• Moderated statistics
• Experimental design

Note, that the R-code is included for learners who are aiming to develop R/markdown scripts to automate their quantitative proteomics data analyses. According to the target audience of the course we either work with a graphical user interface (GUI) in a R/shiny App msqrob2gui (e.g. Proteomics Bioinformatics course of the EBI and the Proteomics Data Analysis course at the Gulbenkian institute) or with R/markdowns scripts (e.g. Bioinformatics Summer School at UCLouvain or the Statistical Genomics Course at Ghent University).

1 Francisella tularensis experiment

![Image of Francisella tularensis](image)

• Pathogen: causes tularemia
• Metabolic adaptation key for intracellular life cycle of pathogenic microorganisms.
• Upon entry into host cells quick phasomal escape and active multiplication in cytosolic compartment.
• Franciscella is auxotroph for several amino acids, including arginine.
• Inactivation of arginine transporter delayed bacterial phagosomal escape and intracellular multiplication.
• Experiment to assess difference in proteome using 3 WT vs 3 ArgP KO mutants

1.1 Import the data in R

Click to see code
1. Load libraries

```r
library(tidyverse)
library(limma)
library(QFeatures)
library(msqrob2)
library(plotly)
library(ggplot2)
```

2. We use a peptides.txt file from MS-data quantified with maxquant that contains MS1 intensities summarized at the peptide level.

```r
peptidesFile <- "https://raw.githubusercontent.com/statOomics/PDA/data/quantification/francisella/peptides.txt"
```

3. Maxquant stores the intensity data for the different samples in columns that start with Intensity. We can retrieve the column names with the intensity data with the code below:

```r
ecols <- grep("Intensity\.", names(read.delim(peptidesFile)))
```

4. Read the data and store it in QFeatures object

```r
pe <- readQFeatures(
  table = peptidesFile,
  fnames = 1,
  ecol = ecols,
  name = "peptideRaw", sep="\t"
)
```

5. Update data with information on design

```r
colData(pe)$genotype <- pe[[1]] %>%
  colnames %>%
  substr(12,13) %>%
  as.factor %>%
  relevel("WT")
pe %>% colData
```

## DataFrame with 6 rows and 1 column
### genotype
### <factor>
## Intensity.1WT_20_2h_n3_3  WT
## Intensity.1WT_20_2h_n4_3  WT
## Intensity.1WT_20_2h_n5_3  WT
## Intensity.3D8_20_2h_n3_3  D8
## Intensity.3D8_20_2h_n4_3  D8
## Intensity.3D8_20_2h_n5_3  D8

### 1.2 Preprocessing

Click to see code to log-transform the data
1. Log transform

- Calculate number of non zero intensities for each peptide

```r
data(pe["peptideRaw"])$nNonZero <- rowSums(assay(pe["peptideRaw"]) > 0)
```

- Peptides with zero intensities are missing peptides and should be represent with a `NA` value rather than 0.

```r
pe <- zeroIsNA(pe, "peptideRaw") # convert 0 to NA
```

- Logtransform data with base 2

```r
pe <- logTransform(pe, base = 2, i = "peptideRaw", name = "peptideLog")
```

2. Filtering

- Handling overlapping protein groups

```r
pe <- filterFeatures(pe, ~ Proteins %in% smallestUniqueGroups(data(pe["peptideLog"])$Proteins))
```

- Remove reverse sequences (decoys) and contaminants. Note that this is indicated by the column names `Reverse` and depending on the version of maxQuant with `Potential.contaminants` or `Contaminants`.

```r
pe <- filterFeatures(pe, ~ Reverse != "+")
ppe <- filterFeatures(pe, ~ Contaminant != "+")
```

- Drop peptides that were only identified in one sample

```r
pe <- filterFeatures(pe, ~ nNonZero >= 2)
nrow(pe["peptideLog"])
```

```r
## [1] 6525
```

We keep 6525 peptides upon filtering.

3. Normalization by median centering

```r
pe <- normalize(pe,
i = "peptideLog",
name = "peptideNorm",
method = "center.median")
```

4. Summarization. We use the standard summarisation in aggregateFeatures, which is a robust summarisation method.
pe <- aggregateFeatures(pe,
  i = "peptideNorm",
  fcol = "Proteins",
  na.rm = TRUE,
  name = "protein")

## Your quantitative and row data contain missing values. Please read the
## relevant section(s) in the aggregateFeatures manual page regarding the
## effects of missing values on data aggregation.

