

# Recap general linear model

Lieven Clement

statOmics, Ghent University (<https://statomics.github.io>)

## Contents

<b>1</b>	<b>Breast cancer example</b>	<b>1</b>
<b>2</b>	<b>Data Exploration</b>	<b>7</b>
2.1	Import . . . . .	7
2.2	Summary statistics . . . . .	7
2.3	Visualisation . . . . .	8
2.4	Research questions . . . . .	10
2.5	Estimation of effect size and standard error . . . . .	11
<b>3</b>	<b>Statistical Inference</b>	<b>11</b>
3.1	Log transformation . . . . .	15
3.2	Conclusion . . . . .	18
<b>4</b>	<b>General Linear Model</b>	<b>20</b>
4.1	Implementation in R . . . . .	20
4.2	Assumptions . . . . .	21
4.3	Breast cancer example . . . . .	24
<b>5</b>	<b>Linear regression in matrix form</b>	<b>25</b>
5.1	Scalar form . . . . .	25
5.2	Matrix form . . . . .	25
5.3	Least Squares (LS) . . . . .	26
5.4	Variance Estimator? . . . . .	35
5.5	Contrasts . . . . .	35
<b>6</b>	<b>Homework: Adopt the gene analysis on log scale in matrix form!</b>	<b>36</b>
6.1	Inspiration . . . . .	36

This is part of the online course Statistical Genomics 2022 (SGA)

## 1 Breast cancer example

- part of study <https://doi.org/10.1093/jnci/djj052>)
- Histologic grade in breast cancer clinically prognostic. Association of histologic grade on expression of KPNA2 gene that is known to be associated with poor BC prognosis.
- Population: all current and future breast cancer patients



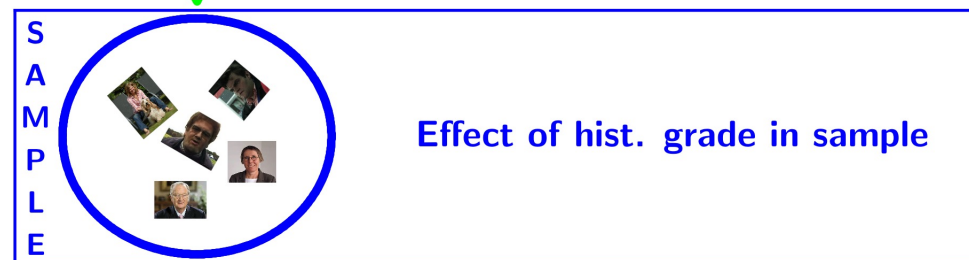


**EXP. DESIGN**





**EXP. DESIGN**









## 2 Data Exploration

### 2.1 Import

```
library(tidyverse)
gene <- read.table("https://raw.githubusercontent.com/statOmics/SGA21/master/data/kpna2.txt", header=TRUE)
head(gene)
```

```
##   grade node    gene
## 1     3     1 367.8179
## 2     3     1 590.3576
## 3     1     1 346.6583
## 4     1     1 258.4455
## 5     1     0 153.8416
## 6     3     0 643.6799
```

We will transform the variable grade and node to a factor

```
gene$grade <- as.factor(gene$grade)
gene$node <- as.factor(gene$node)
```

### 2.2 Summary statistics

```
geneSum <- gene %>%
  group_by(grade) %>%
```

```

summarize(mean = mean(gene),
          sd = sd(gene),
          n=length(gene)
          ) %>%
mutate(se = sd/sqrt(n))
geneSum

```

```

## # A tibble: 2 x 5
##   grade mean    sd     n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 1      233.  65.5    12  18.9
## 2 3      561. 144.    12  41.4

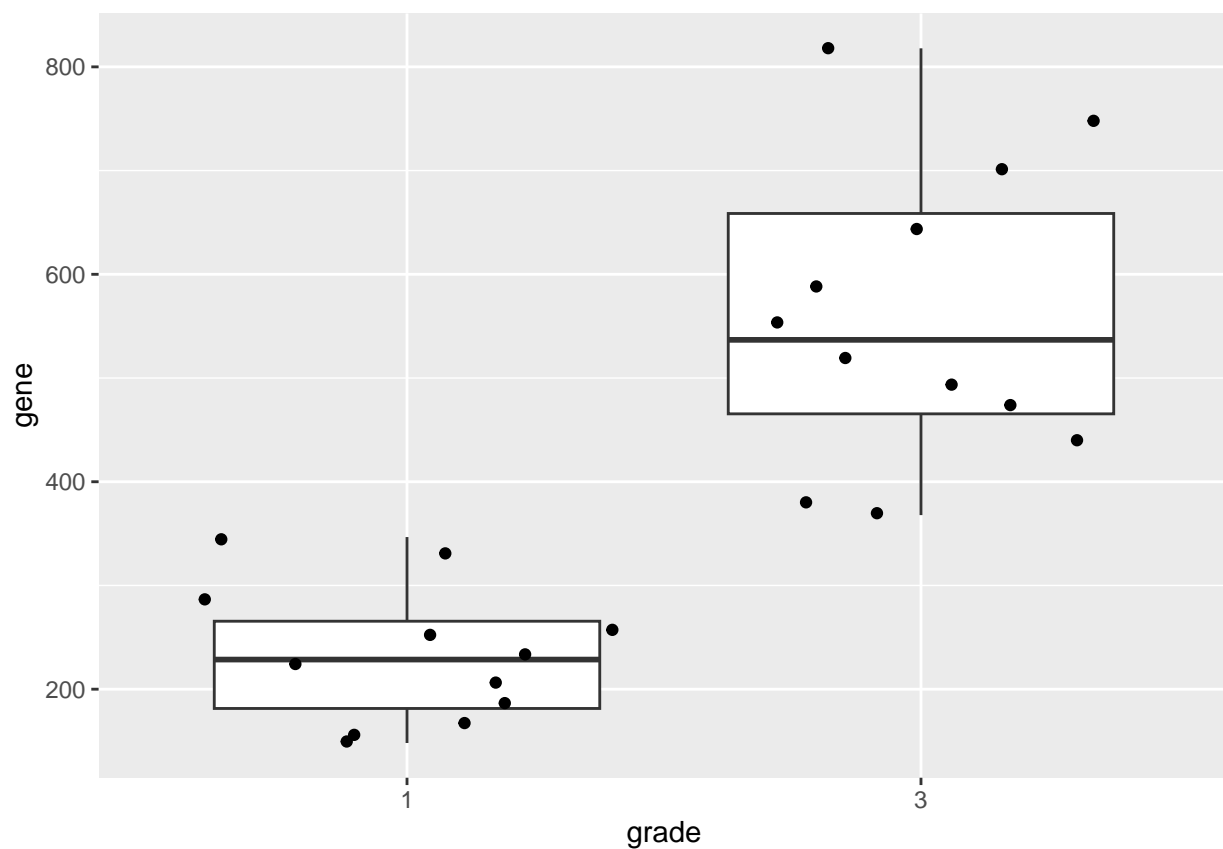
```

