

# **EMImR: a Shiny Application for Identifying Transcriptomic and Epigenomic Changes**

## **About EMImR**

EMImR is a Shiny Application for Transcriptomic and Epigenomic Changes Identification and data correlation.

The application's main function is to identify the intersection between genetic and epigenetic modifications, including :

- Identify the differentially expressed genes (DEGs)
- Identify the differentially methylated genes (DMGs)
- Determine DEGs associated with DMGs
- Identify the genes associated to differentially expressed interfering miRNA (GDEImRs).
- Determine DEGs associated with differentially expressed interfering miRNA

## **User Interface**

The user interface is simple and easy to use. The first step is to define the type of epigenomics data available : (1) methylation data, (2) Micro RNA data, or (3) both data types. Second, the user needs to upload the data as csv files.

The user also needs to define the p-value (or p-adjust) and the LogFC values to define the differentially expressed genes (DEGs), the differentially methylated genes (DMGs), and the genes associated with differentially expressed microRNAs (DEImRs).

### Select Data Type

Select Data to Analyze:

☒ Methylation

☒ MicroRNA

### Select Species

Species

Homo sapiens

#### Import Expression data CSV File

Browse... expression.csv

Upload complete

#### Import Methylation data CSV File

Browse... methylation.csv

Upload complete

#### Import MicroRNA data CSV File

Browse... miRNA.csv

Upload complete

### DEGs filtering parameters

pval value:

0 0.05 1

Log value:

0 1 2

### DMGs filtering parameters

pval value:

0 0.05 1

Log value:

0 1 2

### DEImRs filtering parameters

pval value:

0 0.05 1

Log value:

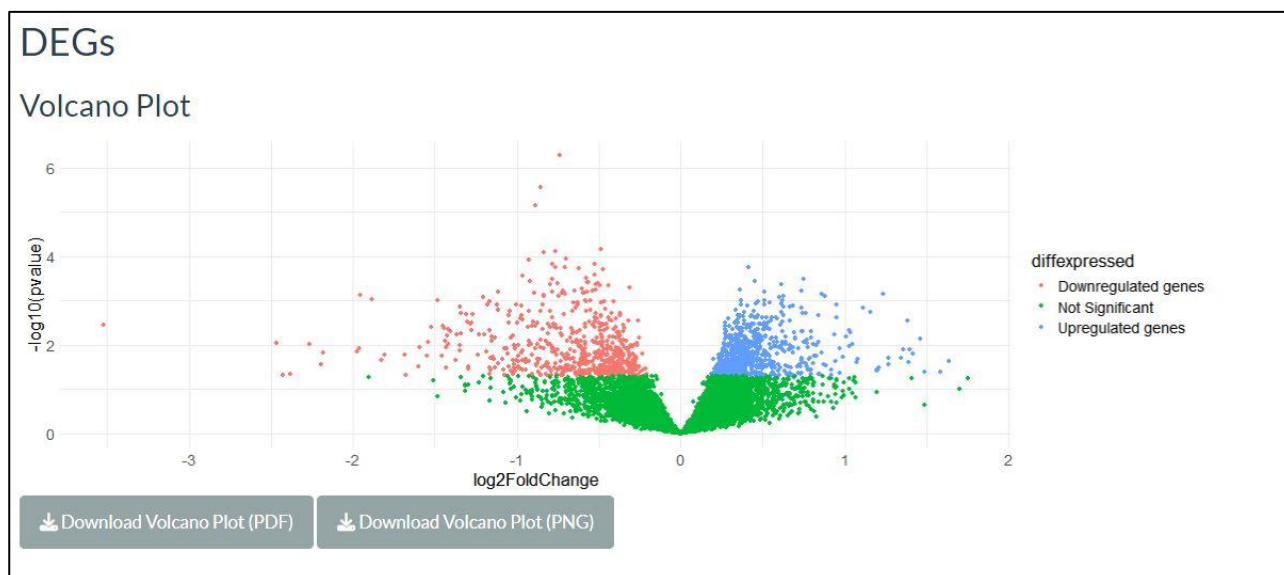
0 2 5

Submit

**Figure 1. The sidebar of the application's user interface**

The outputs are displayed in the application's main panel, which is divided into three sections.

