

Differential Gene Expression Workflow

Workshop on RNA-Seq

NBIS | 16-Nov-2020

NBIS, SciLifeLab

Contents

- Preprocessing
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Raw data

- Raw count table

```
##                               Sample_1 Sample_2 Sample_3 Sample_4 Sample_5 Sample_6
## ENSG000000000003          321    303    204    492    455    359
## ENSG000000000005           0      0      0      0      0      0
## ENSG000000000419          696    660    472    951    963    689
## ENSG000000000457          59     54     44    109     73     66
## ENSG000000000460          399    405    236    445    454    374
## ENSG000000000938           0      0      0      0      0      1
```

- Metadata

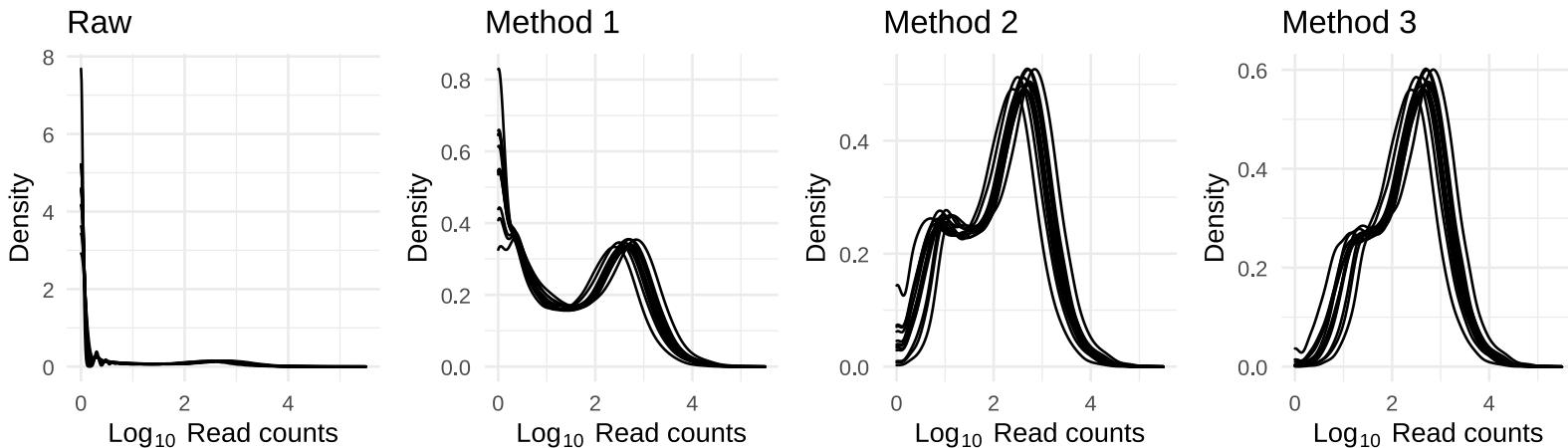
```
##                               Sample_ID Sample_Name Time Replicate Cell
## Sample_1   Sample_1            t0_A    t0        A A431
## Sample_2   Sample_2            t0_B    t0        B A431
## Sample_3   Sample_3            t0_C    t0        C A431
## Sample_4   Sample_4            t2_A    t2        A A431
## Sample_5   Sample_5            t2_B    t2        B A431
## Sample_6   Sample_6            t2_C    t2        C A431
```

Preprocessing

- Remove genes and samples with low counts

```
cf1 <- cr[rowSums(cr>0) >= 2, ]  
cf2 <- cr[rowSums(cr>5) >= 2, ]  
cf3 <- cr[rowSums(edgeR::cpm(cr)>1) >= 2, ]
```