Plot of preprocessed data

pe[["peptideNorm"]]
  %>%
  assay
  %>%
  as.data.frame
  %>%
  gather(sample, intensity)
  %>%
  mutate(genotype = colData(pe)[sample,"genotype"])
  %>%
  ggplot(aes(x = intensity, group = sample, color = genotype)) +
  geom_density() +
  ggtitle("Peptide-level")

## Warning: Removed 7561 rows containing non-finite values (stat_density).

Peptide-level

<table>
<thead>
<tr>
<th>density</th>
<th>intensity</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.00</td>
<td>-5</td>
</tr>
<tr>
<td>0.05</td>
<td>-2.5</td>
</tr>
<tr>
<td>0.10</td>
<td>0</td>
</tr>
<tr>
<td>0.15</td>
<td>2.5</td>
</tr>
<tr>
<td>0.20</td>
<td>5</td>
</tr>
</tbody>
</table>

genotype

- WT
- D8
pe["protein"] %>%
  assay %>%
  as.data.frame() %>%
  gather(sample, intensity) %>%
  mutate(genotype = colData(pe)[sample,"genotype"])
  %>%
  ggplot(aes(x = intensity,group = sample,color = genotype)) +
    geom_density() +
    ggtitle("Protein-level")

## Warning: Removed 428 rows containing non-finite values (stat_density).

![Protein-level density plot](image)

1.3  Summarized data structure

1.3.1  Design

pe %>%
  colData %>%
  knitr::kable()
WT vs KO  
3 vs 3 repeats

### 1.3.2 Summarized intensity matrix

```r
pe[['protein']] %>% assay() %>% head() %>% knitr::kable()
```

<table>
<thead>
<tr>
<th></th>
<th>Intensity.1WT_20_2h_n3_3</th>
<th>Intensity.1WT_20_2h_n4_3</th>
<th>Intensity.1WT_20_2h_n5_3</th>
<th>Intensity.3D8_20_2h_n3_3</th>
<th>Intensity.3D8_20_2h_n4_3</th>
<th>Intensity.3D8_20_2h_n5_3</th>
</tr>
</thead>
<tbody>
<tr>
<td>WP_003013731</td>
<td>-0.0856247</td>
<td>0.1595370</td>
<td>-0.2809009</td>
<td>0.0035526</td>
<td>0.0567110</td>
<td></td>
</tr>
<tr>
<td>WP_003013860</td>
<td>NA</td>
<td>-0.2512039</td>
<td>NA</td>
<td>NA</td>
<td>-0.4865646</td>
<td></td>
</tr>
<tr>
<td>WP_003013909</td>
<td>-0.8161658</td>
<td>-0.7557906</td>
<td>-0.4591476</td>
<td>-0.5449424</td>
<td>-0.4962482</td>
<td></td>
</tr>
<tr>
<td>WP_003014086</td>
<td>0.8522239</td>
<td>1.1344852</td>
<td>0.5459176</td>
<td>0.9187714</td>
<td>0.5974741</td>
<td></td>
</tr>
<tr>
<td>WP_003014122</td>
<td>-1.0430741</td>
<td>-0.8091715</td>
<td>-1.1743951</td>
<td>-1.1924725</td>
<td>-1.2565893</td>
<td></td>
</tr>
<tr>
<td>WP_003014123</td>
<td>-0.3361704</td>
<td>-0.2151930</td>
<td>-0.3855747</td>
<td>-0.2802011</td>
<td>-0.5801771</td>
<td></td>
</tr>
</tbody>
</table>

- 1115 proteins
1.3.3 Hypothesis testing: a single protein

1.3.3.1 T-test

\[
\begin{align*}
\log_2 \text{FC} &= \bar{y}_{p1} - \bar{y}_{p2} \\
T_g &= \frac{\log_2 \text{FC}}{\text{se}_{\log_2 \text{FC}}} \\
T_g &= \frac{\text{signal}}{\text{Noise}}
\end{align*}
\]

If we can assume equal variance in both treatment groups:

\[
\text{se}_{\log_2 \text{FC}} = \text{SD} \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}
\]

WP_003023392 <- data.frame(
  intensity = assay(pe[["protein"]]["WP_003023392",]) %>% c(),
  genotype = colData(pe)[,1])

WP_003023392 %>%
  ggplot(aes(x=genotype,y=intensity)) +
  geom_point() +
  ggtitle("Protein WP_003023392")
Protein WP_003023392

\[ t = \frac{\log_2 \hat{FC} \div \text{se}_{\log_2 FC}}{-1.43} = -24.7 \]

- Is \( t = -24.7 \) indicating that there is an effect?
- How likely is it to observe \( t = -24.7 \) when there is no effect of the argP KO on the protein expression?

