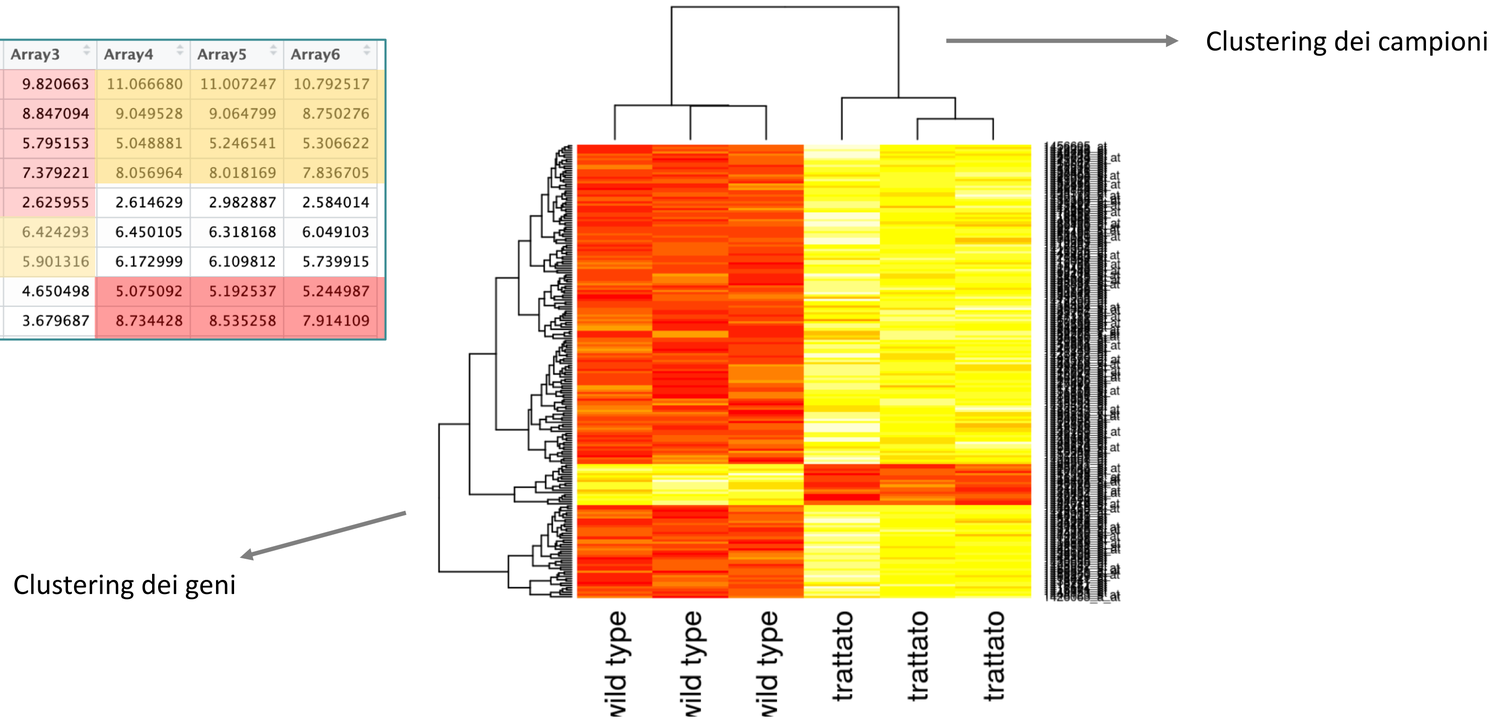
1405_i_at	3.339094	3.189086	3.679687	8.734428	8.535258	7.914109



Heatmap: una rappresentazione grafica dei dati dove ogni singolo valore nella matrice di espressione è rappresentato da un colore in una scala di colori (es dal giallo al rosso)

Applications

Differential Expression Analysis

=MEDIA(num1; num2; num3; …)