- Inspect distribution

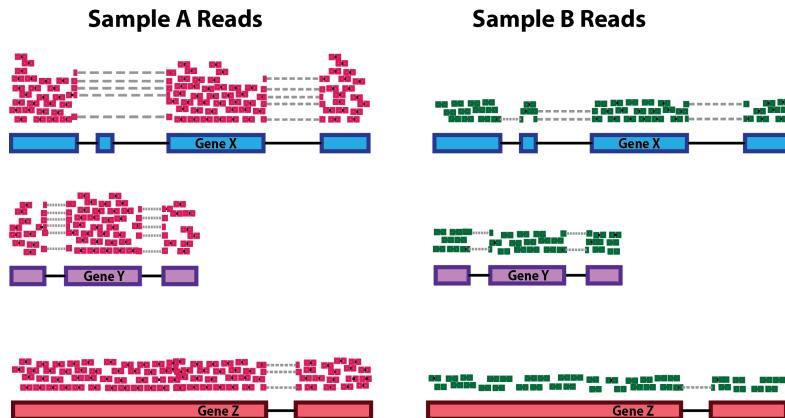


- Inspect the number of rows

```
## Raw: 59573, Method 1: 24194, Method 2: 16519, Method 3: 14578
```

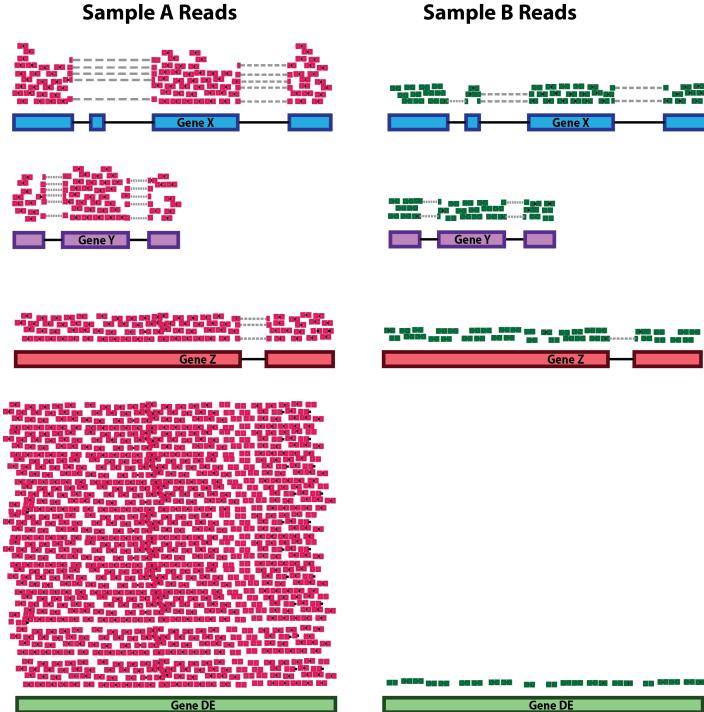
Normalisation

- Make counts comparable across samples
- Control for sequencing depth



```
##   s1 s2 s1_tc s2_tc
## x 20 6 0.33 0.38
## y 25 6 0.42 0.38
## z 15 4 0.25 0.25
```

