R Notebook

Code ▾

This is an R Markdown (http://rmarkdown.rstudio.com) Notebook. When you execute code within the notebook, the results appear beneath the code.

Hide

```
View(Data)
```

Hide

```
library(ggplot2)
library(dplyr)
```

```
Attaching package: 'dplyr'

The following object is masked from 'package:Biobase':

    combine

The following object is masked from 'package:matrixStats':

    count

The following objects are masked from 'package:GenomicRanges':

    intersect, setdiff, union

The following object is masked from 'package:GenomeInfoDb':

    intersect

The following objects are masked from 'package:IRanges':

    collapse, desc, intersect, setdiff, slice, union

The following objects are masked from 'package:S4Vectors':

    first, intersect, rename, setdiff, setequal, union

The following objects are masked from 'package:BiocGenerics':

    combine, intersect, setdiff, union

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```
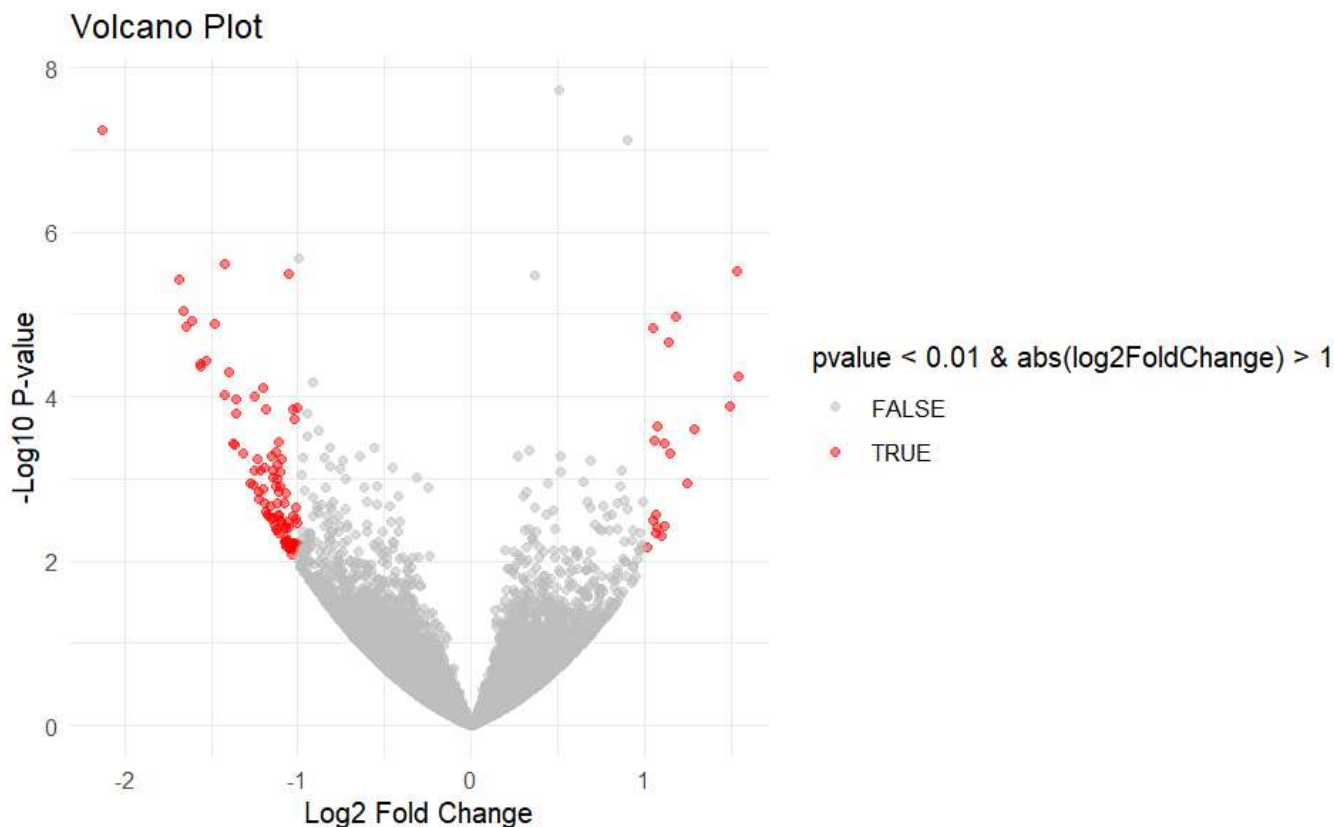
Hide

```
# Create a Volcano plot
ggplot(Data, aes(x = log2FoldChange, y = -log10(pvalue))) +
  geom_point(aes(color = pvalue < 0.01 & abs(log2FoldChange) > 1), alpha = 0.5) +
  scale_color_manual(values = c("grey", "red")) +
  labs(title = "Volcano Plot", x = "Log2 Fold Change", y = "-Log10 P-value") +
  theme_minimal()
```

Volcano Plot

Upregulated genes

```
# Upregulated genes
upregulated_genes <- Data %>%
  filter(log2FoldChange > 1 & pvalue < 0.01)

# View upregulated genes
print(upregulated_genes)
```

Gene <chr>	log2FoldChange <dbl>	pvalue <dbl>	padj <dbl>
EMILIN2	1.534	2.976e-06	0.006809
POU3F4	1.181	1.062e-05	0.015840
LOC285954	1.050	1.456e-05	0.015920
VEPH1	1.137	2.211e-05	0.022670
DTHD1	1.540	5.594e-05	0.043710
PI16	1.495	1.297e-04	0.077940
GALNTL2	1.075	2.298e-04	0.110900
C4orf45	1.288	2.472e-04	0.115900
PDE1B	1.053	3.356e-04	0.144900
BCAN	1.117	3.698e-04	0.147700

1-10 of 19 rows   Previous   **1**   2   Next

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```
# Downregulated genes
downregulated_genes <- Data %>%
  filter(log2FoldChange < -1 & pvalue < 0.01)

# View downregulated genes
print(downregulated_genes)
```

Gene <chr>	log2FoldChange <dbl>	pvalue <dbl>	padj <dbl>
TBX5	-2.129	5.655e-08	0.0004191

Gene <chr>	log2FoldChange <dbl>	pvalue <dbl>	padj <dbl>
IFITM1	-1.687	3.735e-06	0.0068090
LAMA2	-1.425	2.390e-06	0.0068090
CAV2	-1.052	3.213e-06	0.0068090
TNN	-1.658	8.973e-06	0.0147200
COL13A1	-1.647	1.394e-05	0.0159200
IFITM3	-1.610	1.202e-05	0.0159200
SHISA3	-1.477	1.310e-05	0.0159200
ARHGAP29	-1.526	3.675e-05	0.0354700
KIAA1755	-1.562	3.972e-05	0.0362000

1-10 of 91 rows   Previous **1** 2 3 4 5 6 … 10 Next

Gene <chr>	log2FoldChange <dbl>	pvalue <dbl>	padj <dbl>
		3.735e-06	
		2.390e-06	
		3.213e-06	
		8.973e-06	
		1.394e-05	
		1.202e-05	
		1.310e-05	
		3.675e-05	
		3.972e-05	