In the first section, the differentially expressed genes are visualized in a volcano plot.



**Figure 2. Volcano Plot visualizing the DEGs.**

The second section includes two tables summarizing the genes that are simultaneously differentially expressed and differentially methylation.

DEGs	intersection DEGs and DMGs	intersection DEGs and DEImR
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Up-Regulated and Hypo-Methylated Genes

Download Table (CSV)

Show 10 entries

Search:

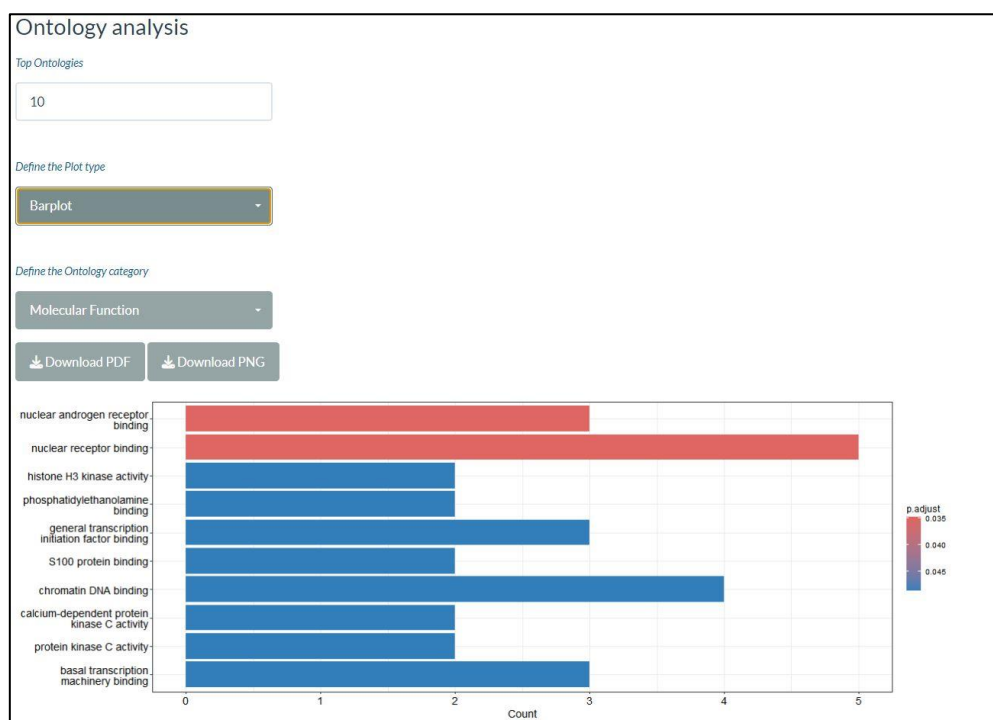
	gene	ID	p.adjust	expression_pvalue	expression_log2FoldChange	GI	cpg	methylation_pvalue	methylation_log2FoldChange	relation.to.CpG.Island
1	AACS	ILMN_1698554	0.30729	0.0265	0.54451	985701019	cg27037969	0.00666	-0.0396	Island
2	ABHD14A	ILMN_1794213	0.35276	0.0444	0.3077989	226437570	cg26791985	0.0272	-0.0267	Island
3	ACP1	ILMN_2344956	0.31908	0.0304	0.3688161	197102727	cg19372772	0.03	-0.00818	Island
4	ACTG1	ILMN_1704961	0.34381	0.041	0.255798	316659407	cg19415364	0.027	-0.0299	Island
5	ACTG1	ILMN_1704961	0.34381	0.041	0.255798	316659407	cg26857837	0.0226	-0.0269	N_Shore
6	AFG3L2	ILMN_2066124	0.31294	0.0282	0.3519276	300192932	cg13397649	0.00624	-0.0352	Island
7	ANXA6	ILMN_1678612	0.27856	0.0188	0.4363789	302129650	cg23481438	0.0194	-0.0106	S_Shore
8	AP3B1	ILMN_1768867	0.29441	0.0233	0.2631009	419636270	cg17417198	0.000922	-0.0492	S_Shore
9	AP3B1	ILMN_1768867	0.29441	0.0233	0.2631009	419636270	cg27312727	0.00769	-0.0338	S_Shore
10	AP3B1	ILMN_1768867	0.29441	0.0233	0.2631009	419636270	cg07757096	0.0409	-0.0122	S_Shore