Probe.id	trattato1	trattato2	trattato3	controllo1	controllo2	controllo3	mean exp trattato	mean exp controllo
1415670_at	10.32095475	10.3348446	10.32643855	10.0755224	10.103059	10.15155883		
1415671_at	11.55659724	11.21470877	11.6095877	11.33865796	11.33715745	11.47039553		
1415672_at	11.54761726	11.57386469	11.44209389	11.44663589	11.58652392	11.52606895		
1415673_at	9.92847925	7.720741249	7.620332624	7.817102331	8.009357375	7.837974306		
1415674_a_at	10.88265313	10.61796162	10.66808788	10.56361125	10.71527994	10.55999493		
1415675_at	9.733159903	9.807113078	10.03279695	9.858790847	10.03756243	10.00587701		
1415676_a_at	12.2327371	12.08600143	12.39492531	12.12988021	12.15886086	12.09462057		
1415677_at	8.494620928	7.57074354	8.532571262	7.877672468	8.006344756	7.969195083		
1415678_at	10.78227494	10.5624431	10.86456977	10.3011318	10.40717798	10.50016997		
1415679_at	11.69570084	11.63114164	11.67969986	11.60829637	11.6649613	11.64915692		
1415680_at	10.90050271	10.99138343	10.77633482	10.81999107	11.03762005	11.01180531		
1415681_at	10.85069521	11.06834829	10.98970299	10.84059181	10.94414474	10.87226999		
1415682_at	9.556735053	9.315819843	9.64109681	8.307379153	8.426017105	8.541887088		
1415683_at	11.59546026	11.73032524	11.44292373	11.55537457	11.76600437	11.65426006		
1415684_at	8.869762455	8.655886981	9.097590276	8.651620784	9.016728456	8.909072845		

Applications

Differential Expression Analysis

	A	B	C	D	E	F	G	H	I
1	**Probe.id**	**trattato1**	**trattato2**	**trattato3**	**controllo1**	**controllo2**	**controllo3**	**mean exp trattato**	**mean exp controllo**
2	1415670_at	10.32095475	10.3348446	10.32643855	10.0755224	10.103059	10.15155883	=MEDIA(B2:D2)	
3	1415671_at	11.55659724	11.21470877	11.6095877	11.33865796	11.33715745	11.47039553		
4	1415672_at	11.54761726	11.57386469	11.44209389	11.44663589	11.58652392	11.52606895		
5	1415673_at	9.92847925	7.720741249	7.620332624	7.817102331	8.009357375	7.837974306		
6	1415674_a_at	10.88265313	10.61796162	10.66808788	10.56361125	10.71527994	10.55999493		
7	1415675_at	9.733159903	9.807113078	10.03279695	9.858790847	10.03756243	10.00587701		

MEDIA(**num1**; [num2]; ...)

	A	B	C	D	E	F	G	H	I
1	**Probe.id**	**trattato1**	**trattato2**	**trattato3**	**controllo1**	**controllo2**	**controllo3**	**mean exp trattato**	**mean exp controllo**
2	1415670_at	10.32095475	10.3348446	10.32643855	10.0755224	10.103059	10.15155883	10.32741263	=MEDIA(E2:G2)
3	1415671_at	11.55659724	11.21470877	11.6095877	11.33865796	11.33715745	11.47039553		
4	1415672_at	11.54761726	11.57386469	11.44209389	11.44663589	11.58652392	11.52606895		
5	1415673_at	9.92847925	7.720741249	7.620332624	7.817102331	8.009357375	7.837974306		
6	1415674_a_at	10.88265313	10.61796162	10.66808788	10.56361125	10.71527994	10.55999493		
7	1415675_at	9.733159903	9.807113078	10.03279695	9.858790847	10.03756243	10.00587701		
8	1415676_a_at	12.2327371	12.08600143	12.39492531	12.12988021	12.15886086	12.09462057		

Applications

Differential Expression Analysis

	A	B	C	D	E	F	G	H	I	J
1	**Probe.id**	**trattato1**	**trattato2**	**trattato3**	**controllo1**	**controllo2**	**controllo3**	**mean exp trattato**	**mean exp controllo**	**Fold change**
2	1415670_at	10.32095475	10.3348446	10.32643855	10.0755224	10.103059	10.15155883	10.32741263	10.11004674	=H2-I2
3	1415671_at	11.55659724	11.21470877	11.6095877	11.33865796	11.33715745	11.47039553	11.4602979	11.38207031	
4	1415672_at	11.54761726	11.57386469	11.44209389	11.44663589	11.58652392	11.52606895	11.52119195	11.51974292	
5	1415673_at	9.92847925	7.720741249	7.620332624	7.817102331	8.009357375	7.837974306	8.423184375	7.888144671	
6	1415674_a_at	10.88265313	10.61796162	10.66808788	10.56361125	10.71527994	10.55999493	10.72290088	10.61296204	
7	1415675_at	9.733159903	9.807113078	10.03279695	9.858790847	10.03756243	10.00587701	9.857689977	9.967410096	
8	1415676_a_at	12.2327371	12.08600143	12.39492531	12.12988021	12.15886086	12.09462057	12.23788795	12.12778722	
9	1415677_at	8.494620928	7.57074354	8.532571262	7.877672468	8.006344756	7.969195083	8.19931191	7.951070769	
10	1415678_at	10.78227494	10.5624431	10.86456977	10.3011318	10.40717798	10.50016997	10.73642927	10.40282659	

