

Differential expression using RNA-seq data

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Packages

We have to load the package **SummarizedExperiment** to use the class **RangedSummarizedExperiment** or simply **SummarizedExperiment**.

```
pacman::p_load(tami, SummarizedExperiment)
```

Data

The RNA-seq dataset used in this vignette is **PRJNA297664** and can be loaded from **tami-data**.

```
data(PRJNA297664, package="tamidata")
```

The phenotypic covariables are

```
colData(PRJNA297664)
```

DataFrame with 6 rows and 4 columns

```
  SampleName      Run      treatment replication
<character> <character>      <factor>      <numeric>
1 GSM1900735 SRR2549634 Wild                1
2 GSM1900737 SRR2549636 Wild                3
3 GSM1900739 SRR2549638 SEC66 deletion        2
4 GSM1900736 SRR2549635 Wild                2
5 GSM1900738 SRR2549637 SEC66 deletion        1
6 GSM1900740 SRR2549639 SEC66 deletion        3
```

The covariable `colData(x)[,"treatment"]` will be used as the experimental factor giving the group or condition of each sample.

Marginal differential expression using edgeR

Common dispersion

We can consider a common dispersion.

```
PRJNA297664_common_deo =
  tami::dema(x=PRJNA297664,y="treatment",test = edgercommon,
            correction = "BH",fdr= 0.01,foutput = "output")
```

A data.frame with the results is obtained with

```
df1 = tidy(PRJNA297664_common_deo)
```

The same report in a html file is obtained with

```
glimpse(PRJNA297664_common_deo)
```

```
Warning: replacing previous import 'utils::findMatches' by
'S4Vectors::findMatches' when loading 'AnnotationDbi'
```

```
Warning: replacing previous import 'utils::findMatches' by
'S4Vectors::findMatches' when loading 'AnnotationForge'
```

```
Registered S3 method overwritten by 'GGally':  
  method from  
+ .gg    ggplot2
```

```
[1] "./reports/output.html"
```

We can open the file with

```
browseURL(glimpse(PRJNA297664_common_deo))
```

Tagwise dispersion

The second choice is to consider a different dispersion parameter per gene.

```
PRJNA297664_tagwise_deo =  
  dema(x=PRJNA297664,y="treatment",test = edgertagwise,  
        correction = "BH",fdr= 0.01,foutput = "output")
```

A data.frame with the results is obtained with

```
df1 = tidy(PRJNA297664_tagwise_deo)
```

The same report in a html file is obtained with

```
glimpse(PRJNA297664_tagwise_deo)
```

```
[1] "./reports/output.html"
```

We can open the file with

```
browseURL(glimpse(PRJNA297664_tagwise_deo))
```