- Control for sequencing bias

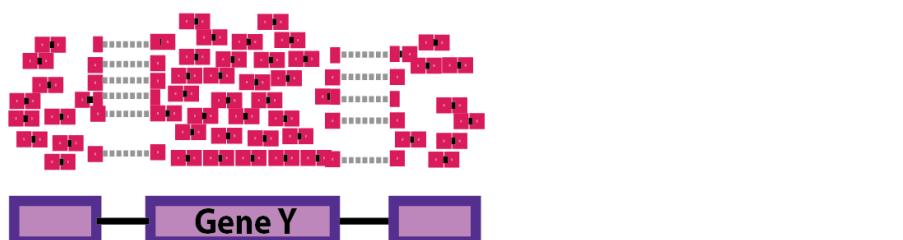
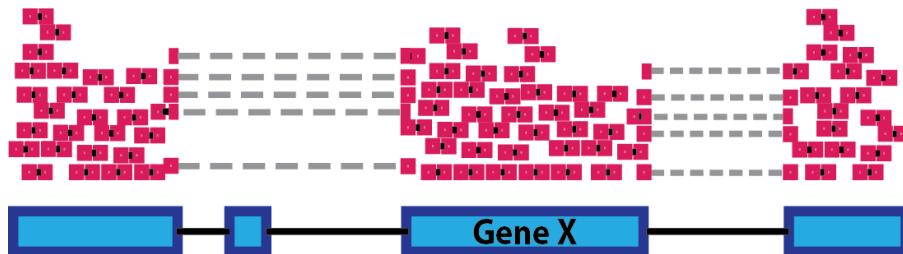


```
##   s1 s2 s1_tc s2_tc
## x 20 20 0.12 0.39
## y 25 25 0.16 0.49
## z 15 4 0.09 0.08
## de 100 2 0.62 0.04
```

Normalisation

- Make counts comparable across features (genes)

Sample A Reads



```
##   counts gene_length norm_counts
## 1     50          10        5
## 2     25           5        5
```

- Bring counts to a human-friendly scale

Normalisation

- CPM, RPKM, FPKM, TPM, RLE, MRN, Q, UQ, TMM, VST, RLOG, VOOM ... Too many...
- **CPM:** Controls for sequencing depth when dividing by total count. Not for within-sample comparison or DE.
- **RPKM/FPKM:** Controls for sequencing depth and gene length. Good for technical replicates, not good for sample-sample due to compositional bias. Assumes total RNA output is same in all samples. Not for DE.
- **TPM:** Similar to RPKM/FPKM. Corrects for sequencing depth and gene length. Also comparable between samples but no correction for compositional bias.
- **TMM/RLE/MRN:** Improved assumption: The output between samples for a core set only of genes is similar. Corrects for compositional bias. Used for DE. RLE and MRN are very similar and correlates well with sequencing depth. `edgeR::calcNormFactors()` implements TMM, TMMwzp, RLE & UQ. `DESeq2::estimateSizeFactors` implements median ratio method (RLE). Does not correct for gene length.
- **VST/RLOG/VOOM:** Variance is stabilised across the range of mean values. For use in exploratory analyses. Not for DE. `vst()` and `rlog()` functions from *DESeq2*. `voom()` function from *Limma* converts data to normal distribution.
- **geTMM:** Gene length corrected TMM.