Applications

Differential Expression Analysis

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	**Probe.id**	**trattato1**	**trattato2**	**trattato3**	**controllo1**	**controllo2**	**controllo3**	**mean exp trattato**	**mean exp controllo**	**Fold change**	**pValue**		
2	1415670_at	10.32095475	10.3348446	10.32643855	10.0755224	10.103059	10.15155883	10.32741263	10.11004674	0.217365888	=TESTT(B2:D2)		
3	1415671_at	11.55659724	11.21470877	11.6095877	11.33865796	11.33715745	11.47039553	11.4602979	11.38207031	0.07822759	TESTT(**matrice1**; matrice2; coda; tipo)		
4	1415672_at	11.54761726	11.57386469	11.44209389	11.44663589	11.58652392	11.52606895	11.52119195	11.51974292	0.001449029			
5	1415673_at	9.92847925	7.720741249	7.620332624	7.817102331	8.009357375	7.837974306	8.423184375	7.888144671	0.535039704			
6	1415674_a_at	10.88265313	10.61796162	10.66808788	10.56361125	10.71527994	10.55999493	10.72290088	10.61296204	0.109938836			

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	**Probe.id**	**trattato1**	**trattato2**	**trattato3**	**controllo1**	**controllo2**	**controllo3**	**mean exp trattato**	**mean exp controllo**	**Fold change**	**pValue**		
2	1415670_at	10.32095475	10.3348446	10.32643855	10.0755224	10.103059	10.15155883	10.32741263	10.11004674	0.217365888	=TESTT(B2:D2; E2:G2)		
3	1415671_at	11.55659724	11.21470877	11.6095877	11.33865796	11.33715745	11.47039553	11.4602979	11.38207031	0.07822759	TESTT(matrice1; **matrice2**; coda; tipo)		
4	1415672_at	11.54761726	11.57386469	11.44209389	11.44663589	11.58652392	11.52606895	11.52119195	11.51974292	0.001449029			
5	1415673_at	9.92847925	7.720741249	7.620332624	7.817102331	8.009357375	7.837974306	8.423184375	7.888144671	0.535039704			
6	1415674_a_at	10.88265313	10.61796162	10.66808788	10.56361125	10.71527994	10.55999493	10.72290088	10.61296204	0.109938836			

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	**Probe.id**	**trattato1**	**trattato2**	**trattato3**	**controllo1**	**controllo2**	**controllo3**	**mean exp trattato**	**mean exp controllo**	**Fold change**	**pValue**		
2	1415670_at	10.32095475	10.3348446	10.32643855	10.0755224	10.103059	10.15155883	10.32741263	10.11004674	0.217365888	=TESTT(B2:D2; E2:G2; 2; 3)		
3	1415671_at	11.55659724	11.21470877	11.6095877	11.33865796	11.33715745	11.47039553	11.4602979	11.38207031	0.07822759	TESTT(matrice1; matrice2; coda; **tipo**)		
4	1415672_at	11.54761726	11.57386469	11.44209389	11.44663589	11.58652392	11.52606895	11.52119195	11.51974292	0.001449029			
5	1415673_at	9.92847925	7.720741249	7.620332624	7.817102331	8.009357375	7.837974306	8.423184375	7.888144671	0.535039704			
6	1415674_a_at	10.88265313	10.61796162	10.66808788	10.56361125	10.71527994	10.55999493	10.72290088	10.61296204	0.109938836			

