

# MExpResso: differential expression and methylation analysis

Case study using RTCGA data

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## 1 Package (Abstract?)

It is considered that the result of increased methylation is decreased gene expression. While, recent studies suggest that the relationship between methylation and expression is more complex than was previously thought. The package **MExpResso** provides methods to test for differential expression and methylation by use of the negative binomial distribution and t-test. Additionally **MExpResso** allows to visualize results in a simple way.

## 2 Standard Workflow

In this vignette we will work with the data sets containing information about gene expression and methylation for patients with breast cancer. We will analyze differences in methylation and expression for patients with different subtypes of BRCA cancer.

### 2.0.0.1 BRCA\_methylation\_chr17 data set

In this section, we will work with the methylation level data from TCGA database. Package contains **BRCA\_methylation\_all** dataset. **BRCA\_methylation\_all** contains information about methylation of CpG islands for patients with breast cancer. Rows of this data set correspond to patients, more precisely, to samples taken from patients. First column **SUBTYPE** corresponds to a subtype of BRCA cancer, next columns correspond to CpG islands. Values inside the table indicate the methylation level of CpG island for specified sample.

```
library(MetExpr)
```

```
## Setting options('download.file.method.GEOquery'='auto')
```

```
## Setting options('GEOquery.inmemory.gpl'=FALSE)
```

```
## Warning: namespace 'bit64' is not available and has been replaced
```

```
## by .GlobalEnv when processing object 'silent'
```

```
## Warning: namespace 'bit64' is not available and has been replaced
## by .GlobalEnv when processing object 'silent'

## No methods found in "genoset" for requests: toGenomeOrder

##
```

```
head(BRCA_methylation_all)[1:5,1:4]
```

```
##                               SUBTYPE cg00000292 cg00002426 cg00003994
## TCGA-A1-A0SD-01A-11D-A112-05    LumA  0.6055526 0.06197412 0.33345006
## TCGA-A2-A04N-01A-11D-A112-05    LumA  0.7433957 0.07044132 0.32317983
## TCGA-A2-A04P-01A-31D-A032-05    Basal  0.2897206 0.25927969 0.02402149
## TCGA-A2-A04Q-01A-21D-A032-05    Basal  0.7898920 0.63619354 0.10885097
## TCGA-A2-A04T-01A-21D-A032-05    Basal  0.6512270 0.27268734 0.03413620
```

In this analysis we would like to find genes with different methylation and expression. At first we need to use function `map_to_gene`, which generates new data frame with CpG islands mapped to genes.

```
BRCA_methylation_gen <- map_to_gene(BRCA_methylation_all[, -1])
head(BRCA_methylation_gen)[1:5,1:4]
```

```
##                               c.0.627525304291071..0.61889803781234..0.561973209745455..0.646872541683
## TCGA-A1-A0SD-01A-11D-A112-05                                0.6
## TCGA-A2-A04N-01A-11D-A112-05                                0.6
## TCGA-A2-A04P-01A-31D-A032-05                                0.5
## TCGA-A2-A04Q-01A-21D-A032-05                                0.6
## TCGA-A2-A04T-01A-21D-A032-05                                0.6
##                               X7A5      A1BG      A2BP1
## TCGA-A1-A0SD-01A-11D-A112-05 0.13199966 0.9686056 0.03378443
## TCGA-A2-A04N-01A-11D-A112-05 0.11862215 0.9785676 0.06679088
## TCGA-A2-A04P-01A-31D-A032-05 0.08032758 0.9793897 0.29396794
## TCGA-A2-A04Q-01A-21D-A032-05 0.08958826 0.9718291 0.21287231
## TCGA-A2-A04T-01A-21D-A032-05 0.13135664 0.9801575 0.21864058
```

In this case we have two conditions, connected with subtypes of breast cancer.

Before we go to the testing, we need to define condition values for each sample. We would like to test for differences between LumA subtype and other subtypes of breast cancer, so we create a vector, which each element corresponds to a sample. Our division into this two groups relies on numbers of occurrences of each subtype. The LumA subtype is the most common, in case of breast cancer.

```
condition_met <- ifelse(BRCA_methylation_all$SUBTYPE=="LumA", "LumA", "other")
head(condition_met, 8)
```

```
## [1] "LumA" "LumA" "other" "other" "other" "other" "LumA" "other"
```

### 2.0.0.2 BRCA\_mRNAseq\_all data set

Data set `BRCA_mRNAseq_all` contains information about gene expression. This data set contains per-gene read counts computed for genes for 736 patients with breast cancer. Rows of this data set correspond to samples taken from patients. First column `SUBTYPE` corresponds to a subtype of BRCA cancer, next columns correspond to genes.

```
BRCA_mRNAseq_all[1:5,1:5]
```

```
##                               SUBTYPE A1BG A1CF A2BP1 A2LD1
## TCGA-A1-A0SB-01A-11R-A144-07    Normal  164    0    22   127
## TCGA-A1-A0SD-01A-11R-A115-07    LumA   546    0     1   331
```

```
## TCGA-A1-A0SE-01A-11R-A084-07    LumA 1341    0    2    498
## TCGA-A1-A0SF-01A-11R-A144-07    LumA  836    1    0    526
## TCGA-A1-A0SG-01A-11R-A144-07    LumA  512    3   25    451
```