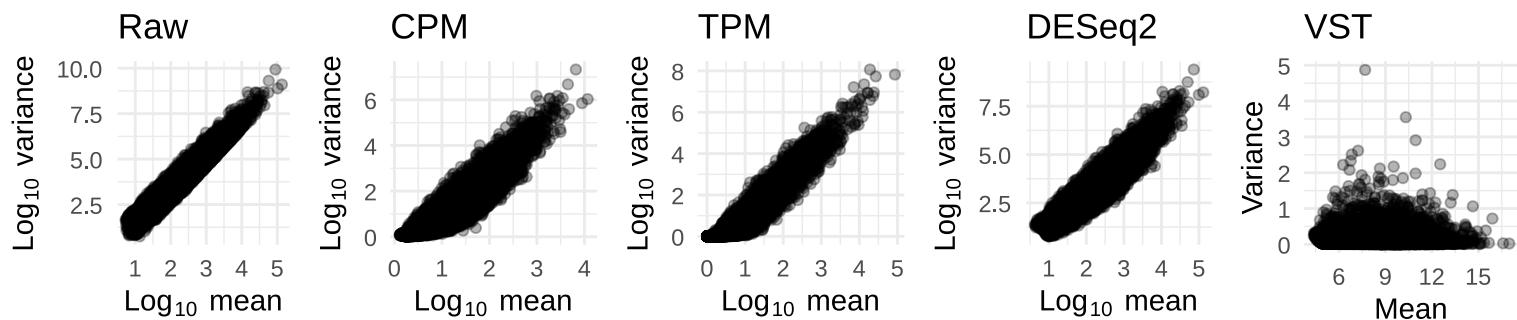
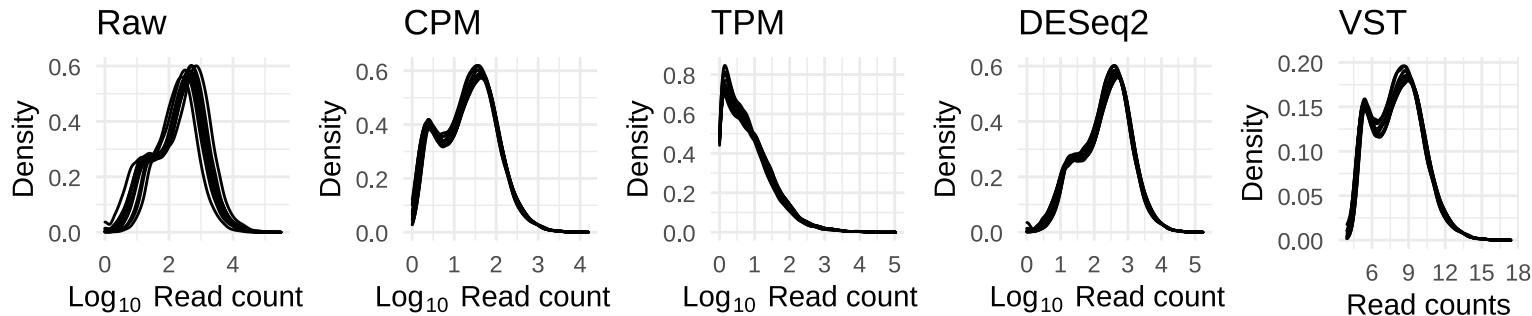
DOI: Dillies, Marie-Agnes, et al. "A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis." *Briefings in bioinformatics* 14.6 (2013): 671-683

DOI: Evans, Ciaran, Johanna Hardin, and Daniel M. Stoebel. "Selecting between-sample RNA-Seq normalization methods from the perspective of their assumptions." *Briefings in bioinformatics* (2017)

