

MA5111 Assessment 3 - Shiny

You are to design and build a small Shiny app that will allow a user to explore and visualise the results of a differential expression analysis. An example of what this might look like is shown below.

Microarray Analysis

Choose CSV File

Browse...

All_list.csv

Upload complete

Number of Genes to Display:

10

10

Plot Thresholds:

Adj. P-Value:

0.0001

0.045

0.1

log2FC:

0

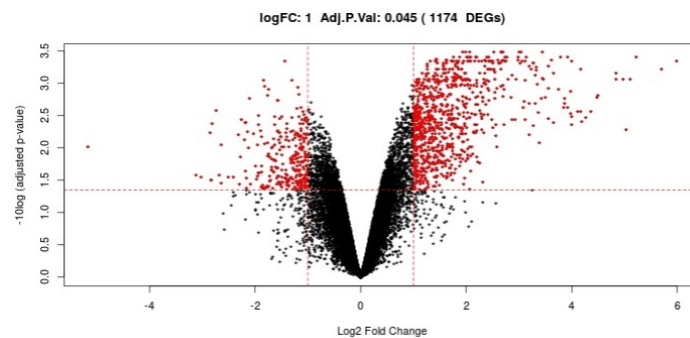
1

8

Gene List

symbol	desc	logFC	adj.P.Val	B
KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	2.67	0.00	9.37
P2RY10	purinergic receptor P2Y, G-protein coupled, 10	3.44	0.00	9.31
CD3D	CD3d molecule, delta (CD3-TCR complex)	2.70	0.00	9.07
CD2	CD2 molecule	2.65	0.00	8.82
SP140	SP140 nuclear body protein	1.98	0.00	8.79
CD3E	CD3e molecule, epsilon (CD3-TCR complex)	3.03	0.00	8.43
IKZF3	IKAROS family zinc finger 3 (Aiolos)	3.00	0.00	8.39
MAP4K1	mitogen-activated protein kinase kinase kinase 1	2.07	0.00	8.35
FMNL1	formin-like 1	1.93	0.00	8.30
THEMIS	thymocyte selection associated	2.52	0.00	8.29

Volcano Plot



The app will allow the user to upload a csv similar to the one provided and should function as follows:

- The data will be read in using a reactive function.
- The desired number of genes (specified by a numeric input field) will be displayed in a table.
- Sliders should be provided to allow the user to set thresholds for adjusted p-values and logFC values. A volcano plot showing the thresholds set and highlighting the differentially expressed genes at those thresholds should be displayed. The thresholds set and number of differentially expressed genes should be shown in the plot title.
- Include one other feature of your choice.

Marks will be awarded for:

Design (layout, use of formatting and overall visual appeal of app)	15
Functionality (as specified above)	70
Code (readability, use of meaningful variable names, comments etc.)	15

You should submit a single app.R file to Blackboard.