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 modififcations, 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).

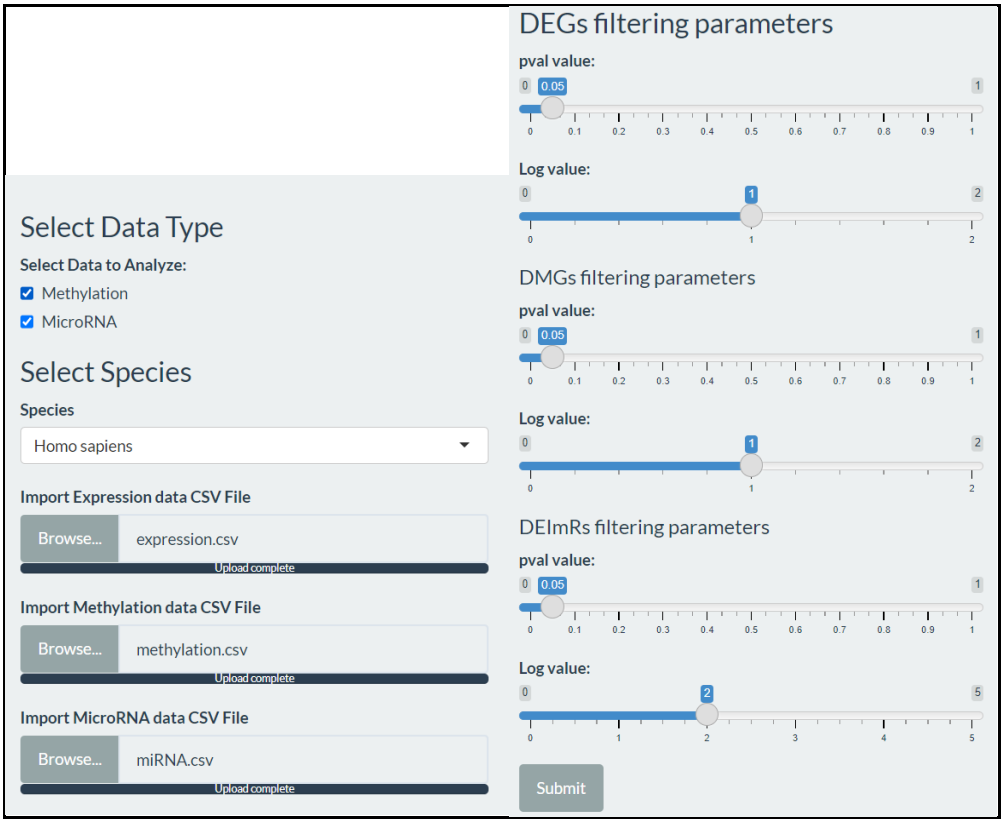

Figure 1. The sidebar of the application's user interface

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.

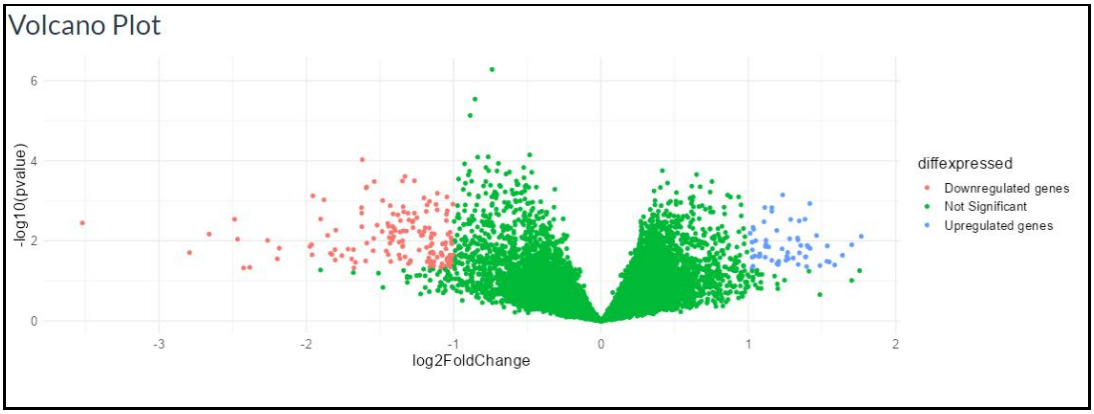

Figure 2. Volcano Plot visualizing the DEGs.

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

Down-Regulated and Hyper-Methylated Genes

Show 25 entries Search:

	gene	ID	p.adj	expression_pvalue	expression_log2FoldChange	Name	methylation_pvalue	methylation_log2FoldChange
1	ADI1	ILMN_1813975	0.3203	0.0319	-1.1635857	cg07737964	0.01382319	0.0217
2	ASH1L	ILMN_1782032	0.32908	0.0359	-1.1570542	cg23821590	0.01869074	0.00988
3	ASH1L	ILMN_1782032	0.32908	0.0359	-1.1570542	cg09410084	0.0398078	0.00859
4	C9orf64	ILMN_1777318	0.35294	0.0447	-1.1627335	cg01614478	0.03880537	0.0126
5	EBF2	ILMN_1844919	0.33685	0.0391	-1.0333316	cg17203647	0.03388374	0.014
6	EBF2	ILMN_1844919	0.33685	0.0391	-1.0333316	cg22280475	0.03021872	0.018
7	NGB	ILMN_1800332	0.29074	0.0218	-1.8265885	cg02400572	0.03500265	0.0265
8	NGB	ILMN_1800332	0.29074	0.0218	-1.8265885	cg08025100	0.04289689	0.0372
9	NGB	ILMN_1800332	0.29074	0.0218	-1.8265885	cg12623422	0.00167966	0.0468
10	NGB	ILMN_1800332	0.29074	0.0218	-1.8265885	cg02181639	0.01318731	0.0282
11	PCDHB9	ILMN_2047885	0.17026	0.00311	-1.0497395	cg09975352	0.04383017	0.0334
12	SPC24	ILMN_2181432	0.13657	0.00127	-1.1806279	cg13932035	0.01154828	0.0103