Normalisation

Recommendations

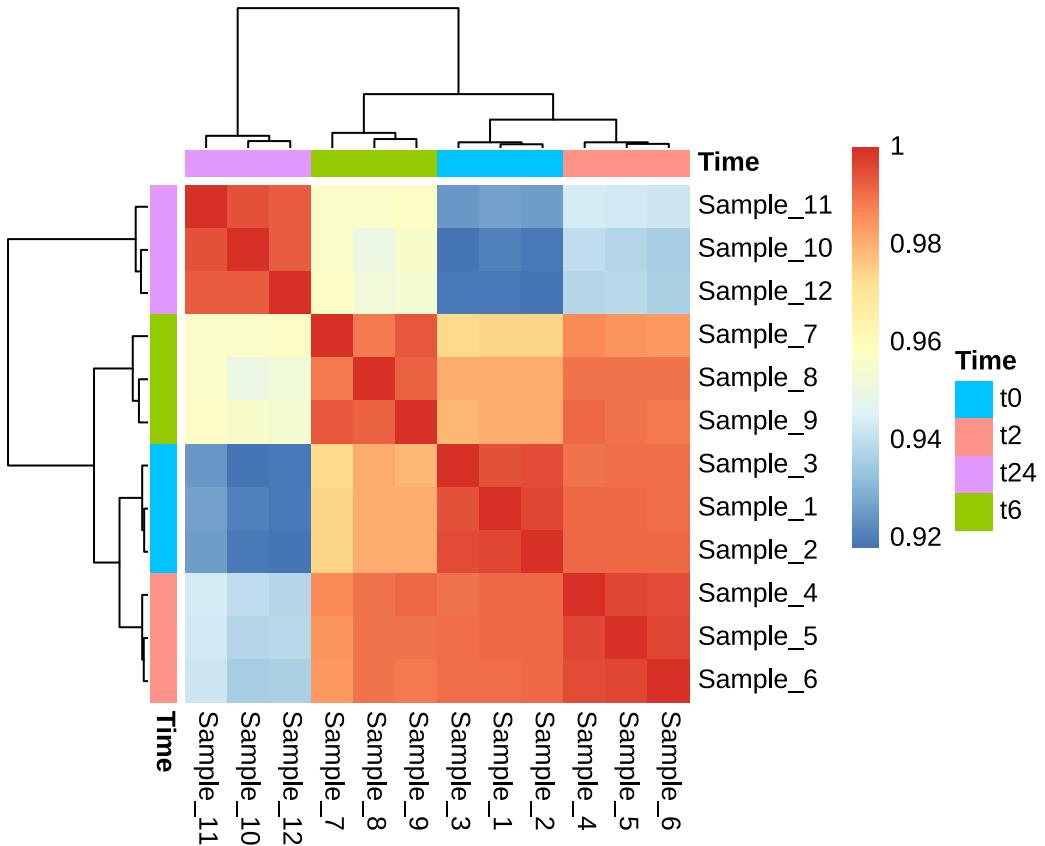
- For DGE using DGE R packages (DESeq2, edgeR, Limma etc), use raw counts
- For visualisation (PCA, clustering, heatmaps etc), use VST or RLOG
- For own analysis with gene length correction, use TPM (maybe geTMM?)
- Other solutions: spike-ins/house-keeping genes



Exploratory | Correlation

- Correlation between samples

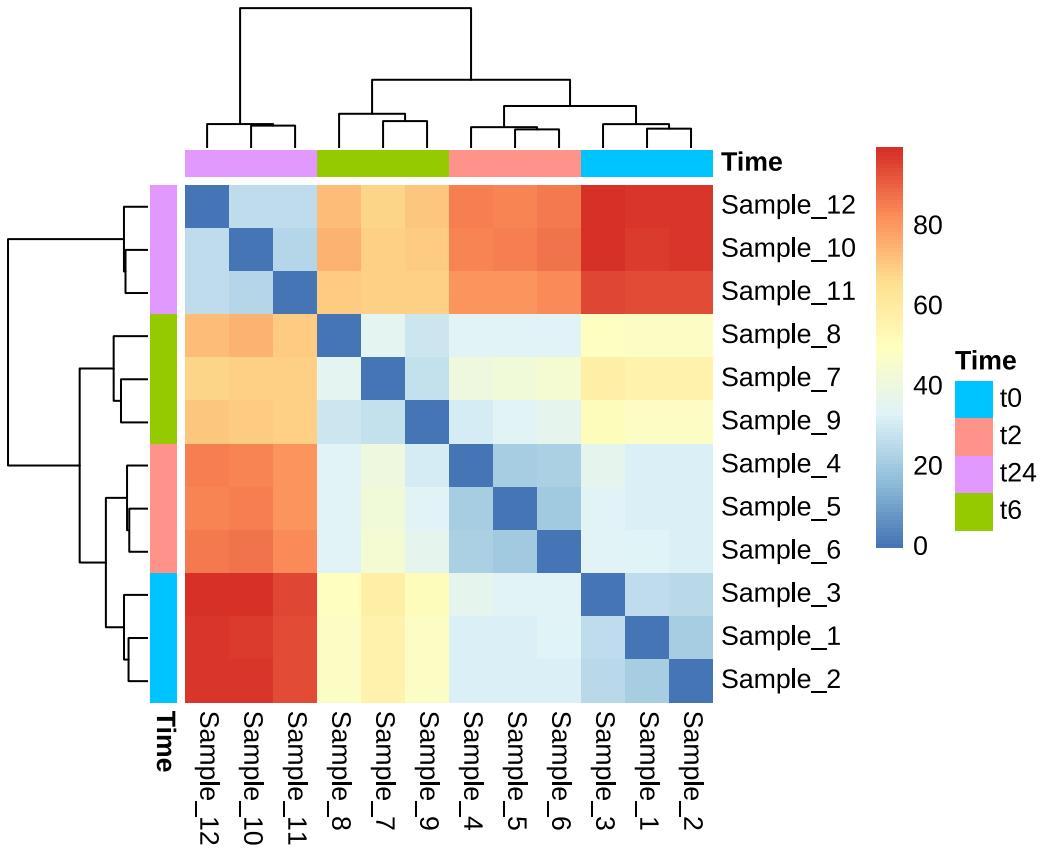
```
dmat <- as.matrix(cor(cv,method="spearman"))
pheatmap::pheatmap(dmat,border_color=NA,annotation_col=mr[, "Time",drop=F],
                   annotation_row=mr[, "Time",drop=F],annotation_legend=T)
```