1.3.3.2 Null hypothesis (\( H_0 \)) and alternative hypothesis (\( H_1 \))

- With data we can never prove a hypothesis (falsification principle of Popper)
- With data we can only reject a hypothesis
- In general we start from alternative hypothesis \( H_1 \): we want to show an effect of the KO on a protein

\( H_1 \): On average the protein abundance in WT is different from that in KO
- But, we will assess this by falsifying the opposite:
  \( H_0 \): On average the protein abundance in WT is equal to that in KO

\[
\text{t.test(intensity ~ genotype, data = WP_003023392, var.equal=TRUE)}
\]

##
## Two Sample t-test
### Data: intensity by genotype

* t = 24.747, df = 4, p-value = 1.582e-05

* Alternative hypothesis: true difference in means between group WT and group D8 is not equal to 0

* 95 percent confidence interval:

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1.267666</td>
<td>1.588058</td>
</tr>
</tbody>
</table>

* Sample estimates:

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>-0.1821147</td>
<td>-1.6099769</td>
</tr>
</tbody>
</table>

- How likely is it to observe an equal or more extreme effect than the one observed in the sample when the null hypothesis is true?

- When we make assumptions about the distribution of our test statistic we can quantify this probability: *p-value*. The *p*-value will only be calculated correctly if the underlying assumptions hold!

- When we repeat the experiment, the probability to observe a fold change for this gene that is more extreme than a 2.69 fold (log₂ FC = −1.43) down or up regulation by random change (if H₀ is true) is 16 out of 1 000 000.

- If the *p*-value is below a significance threshold α we reject the null hypothesis. *We control the probability on a false positive result at the α-level (type I error)*

- Note, that the *p*-values are uniform under the null hypothesis, i.e. when H₀ is true all *p*-values are equally likely.

## 1.4 Multiple hypothesis testing

- Consider testing DA for all m = 1066 proteins simultaneously

- What if we assess each individual test at level α? → Probability to have a false positive (FP) among all m simultaneous tests >>> α = 0.05

- Indeed for each non DA protein we have a probability of 5% to return a FP.

- In a typical experiment the majority of the proteins are non DA.

- So an upperbound of the expected FP is m × α or 1066 × 0.05 = 53.

→ Hence, we are bound to call many false positive proteins each time we run the experiment.

### 1.4.1 Multiple testing

#### 1.4.1.1 Family-wise error rate

The family-wise error rate (FWER) addresses the multiple testing issue by no longer controlling the individual type I error for each protein, instead it controls:

\[
\text{FWER} = P[FP \geq 1].
\]

The Bonferroni method is widely used to control the type I error:

- assess each test at

\[
\alpha_{\text{adj}} = \frac{\alpha}{m}
\]
• or use adjusted p-values and compare them to $\alpha$:

$$p_{\text{adj}} = \min (p \times m, 1)$$

Problem, the method is very conservative!

### 1.4.1.2 False discovery rate

- FDR: Expected proportion of false positives on the total number of positives you return.
- An FDR of 1% means that on average we expect 1% false positive proteins in the list of proteins that are called significant.

The **False Discovery Proportion (FDP)** is the fraction of false positives that are returned, i.e.

$$FDP = \frac{FP}{R}$$

- However, this quantity cannot be observed because in practice we only know the number of proteins for which we rejected $H_0$, $R$.
- But, we do not know the number of false positives, $FP$.

Therefore, Benjamini and Hochberg, 1995, defined the **False Discovery Rate (FDR)** as

$$\text{FDR} = E \left[ \frac{FP}{R} \right] = E[FDP]$$

the expected FDP.

- Controlling the FDR allows for more discoveries (i.e. longer lists with significant results), while the fraction of false discoveries among the significant results in well controlled on average. As a consequence, more of the true positive hypotheses will be detected.

