

# Dirichlet-multinomial framework for differential splicing and SQTl analysis.

Malgorzata Nowicka, Mark Robinson\*

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## 1 Dirichlet-multinomial workflow to detect differential splicing (DS) in RNA-seq data

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Load *DM* package.

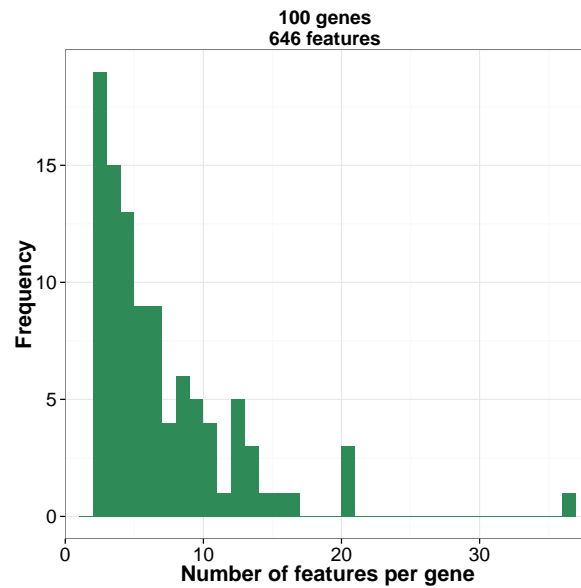
```
suppressPackageStartupMessages(library(DM))
```

Create a `dmDSdata` object that contains counts.

```
counts <- dataDS_counts[, -1]
group_id <- dataDS_counts[, 1]
group_split <- limma::strsplit2(group_id, ":")
gene_id <- group_split[, 1]
feature_id <- group_split[, 2]
sample_id = dataDS_metadata$sample_id
group = dataDS_metadata$group
d <- dmDSdata(counts = counts, gene_id = gene_id, feature_id = feature_id,
  sample_id = sample_id, group = group)
plotData(d)
```

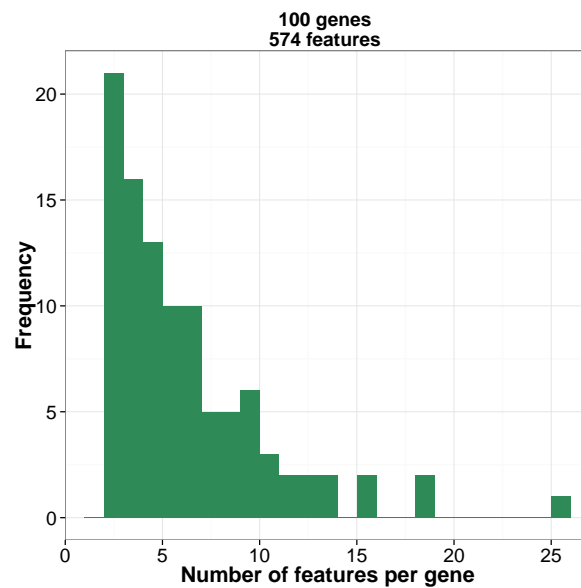
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\*[gosia.nowicka@uzh.ch](mailto:gosia.nowicka@uzh.ch)



Filter genes and transcripts with low expression.

```
d <- dmFilter(d)
plotData(d)
```



Estimate dispersion.