Showing 1 to 10 of 295 entries

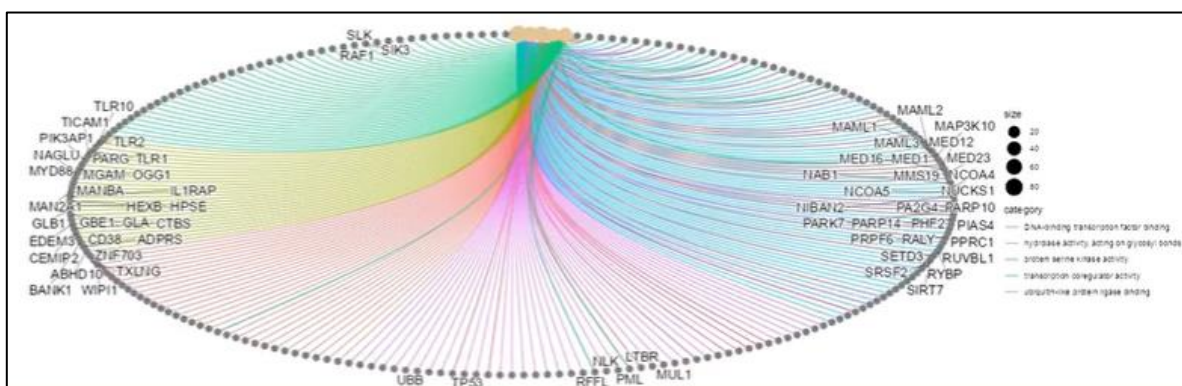
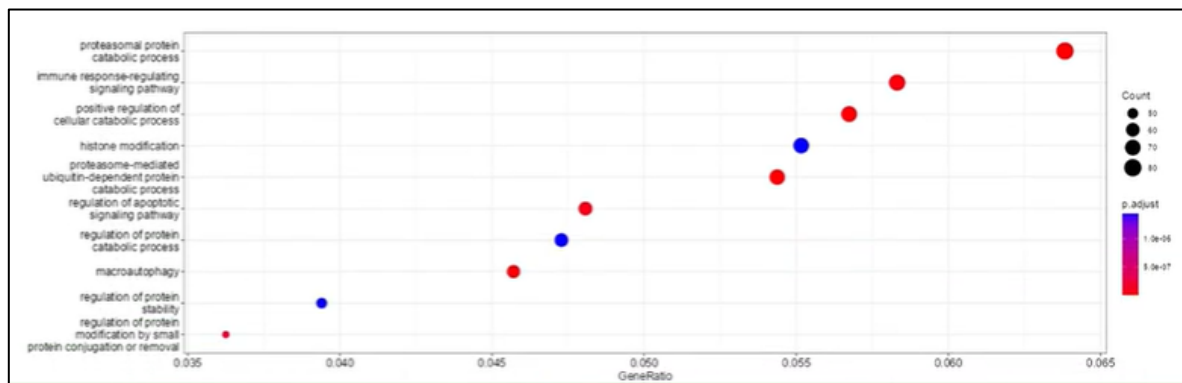
Previous 1 2 3 4 5 ... 30 Next

**Table 3. Table summarizing the genes that are simultaneously differentially expressed and differentially methylation.**

Additionally, ontology analysis is performed. The user needs to define the ontology category between (a) biological Process, (2) cellular components, and (3) molecular functions. The results could be visualized as barplot, dotplot, or cnetplot.



**Figure 4. Ontology analysis data visualization as barplot**



The third section includes have similar tables and ontology analysis plots for the genes that are simultaneously differentially expressed and associated with differentially expressed micro RNA.

All generated data tables could be downloaded as csv files and the generated plots could be downloaded as PDF or PNG files.