### 1.4.1.3 Intuition of BH-FDR procedure

Consider $m = 1000$ tests

- Suppose that a researcher rejects all null hypotheses for which $p < 0.01$.
- If we use $p < 0.01$, we expect $0.01 \times m_0$ tests to return false positives.
- A conservative estimate of the number of false positives that we can expect can be obtained by considering that the null hypotheses are true for all features, $m_0 = m = 1000$.
- We then would expect $0.01 \times 1000 = 10$ false positives ($FP = 10$).
- Suppose that the researcher found 200 genes with $p < 0.01$ ($R = 200$).
- The proportion of false positive results ($FDP = \text{false positive proportion}$) among the list of $R = 200$ genes can then be estimated as

$$FDP = \frac{FP}{R} = \frac{10}{200} = \frac{0.01 \times 1000}{200} = 0.05.$$
1.4.1.4 Benjamini and Hochberg (1995) procedure for controlling the FDR at $\alpha$

1. Let $p(1) \leq \ldots \leq p(m)$ denote the ordered $p$-values.

2. Find the largest integer $k$ so that

$$\frac{p(k) \times m}{k} \leq \alpha$$

or

$$p(k) \leq k \times \alpha/m$$

3. If such a $k$ exists, reject the $k$ null hypotheses associated with $p(1), \ldots, p(k)$. Otherwise none of the null hypotheses is rejected.

The adjusted $p$-value (also known as the $q$-value in FDR literature):

$$q(i) = \tilde{p}(i) = \min \left[ \min_{j=i, \ldots, m} \left( m p(j)/j \right), 1 \right].$$

In the hypothetical example above: $k = 200$, $p(k) = 0.01$, $m = 1000$ and $\alpha = 0.05$.

1.4.1.5 Francisella Example  

Click to see code

ttestMx <- function(y,group) {
  test <- try(t.test(y[group],y[!group],var.equal=TRUE),silent=TRUE)
  if(is(test,"try-error")) {
    return(c(log2FC=NA,se=NA,tstat=NA,p=NA))
  } else {
    return(c(log2FC= (test$estimate%*%c(1,-1)),se=test$stderr,tstat=test$statistic,pval=test$p.value))
  }
}

res <- apply(assay(pe["protein"]),1,ttestMx,group = colData(pe)$genotype=="D8") %>%
t
colnames(res) <- c("logFC","se","tstat","pval")
res <- res %>% as.data.frame %>% na.exclude %>% arrange(pval)
res$adjPval <- p.adjust(res$pval, "fdr")
alpha <- 0.05
res$adjAlphaForm <- paste0(1:nrow(res)," x ",alpha,"/",nrow(res))
res$adjAlpha <- alpha * (1:nrow(res))/nrow(res)
res$pval < adjAlpha" <- res$pval < res$adjAlpha
res$adjPval < alpha" <- res$adjPval < alpha

FWER: Bonferroni method: $\alpha_{adj} = \alpha/m = 0.05/1066 = 5 \times 10^{-5}$

<table>
<thead>
<tr>
<th></th>
<th>logFC</th>
<th>pval</th>
<th>adjPval</th>
<th>adjAlphaForm</th>
<th>adjAlpha</th>
<th>pval &lt; adjAlpha</th>
<th>adjPval &lt; alpha</th>
</tr>
</thead>
<tbody>
<tr>
<td>WP_003038940</td>
<td>-0.2876290</td>
<td>0.0000146</td>
<td>0.0084347</td>
<td>1 x</td>
<td>0.0000469</td>
<td>TRUE</td>
<td>TRUE</td>
</tr>
<tr>
<td></td>
<td>0.2876290</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>logFC</td>
<td>pval</td>
<td>adjPval</td>
<td>adjAlphaForm</td>
<td>adjAlpha</td>
<td>pval &lt; adjAlpha</td>
<td>adjPval &lt; alpha</td>
<td></td>
</tr>
<tr>
<td>---------------</td>
<td>---------</td>
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<td>--------------</td>
<td>----------</td>
<td>----------------</td>
<td>-----------------</td>
<td></td>
</tr>
<tr>
<td>WP_003023392</td>
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<td>0.0291520</td>
<td>3 x</td>
<td>0.0001407</td>
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<tr>
<td>WP_003026016</td>
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<td>0.0001395</td>
<td>0.0346124</td>
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<td>0.0001876</td>
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<tr>
<td>WP_003039615</td>
<td>0.3923262</td>
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<td>0.0407034</td>
<td>6 x</td>
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<tr>
<td>WP_001173588</td>
<td>0.9843865</td>
<td>0.0003224</td>
<td>0.0440266</td>
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<td></td>
</tr>
<tr>
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<td>0.0004505</td>
<td>0.0489078</td>
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<td>0.0004221</td>
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<td></td>
</tr>
<tr>
<td>WP_003038430</td>
<td>0.2949061</td>
<td>0.0005047</td>
<td>0.0489078</td>
<td>9 x</td>
<td>0.0004690</td>
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<td></td>
</tr>
<tr>
<td>WP_00303975</td>
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<td>0.000547</td>
<td>0.0489078</td>
<td>10 x</td>
<td>0.0005159</td>
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<tr>
<td>WP_001173372</td>
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<td>0.0005629</td>
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</tr>
<tr>
<td>WP_003038679</td>
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<td>0.0007083</td>
<td>0.0580821</td>
<td>12 x</td>
<td>0.0006098</td>
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</tr>
<tr>
<td>WP_00303719</td>
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<td>0.0008426</td>
<td>0.0603810</td>
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<tr>
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<td>0.9985797</td>
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<td>0.0499531</td>
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</tr>
<tr>
<td>WP_003041130</td>
<td>0.0002941</td>
<td>0.9992812</td>
<td>0.9992812</td>
<td>1066 x</td>
<td>0.05</td>
<td>FALSE</td>
<td></td>
</tr>
</tbody>
</table>