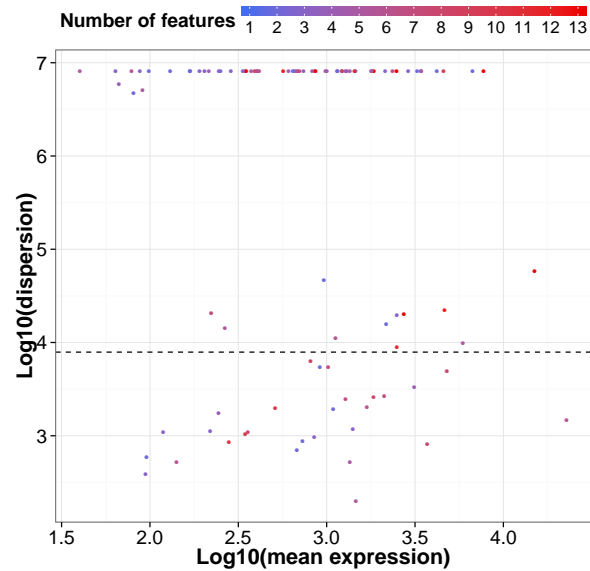
```
d <- dmDispersion(d, BPPARAM = BiocParallel::MulticoreParam(workers = 5))

## * Calculating mean gene expression..
## Took 0.624 seconds.
## * Estimating common dispersion..
## Took 21.475 seconds.

## ! Using common_dispersion = 7884.85 as disp_init in 'grid' mode !

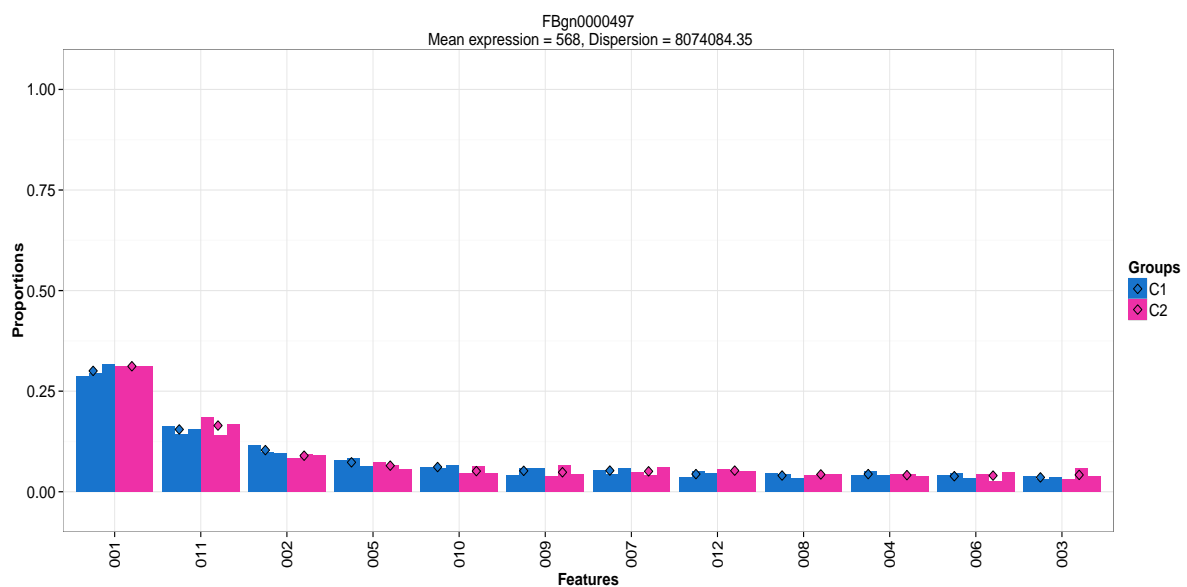
## * Estimating genewise dispersion..
## Took 5.367 seconds.
```

```
plotDispersion(d)
```



Estimate proportions.

```
d <- dmFit(d)
## * Fitting full model..
## Took 14.925 seconds.
gene_id <- names(d)[1]
plotFit(d, gene_id = gene_id, plot_type = "barplot")
## Plot gene 1: FBgn0000497
```



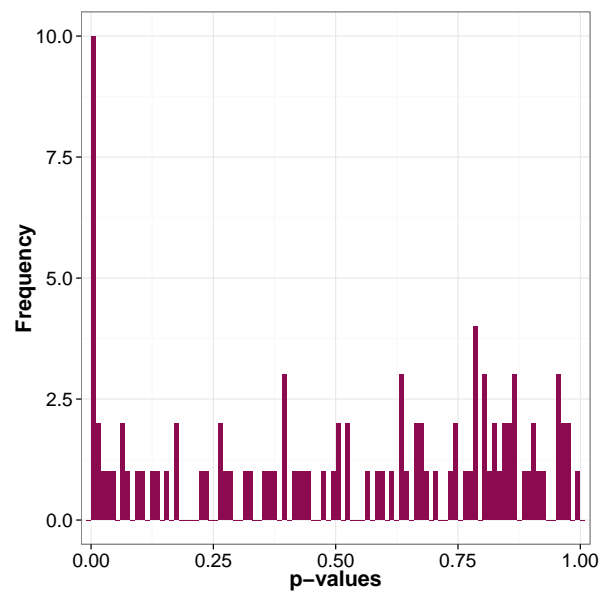
Use likelihood ratio to test for differential splicing.

```
d <- dmLRT(d)

## Running comparison between groups: C1, C2

## * Fitting null model..
## Took 20.617 seconds.
## * Calculating likelihood ratio statistics..
## Took 0.01198125 seconds.

plotLRT(d)
```



```
results <- results(d)

gene_id <- results$gene_id[1]
plotFit(d, gene_id = gene_id)

## Plot gene 1: FBgn0000497
```