In our example we will test for differential expression between groups with LumA breast cancer subtype and other subtypes of that cancer. Again we will use vector `conditions`, which consist of two values corresponds to subtype of breast cancer: LumA and other.

```
condition_exp <- ifelse(BRCA_mRNAseq_all$SUBTYPE=="LumA","LumA","other")
head(condition_exp, 8)
```

```
## [1] "other" "LumA"  "LumA"  "LumA"  "LumA"  "LumA"  "other" "LumA"
```

### 3 Testing

```
genes_comparison <- comparison_table(BRCA_mRNAseq_all[, -1], BRCA_methylation_gen, condition_exp, condi
head(genes_comparison)
```

```
##      id nbinom2.log2.fold  nbinom2.pval ttest.log2.fold  ttest.pval
## 1   A1BG      -0.4855862  7.330514e-13    0.01318900  1.119637e-01
## 2  A2BP1      -0.8461944  4.315880e-07   -0.05677500  1.019935e-02
## 3   A2M       0.2352576  1.675724e-03    0.03310777  1.686741e-01
## 4  A2ML1      4.1919667  8.164823e-201    0.17016379  1.019044e-12
## 5  A4GALT     -0.1927530  9.741784e-03   -0.00841392  5.203636e-01
## 6  A4GNT      0.2208814  8.021080e-02    0.06387711  1.957709e-05
```

#### 3.1 Choosing most different genes

Sorting ...

```
genes_comparison_sorted <- genes_comparison[order(genes_comparison$ttest.pval), ]
head(genes_comparison_sorted)
```

```
##      id nbinom2.log2.fold  nbinom2.pval ttest.log2.fold
## 10601 TNFRSF10A      0.2038466  2.272347e-04    0.1401746
## 10218  TBX19       1.0212930  3.226882e-49   -0.3479977
## 4958  IGFALS      -1.9559531  1.892160e-54   -0.1581887
## 6214  MGST1       0.4688093  8.122084e-08    0.2583506
## 5895  LUC7L      -0.1772576  5.466990e-05    0.1414415
## 8870  RRM2       1.4786220  5.630314e-103   0.1051548
##      ttest.pval
## 10601 2.568571e-22
## 10218 2.252784e-21
## 4958  6.144850e-21
## 6214  7.121403e-20
## 5895  6.298008e-18
## 8870  7.790260e-18
```

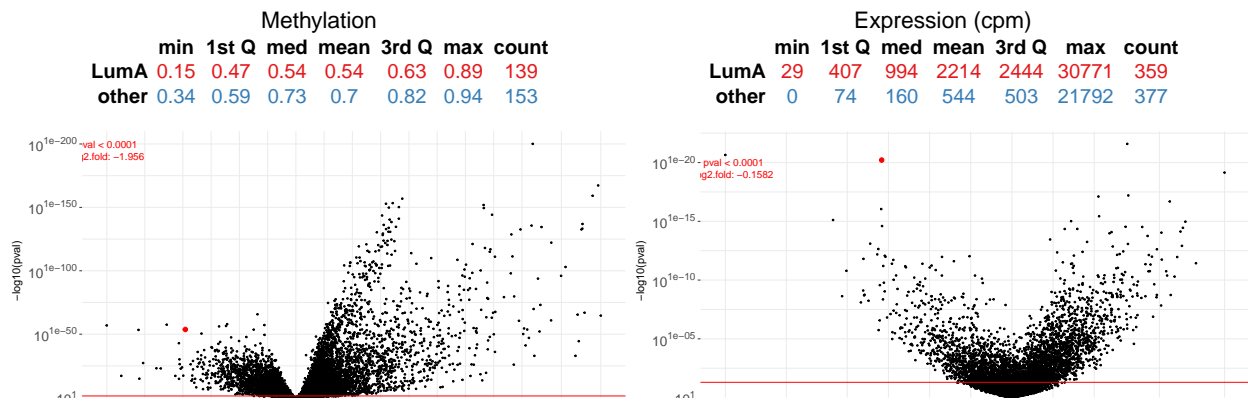
IGFALS!

## 4 Visualization

Visualizing chosen gene - IGFALS.

```
test_exp <- genes_comparison[,c(1,2,3)]
test_met <- genes_comparison[,c(1,4,5)]
```

```
visual_volcano(condition_exp, condition_met,
  BRCA_mRNAseq_all[, -1], BRCA_methylation_all[, -1],
  "IGFALS",
  list(test_exp), list(test_met),
  values=TRUE)
```



Note that visual\_gene methylation require data frame with cpg islands, not genes.

```
visual_gene(condition_exp, condition_met,
  BRCA_mRNAseq_all[, -1], BRCA_methylation_all[, -1],
  "IGFALS")
```