**1.4.1.6 Results**  
Click to see code

```r
volcanoT <- res %>%
ggplot(aes(x = logFC, y = -log10(pval), color = adjPval < 0.05)) +
geom_point(cex = 2.5) +
scale_color_manual(values = alpha(c("black", "red"), 0.5)) +
theme_minimal()
```

volcanoT
1.5 Moderated Statistics

Problems with ordinary t-test

Click to see code

```r
problemPlots <- list()
problemPlots[[1]] <- res %>%
  ggplot(aes(x = logFC, y = se, color = adjPval < 0.05)) +
  geom_point(cex = 2.5) +
  scale_color_manual(values = alpha(c("black", "red"), 0.5)) +
  theme_minimal()

for (i in 2:3)
{
  problemPlots[[i]] <- colData(pe) %>%
    as.data.frame %>%
    mutate(intensity = pe["protein"][[rownames(res)[i]],] %>%
      assay %>%
      c) %>%
    ggplot(aes(x = genotype, y = intensity)) +
    geom_point() +
    ylim(-3, 0) +
    ggtitle(rownames(res)[i])
}
```
problemPlots

## [[1]]

## [[2]]

## [[2]]
WP_003023392

# [3]

## [3]
A general class of moderated test statistics is given by

$$T^{\text{mod}}_g = \frac{\bar{Y}_{g1} - \bar{Y}_{g2}}{C \cdot \bar{S}_g},$$

where $\bar{S}_g$ is a moderated standard deviation estimate.

- $C$ is a constant depending on the design e.g. $\sqrt{1/n_1 + 1/n_2}$ for a t-test and of another form for linear models.
- $\bar{S}_g = S_g + S_0$: add small positive constant to denominator of t-statistic.
- This can be adopted in Perseus.

Click to see code

```r
simI<-sapply(res$se/sqrt(1/3+1/3),function(n,mean,sd) rnorm(n,mean,sd),n=6,mean=0) %>% t
resSim <- apply(
  simI,
  1, 
ttestMx,
  group = colData(pe)$genotype=="D8") %>% t
colnames(resSim) <- c("logFC","se","tstat","pval")
resSim <- as.data.frame(resSim)
tstatSimPlot <- resSim %>%
ggplot(aes(x=tstat)) +
  geom_histogram(aes(y=..density.., fill=..count..),bins=30) +
```

Click to see code
The choice of $S_0$ in Perseus is ad hoc and the t-statistic is no-longer t-distributed. Permutation test, but is difficult for more complex designs. Allows for Data Dredging because user can choose $S_0$
1.5.1 Empirical Bayes

Shrinkage of Standard Deviations

\[
T_{g, \text{mod}} = \frac{\bar{Y}_{g1} - \bar{Y}_{g2}}{C \bar{S}_g},
\]

- empirical Bayes theory provides formal framework for borrowing strength across proteins,
- Implemented in popular bioconductor package \texttt{limma} and \texttt{msqrob2}

\[
\bar{S}_g = \sqrt{\frac{d_g S_g^2 + d_0 S_0^2}{d_g + d_0}},
\]

- \(S_0^2\): common variance (over all proteins)
- Moderated t-statistic is t-distributed with \(d_0 + d_g\) degrees of freedom.
- Note that the degrees of freedom increase by borrowing strength across proteins!