Exploratory | Distance

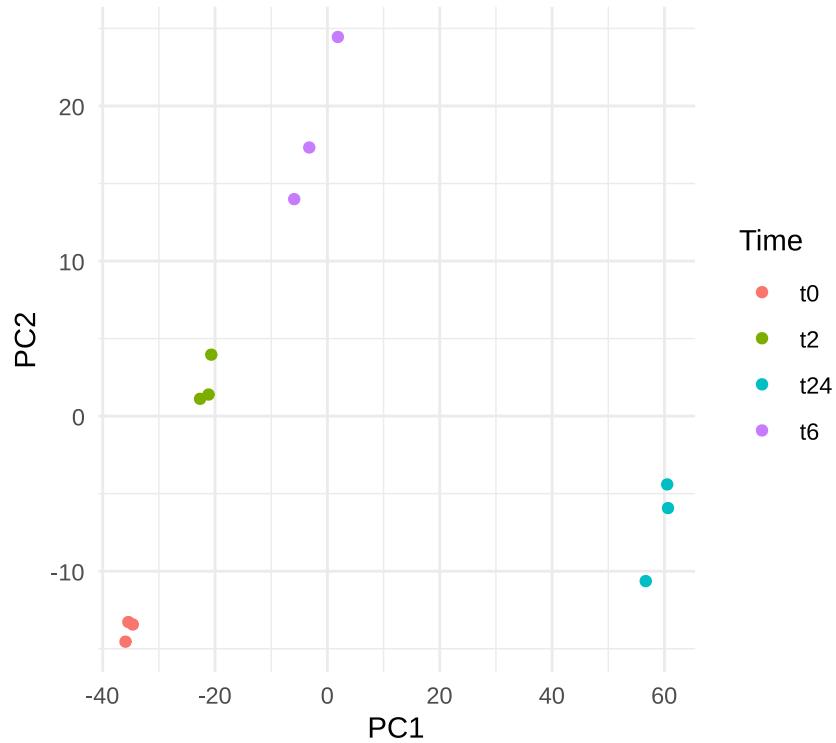
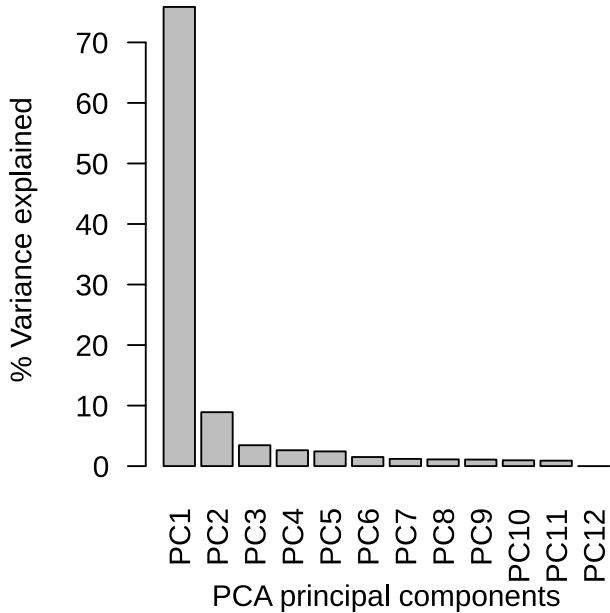
- Similarity between samples

```
dmat <- as.matrix(dist(t(cv)))
pheatmap(dmat,border_color=NA,annotation_col=mr[, "Time",drop=F],
          annotation_row=mr[, "Time",drop=F],annotation_legend=T)
```



