

MLExpResso Cheat Sheet



Expression

Data

Data sets for testing expression differences must contain per gene read counts. Columns should correspond to genes, rows to samples.

As input for tests correspond to expression, the `calculate_test` function expects count data in the form of a matrix of integer values. The value in the *i*-th row and the *j*-th column tells how many reads can be assigned to gene *j* in sample *i*.

Note that for some tests the values in the matrix should be un-normalized counts. so transformed or normalized values such as counts scaled by library size should not be used as input. More idetails is in the documentation of `calculate_test` function.

Tests

Testing for differences.

`MLExpResso::calculate_test(data, condition, test)`

Value	Test
'ttest'	student's t-tets
'nbinom2'	negative binomial test
'lrt'	likelihood-ratio test
'qlf'	quasi-likelihood F-test

Example

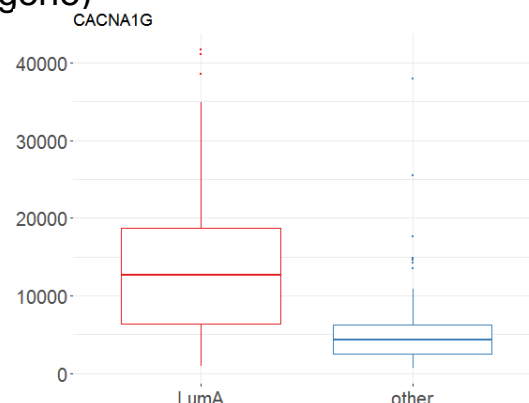
```
library(MLExpResso)
library(MLExpRessodata)
exp <- BRCA_mRNAseq_chr17[, -1]
gr_exp <- BRCA_mRNAseq_chr17[, -1]
gr_exp <- ifelse(group=='LumA', 'LumA', 'other')
calculate_test(exp, gr_exp, 'lrt')
```

Plots

`MLExpResso::plot_diff_boxplot(data, condition, gene)`

Example

```
plot_diff_boxplot(exp, gr_exp, 'CACNA1G')
```



Methylation

Data

`MLExpResso::aggregate_probes(data)`

Tests

Testing for differences.

`MLExpResso::calculate_test(data, condition, test)`

Value	Test
'ttest'	student's t-test
'methanalysis'	quasi-likelihood F-test

Example

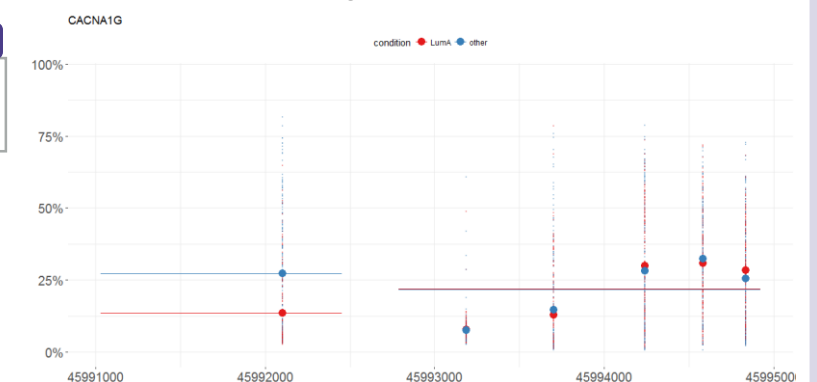
```
library(MLExpResso)
library(MLExpRessodata)
met <-
aggregate_probes(BRCA_methylation_chr17[, -1])
gr_met <- BRCA_methylation_chr17[, -1]
gr_met <- ifelse(group=='LumA', 'LumA', 'other')
calculate_test(met, gr_met, 'ttest')
```

Plots

`MLExpResso::plot_methylation_path(data, condition, gene)`

Example

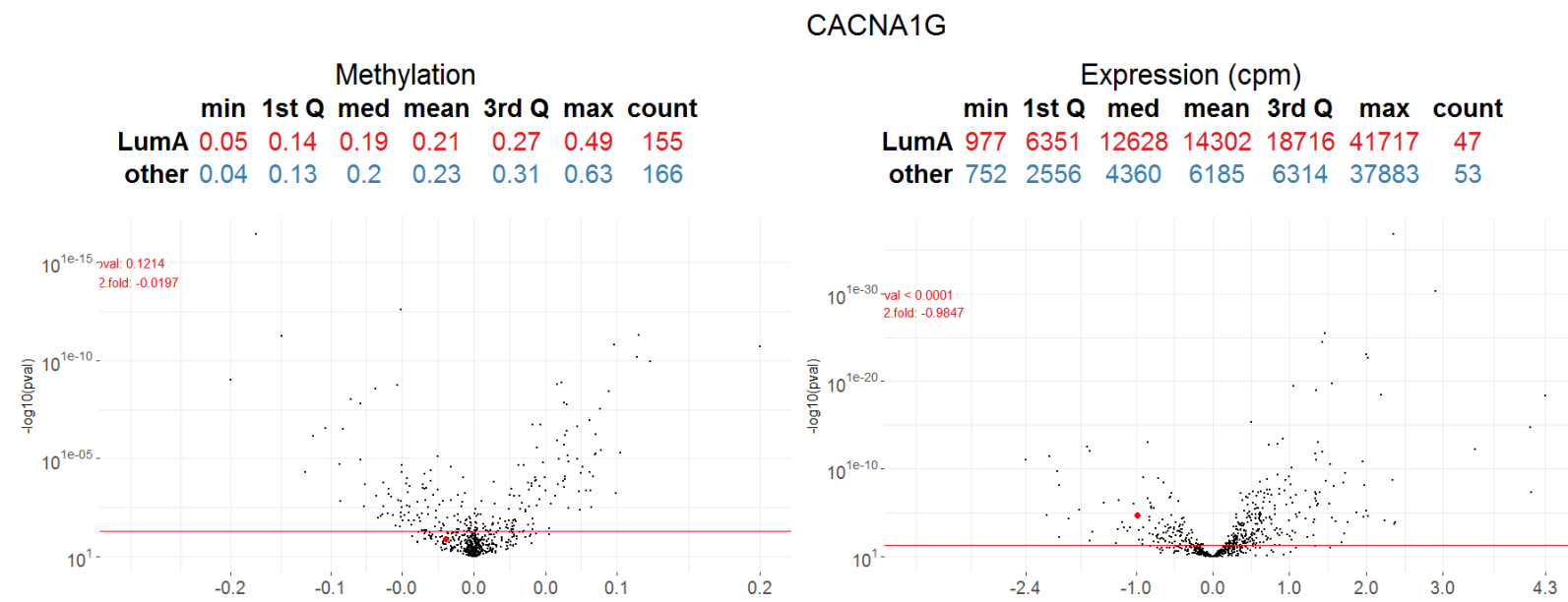
```
plot_methylation_path(met, gr_met,
'CACNA1G')
```



Visualizations

Plot_volcanoes()

`MLEXPRESSO::plot_volcanoes(data.m, data.e, condition.m, condition.e, gene, test.m, test.e)`



Plot_gene()

`MLEXPRESSO::plot_genes(data.m, data.e, condition.m, condition.e, gene)`