Click to see the code

1. We model the protein level expression values using the \texttt{msqrob} function. By default \texttt{msqrob2} estimates the model parameters using robust regression.

We will model the data with a different group mean for every genotype. The group is encoded in the variable \texttt{genotype} of the \texttt{colData}. We can specify this model by using a formula with the factor \texttt{genotype} as its predictor: \texttt{formula = ~genotype}.

Note, that a formula always starts with a symbol `~`.

\texttt{pe <- msqrob(object = pe, i = "protein", formula = ~genotype)}

2. Inference

We first explore the design of the model that we specified using the package \texttt{ExploreModelMatrix}
We have two model parameters, the (Intercept) and genotypeD8. This results in a model with two group means:

1. For the wild type (WT) the expected value (mean) of the log2 transformed intensity \( y \) for a protein will be modelled using

\[
E[Y|\text{genotype} = \text{WT}] = \text{(Intercept)}
\]

2. For the knockout genotype D8 the expected value (mean) of the log2 transformed intensity \( y \) for a protein will be modelled using

\[
E[Y|\text{genotype} = \text{D8}] = \text{(Intercept)} + \text{genotypeD8}
\]

The average log2FC between D8 and WT is thus

\[
\log_2 \text{FC}_{D8-WT} = E[Y|\text{genotype} = \text{D8}] - E[Y|\text{genotype} = \text{WT}] = \text{genotypeD8}
\]

Hence, assessing the null hypothesis that there is no differential abundance between D8 and WT can be reformulated as
We can implement a hypothesis test for each protein in msqrob2 using the code below:

```r
L <- makeContrast("genotypeD8 = 0", parameterNames = c("genotypeD8"))
pe <- hypothesisTest(object = pe, i = "protein", contrast = L)
```

We can show the list with all significant DE proteins at the 5% FDR using

```r
rowData(pe[["protein"]])$genotypeD8 %>%
  arrange(pval) %>%
  filter(adjPval<0.05)
```

```
## logFC  se    df     t   pval    adjPval
## WP_003023392 -1.4278622 0.09546104 6.353267 -14.957538 3.435824e-06 0.003456439
## WP_003040849 -1.2857733 0.12226820 6.236222 -10.516007 3.372825e-05 0.016965307
## WP_003033719 -1.970073 0.13408775 6.220667 -8.927044 8.983461e-05 0.016965307
## WP_003033905 -0.8815374 0.12199689 6.353267 -7.225901 2.740575e-04 0.039385984
## WP_003039713 -0.7635044 0.11307420 6.033034 -6.772410 4.947588e-04 0.041477282
```

We can also visualise the results using a volcanoplot

```r
volcano <- ggplot(
  rowData(pe[["protein"]])$genotypeD8,
  aes(x = logFC, y = -log10(pval), color = adjPval < 0.05)
) +
  geom_point(cex = 2.5) +
  scale_color_manual(values = alpha(c("black", "red"), 0.5)) +
  theme_minimal() +
  ggtitle("msqrob2")
```

```r
gridExtra::grid.arrange(
  volcanoT +
  xlim(-3,3) +
  ggtitle("ordinary t-test"),
  volcano +
  xlim(-3,3),
  nrow=2)
```

## Warning: Removed 109 rows containing missing values (geom_point).
• The volcano plot opens up when using the EB variance estimator
• Borrowing strength to estimate the variance using empirical Bayes solves the issue of returning proteins with a low fold change as significant due to a low variance.

1.5.2 Shrinkage of the variance and moderated t-statistics

```r
qplot(
  sapply(rowData(pe[["protein"]])$msqrobModels,getSigma),
  sapply(rowData(pe[["protein"]])$msqrobModels,getSigmaPosterior)) +
  xlab("SD") +
  ylab("moderated SD") +
  geom_abline(intercept = 0,slope = 1) +
  geom_hline(yintercept = )

## Warning: Removed 109 rows containing missing values (geom_point).
```
• Small variances are shrunken towards the common variance resulting in large EB variance estimates
• Large variances are shrunk towards the common variance resulting in smaller EB variance estimates
• Pooled degrees of freedom of the EB variance estimator are larger because information is borrowed across proteins to estimate the variance

1.6 Plots

```r
sigNames <- rowData(pe["protein"])$genotypeD8 %>%
  rownames_to_column("protein") %>%
  filter(adjPval < 0.05) %>%
  pull(protein)
heatmap(assay(pe["protein"])[sigNames, ])
```
for (protName in sigNames)
{
  pePlot <- pe[protName, , c("peptideNorm", "protein")]
  pePlotDf <- data.frame(longFormat(pePlot))
  pePlotDf$assay <- factor(pePlotDf$assay,
    levels = c("peptideNorm", "protein")
  )
  pePlotDf$genotype <- as.factor(colData(pePlot)[pePlotDf$colname, "genotype"])