Exploratory | PCA

- Relationship between samples



- Create the DESeq2 object

```
library(DESeq2)
mr$Time <- factor(mr$Time)
d <- DESeqDataSetFromMatrix(countData=cf,colData=mr,design=~Time)
d
```

```
## class: DESeqDataSet
## dim: 14578 12
## metadata(1): version
## assays(1): counts
## rownames(14578): ENSG00000000003 ENSG000000000419 ... ENSG00000266865
##   ENSG00000266876
## rowData names():
## colnames(12): Sample_1 Sample_2 ... Sample_11 Sample_12
## colData names(5): Sample_ID Sample_Name Time Replicate Cell
```

- Model must be factors
- `~var`
- `~covar+var`

DGE | Size factors

- Normalisation factors are computed

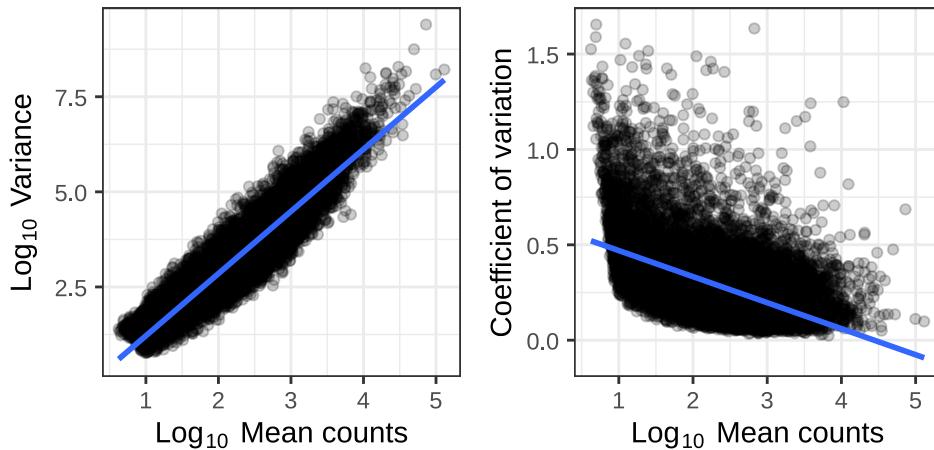
```
d <- DESeq2::estimateSizeFactors(d,type="ratio")
sizeFactors(d)
```

```
## Sample_1 Sample_2 Sample_3 Sample_4 Sample_5 Sample_6 Sample_7 Sample_8
## 0.9003753 0.8437393 0.5106445 1.1276451 1.0941383 0.8133849 0.7553903 1.1744008
## Sample_9 Sample_10 Sample_11 Sample_12
## 1.0189325 1.3642797 1.2325485 1.8555904
```

DGE | Dispersion

- We need a measure variability of gene counts

```
dm <- apply(cd,1,mean)
dv <- apply(cd,1,var)
cva <- function(x) sd(x)/mean(x)
dc <- apply(cd,1,cva)
```