Showing 1 to 12 of 12 entries Previous 1 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.

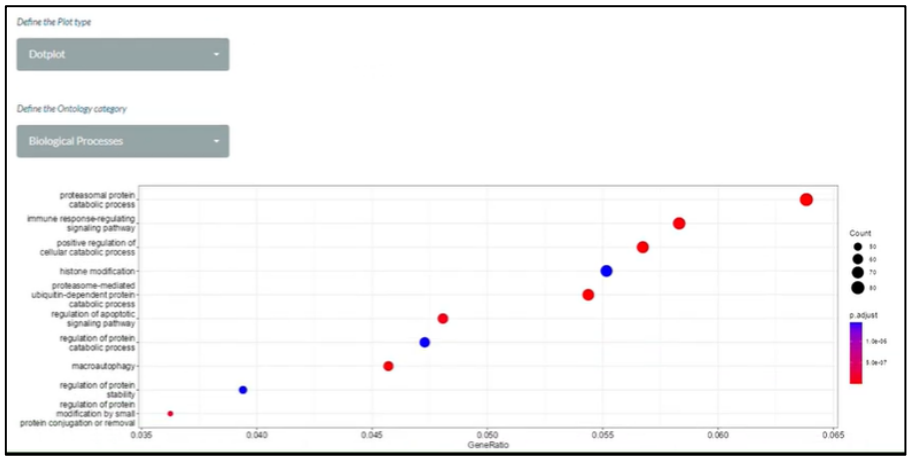

Figure 4. Ontology analysis data visualization as dotplot

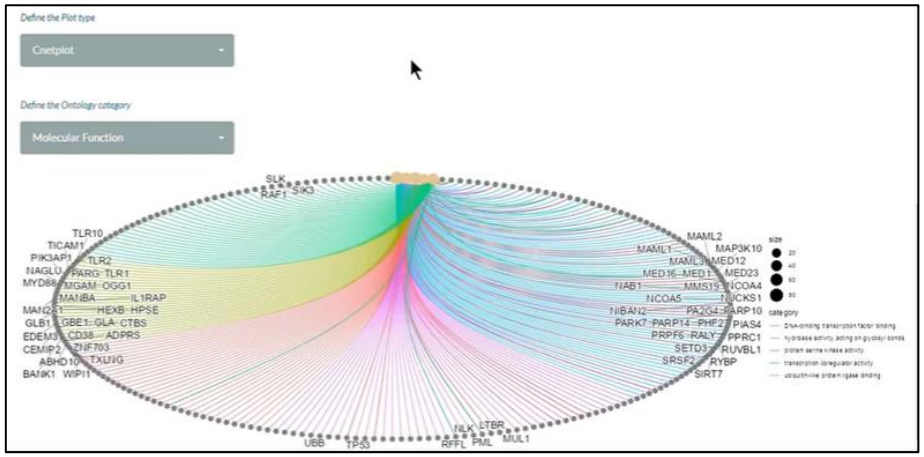

Figure 5. Ontology analysis data visualization as cnetplot

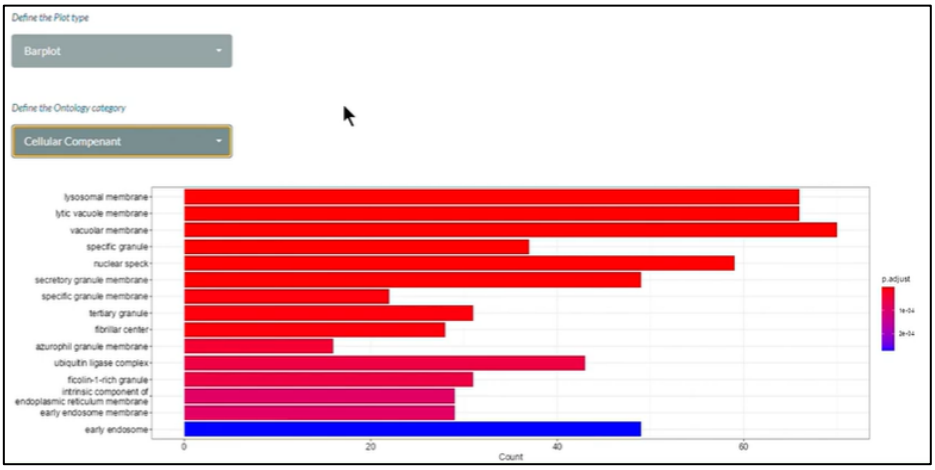

Figure 6. Ontology analysis data visualization as barplot

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.