  # plotting
  p1 <- ggplot(data = pePlotDf,
    aes(x = colname, y = value, group = rowname)
  ) +
    geom_line() +
    geom_point() +
    facet_grid(~assay) +
    theme(axis.text.x = element_text(angle = 70, hjust = 1, vjust = 0.5)) +
    ggtitle(protName)
  print(p1)

  # plotting 2
  p2 <- ggplot(pePlotDf, aes(x = colname, y = value, fill = genotype)) +
    geom_boxplot(outlier.shape = NA) +
    geom_point(
      position = position_jitter(width = .1),
    )

```r
aes(shape = rowname)
)
+ scale_shape_manual(values = 1:nrow(pePlotDf)) +
labs(title = protName, x = "sample", y = "peptide intensity (log2)") +
theme(axis.text.x = element_text(angle = 70, hjust = 1, vjust = 0.5)) +
facet_grid(~assay)
print(p2)
```
WP_003014552

peptideNorm

protein

rowname
○ INSFINNL
△ SEPLQDFLFELK
+ TEDNIQNFFK
× WP_003014552

genotype
- WT
- D8

sample

WT_20_2h_n3_3
WT_20_2h_n4_3
WT_20_2h_n5_3
3D8_20_2h_n3_3
3D8_20_2h_n4_3
3D8_20_2h_n5_3
WP_003023392

<table>
<thead>
<tr>
<th>peptideNorm</th>
<th>protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>genotype</td>
<td></td>
</tr>
<tr>
<td>WT</td>
<td></td>
</tr>
<tr>
<td>D8</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>rowname</th>
</tr>
</thead>
<tbody>
<tr>
<td>○ APFVDLVFGPQTIHR</td>
</tr>
<tr>
<td>△ FDYLPEPK</td>
</tr>
<tr>
<td>+ GPEVNRPFEDVLAECAILAEQGVK</td>
</tr>
<tr>
<td>✗ LQDLLNSNAQIISR</td>
</tr>
<tr>
<td>◇ WP_003023392</td>
</tr>
</tbody>
</table>

Sample:

- WT_20_2h_n3.3
- WT_20_2h_n4.3
- WT_20_2h_n5.3
- 3D8_20_2h_n3.3
- 3D8_20_2h_n4.3
- 3D8_20_2h_n5.3
- WP_003023392

peptide intensity (log2)
### Table

<table>
<thead>
<tr>
<th>genotype</th>
<th>peptideNorm</th>
<th>protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT</td>
<td>[peptide intensity data]</td>
<td>[protein intensity data]</td>
</tr>
<tr>
<td>D8</td>
<td>[peptide intensity data]</td>
<td>[protein intensity data]</td>
</tr>
</tbody>
</table>

### Diagram

- **WP_003026016**
- **peptide intensity (log2)**
- **rowname**
  - DFDQVAEIITEVK
  - EFYPEIITTR
  - FNLLLELLQLPAAPK
  - ILFPQAR
  - KDFDQVAEIITEVK
  - LLTENNATVNSDNFLAK
  - PLTELILQALEIHNK
  - SIPINTLPVK
  - WP_003026016

### Sample Values

<table>
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<tr>
<th>Sample</th>
<th>PeptideNorm</th>
<th>Protein</th>
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<tbody>
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<td>WT</td>
<td>[Data]</td>
<td>[Data]</td>
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<td>[Data]</td>
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### WP_003033719

<table>
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<tr>
<td>WT</td>
<td></td>
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<tr>
<td>D8</td>
<td></td>
</tr>
<tr>
<td>rowname</td>
<td></td>
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<tr>
<td>L TIVDDGYNIDDEIQK</td>
<td>WP_003033719</td>
</tr>
</tbody>
</table>

**Peptide intensity (log2)**

-2.4
-2.0
-1.6
-1.2
-1.0

**Sample**

- WT_20_2h_n3_3
- WT_20_2h_n4_3
- WT_20_2h_n5_3
- 3D8_20_2h_n3_3
- 3D8_20_2h_n4_3
- 3D8_20_2h_n5_3
- WT_20_2h_n3_3
- WT_20_2h_n4_3
- WT_20_2h_n5_3
- 3D8_20_2h_n3_3
- 3D8_20_2h_n4_3
- 3D8_20_2h_n5_3
WP_003033905