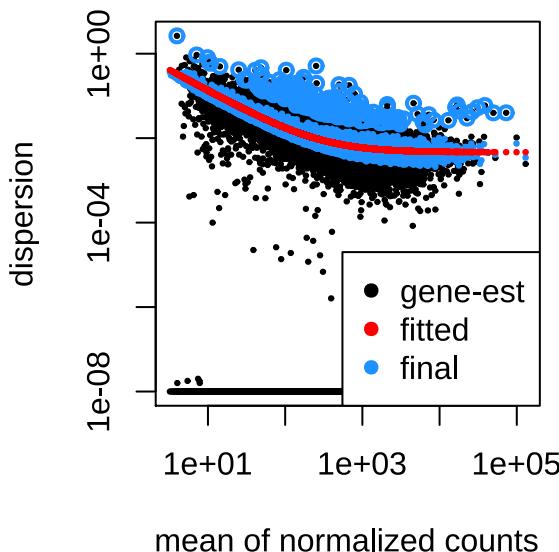


- Dispersion is a measure of variability in gene expression for a given mean

DGE | Dispersion

- D is unreliable for low mean counts
- Genes with similar mean values must have similar dispersion
- Estimate likely (ML) dispersion for each gene based on counts
- Fit a curve through the gene-wise estimates
- Shrink dispersion towards the curve

```
d <- DESeq2::estimateDispersions(d)
{par(mar=c(4,4,1,1))
plotDispEsts(d)}
```



- Log2 fold changes changes are computed after GLM fitting

```
dg <- nbinomWaldTest(d)
resultsNames(dg)
```

```
## [1] "Intercept"      "Time_t2_vs_t0"    "Time_t24_vs_t0"   "Time_t6_vs_t0"
```

- Use `results()` to customise/return results
 - Set coefficients using `contrast` or `name`
 - Filtering by fold change using `lfcThreshold`
 - `cooksCutoff` removes outliers
 - `independentFiltering`
 - `pAdjustMethod`
 - `alpha`

```
res1 <- results(dg, name="Time_t2_vs_t0", alpha=0.05)
summary(res1)
```

```
## 
## out of 14578 with nonzero total read count
## adjusted p-value < 0.05
## LFC > 0 (up)      : 413, 2.8%
## LFC < 0 (down)    : 696, 4.8%
## outliers [1]       : 0, 0%
## low counts [2]     : 2261, 16%
## (mean count < 26)
## [1] see 'cooksCutoff' argument of ?results
## [2] see 'independentFiltering' argument of ?results
```

```
head(res1)
```

```
## log2 fold change (MLE): Time t2 vs t0
## Wald test p-value: Time t2 vs t0
## DataFrame with 6 rows and 6 columns
##           baseMean log2FoldChange      lfcSE      stat     pvalue
## ENSG000000000003  490.0172    0.2206198  0.1127611  1.956524 0.0504034
## ENSG000000000419  817.7807    0.0592720  0.1014813  0.584068 0.5591746
## ENSG000000000457   82.0788    0.2077486  0.2204049  0.942577 0.3458972
## ENSG000000000460  356.0716   -0.1291864  0.1151392 -1.122002 0.2618616
## ENSG000000001036  919.6068    0.0288827  0.0851501  0.339198 0.7344609
## ENSG000000001084  529.5940    0.2119648  0.0929811  2.279655 0.0226281
##          padj
##           <numeric>
## ENSG000000000003  0.263505
## ENSG000000000419  0.830262
## ENSG000000000457  0.689946
## ENSG000000000460  0.612625
## ENSG000000001036  0.909639
## ENSG000000001084  0.159263
```

- Use `lfcShrink()` to correct fold changes for high dispersion genes

Thank you. Questions?

R version 4.0.3 (2020-10-10)

Platform: x86_64-pc-linux-gnu (64-bit)

OS: Ubuntu 18.04.5 LTS

Built on : 📅 16-Nov-2020 at ⏱ 17:15:42

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