EBSeq-two/multiple conditions

Data file input (support .csv, .txt, .tab)

Choose File | no file selected

Condition vector file name (support .csv, .txt, .tab)

Choose File | no file selected

I_g vector for isoform analysis file name (support .csv, .txt, .tab) - Gene analysis will be applied if I_g vector is not provided

Choose File | no file selected

Do you need to normalize data?

- ● Yes
- ○ No

Patterns of interest for - comma delimited (e.g. if you're interested in pattern 1,2,3 from the MultiPattern output, type: '1,2,3'. Default is all possible patterns.)

[   ]

The number of iteration for EM

[5   ⇕]

Target FDR

[0.05   ⇕]

Please select a folder for output :

[Select Output Folder]

Export file name - DE genes only (FDR cutoff) sorted by PPDE

[DEListSortedbyPPDE_TwoCond]

Export file name for two conditions - Output with sorted gene order by PPDE

[OutputSortedbyPPDE_TwoCond]

Export file name for two conditions - Output with original gene order from input file

[OutputOrigFileOrder_TwoCond]

Export file name for multiple conditions - Output with posterior probability of being in each pattern

[OutputPP_MultiCond]

Export file name for multiple conditions - The most likely pattern of each gene

[OutputMAP_MultiCond]

Export file name - normalized expression matrix

[Normalized]

Export file name - Session Info

[Info]

[Submit for processing]