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</table>
WP_003038816

peptideNorm
protein

peptide intensity (log2)

WT
D8

rowname

○ DELQLDSEELLAGLTLAQGK
△ DFSQGLNQDIVTVIK
✚ DVLGQAQTGTGK
✗ DYTVDLPANLSPK
◆ EYIVDQFR
▼ FVLSHVSDECQR
□ NIVGAIAENGISDK
★ NVPNLVACIYGGQYGSQIR
Φ TSTIEVTDLNK
★ WP_003038816
WP_003039530

peptide intensity (log2)

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<th>genotype</th>
<th>sample</th>
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</thead>
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<td>DLQQFIDK</td>
<td>WT</td>
<td>WT_20_2h_n3_3</td>
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<td>LPLEVL YLLK</td>
<td>WT</td>
<td>WT_20_2h_n4_3</td>
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<tr>
<td>NLGLLIIDEEHR</td>
<td>WT</td>
<td>WT_20_2h_n5_3</td>
</tr>
<tr>
<td>VDILFFPNLEILPYDR</td>
<td>WT</td>
<td>3D8_20_2h_n3_3</td>
</tr>
<tr>
<td>WP_003039530</td>
<td>D8</td>
<td>3D8_20_2h_n4_3</td>
</tr>
<tr>
<td>WP_003039530</td>
<td>D8</td>
<td>3D8_20_2h_n5_3</td>
</tr>
</tbody>
</table>
WP_003039713

peptide intensity (log2)

protein

genotype
WT
D8

rowname
DL VEAVYR
WP_003039713
WP_003040790

<table>
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```
WP_003040790

peptideNorm

protein

peptide intensity (log2)

genotype
WT
D8

rowname
GEAINDIWSLFGTNVTLK
NHDITHVLFA TIPFEIR
WP_003040790
```
2 Experimental Design

2.1 Sample size

\[
\log_2 \text{FC} = \bar{y}_p - \bar{y}_n
\]

\[
T_g = \frac{\log_2 \text{FC}}{\text{se}_{\log_2 \text{FC}}}
\]

\[
T_g = \frac{\text{signal}}{\text{Noise}}
\]

If we can assume equal variance in both treatment groups:

\[
\text{se}_{\log_2 \text{FC}} = \text{SD} \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}
\]

→ if number of bio-repeats increases we have a higher power!

- cfr. Study of tamoxifen treated Estrogen Recepter (ER) positive breast cancer patients
2.2 Blocking

\[ \sigma^2 = \sigma^2_{\text{bio}} + \sigma^2_{\text{lab}} + \sigma^2_{\text{extraction}} + \sigma^2_{\text{run}} + \ldots \]

- Biological: fluctuations in protein level between mice, fluctuations in protein level between cells, \ldots
- Technical: cage effect, lab effect, week effect, plasma extraction, MS-run, \ldots

2.3 Nature methods: Points of significance - Blocking

https://www.nature.com/articles/nmeth.3005.pdf

2.4 Mouse example

Duguet et al. (2017) MCP 16(8):1416-1432. doi: 10.1074/mcp.m116.062745

- All treatments of interest are present within block!
- We can estimate the effect of the treatment within block!
- We can isolate the between block variability from the analysis using linear model:

\[ y \sim \text{type} + \text{mouse} \]

- Not possible with Perseus!
2.4.1 Assess the impact of blocking in the tutorial session!

- Completely randomized design with only one cell type per mouse (Treg and Tconv)

¬

- Randomized complete block design assessing Treg and Tconv on each mouse

3 Software & code

- Our R/Bioconductor package msqrob2 can be used in R markdown scripts or with a GUI/shinyApp in the msqrob2gui package.

- The GUI is intended as an introduction to the key concepts of proteomics data analysis for users who have no experience in R.

- However, learning how to code data analyses in R markdown scripts is key for open and reproducible science and for reporting your proteomics data analyses and interpretation in a reproducible way.

- More information on our tools can be found in our papers (L. J. Goeminne, Gevaert, and Clement 2016), (L. J. E. Goeminne et al. 2020) and (Sticker et al. 2020). Please refer to our work when using our tools.

- Clips on the code on importing the data and preprocessing can be found in Part I Preprocessing

- A clip on the code for modelling and statistical inference with msqrob2 is included below

References