Applications

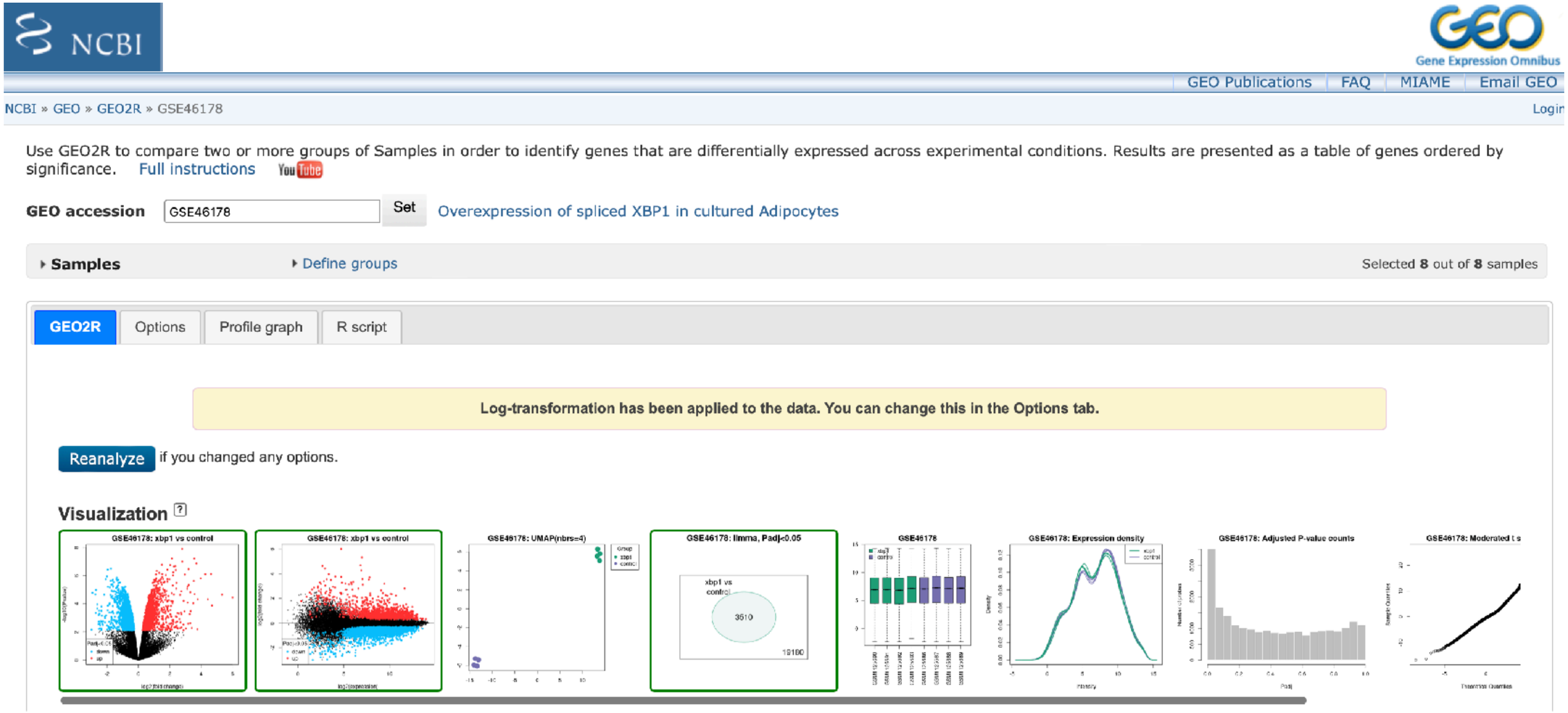
Exercise 1 - differential expression analysis

The Transcription factor Xbp1 was over-expressed in the mouse adipocyte cell line F442A through adenoviral infection. A microarray experiment (GEO series GSE46178) was performed to compare gene expression profiles in cells in which Xbp1 is over-expressed compared to control cells. Four replicates were conducted for each of the two treatments

1. How many genes are upregulated? And how many genes are downregulated? Generate the plots of the differentially expressed genes in the two conditions.
2. With FIMO (https://meme-suite.org/meme/tools/fimo) find among the up genes which is directly regulated by Xbp1

Applications

Exercise 1 - differential expression analysis



Applications

Exercise 3 - Master Regulator analysis

1. Perform a Master regulator off the previous exercise (GEO series GSE46178) to find top regulator mechanism altered by Id2 knockout (Mouse regulons provided from STRING)
2. Get insights about top regulators with https://www.genecards.org

Applications

Exercise 3 - differential expression analysis and Master Regulator

Eye development and photoreceptor maintenance requires the retinal pigment epithelium (RPE), a thin layer of cells that underlies the neural retina (GEO series GSE5048). Three independent replicates of Zebrafish retina with RPE attached consisting of ten samples each at 52hpf (WRR52) were compared with three independent pure retinal samples consisting of ten retinas each at 52hpf (WR52).

1. Analyse the dataset performing a Master Regulator Analysis (Danio Rerio regulons file provided from STRING)
2. Get insights about top regulators with https://www.genecards.org