## 2.3 Visualisation

```

gene %>%
  ggplot(aes(x=grade,y=gene)) +
  geom_boxplot(outlier.shape=NA) +
  geom_jitter()

```



We can also save the plots as objects for later use!

```

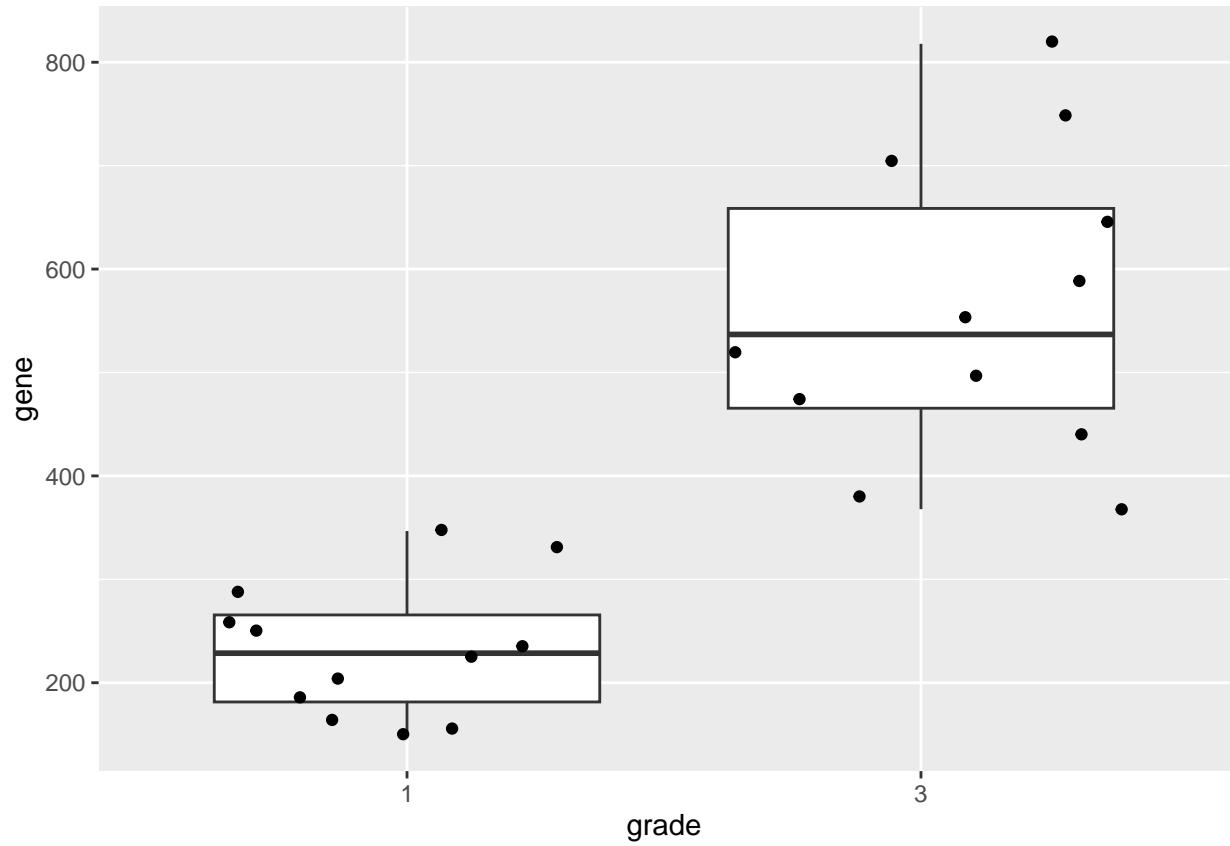
p1 <- gene %>%
  ggplot(aes(x=grade,y=gene)) +
  geom_boxplot(outlier.shape=NA) +
  geom_jitter()

```

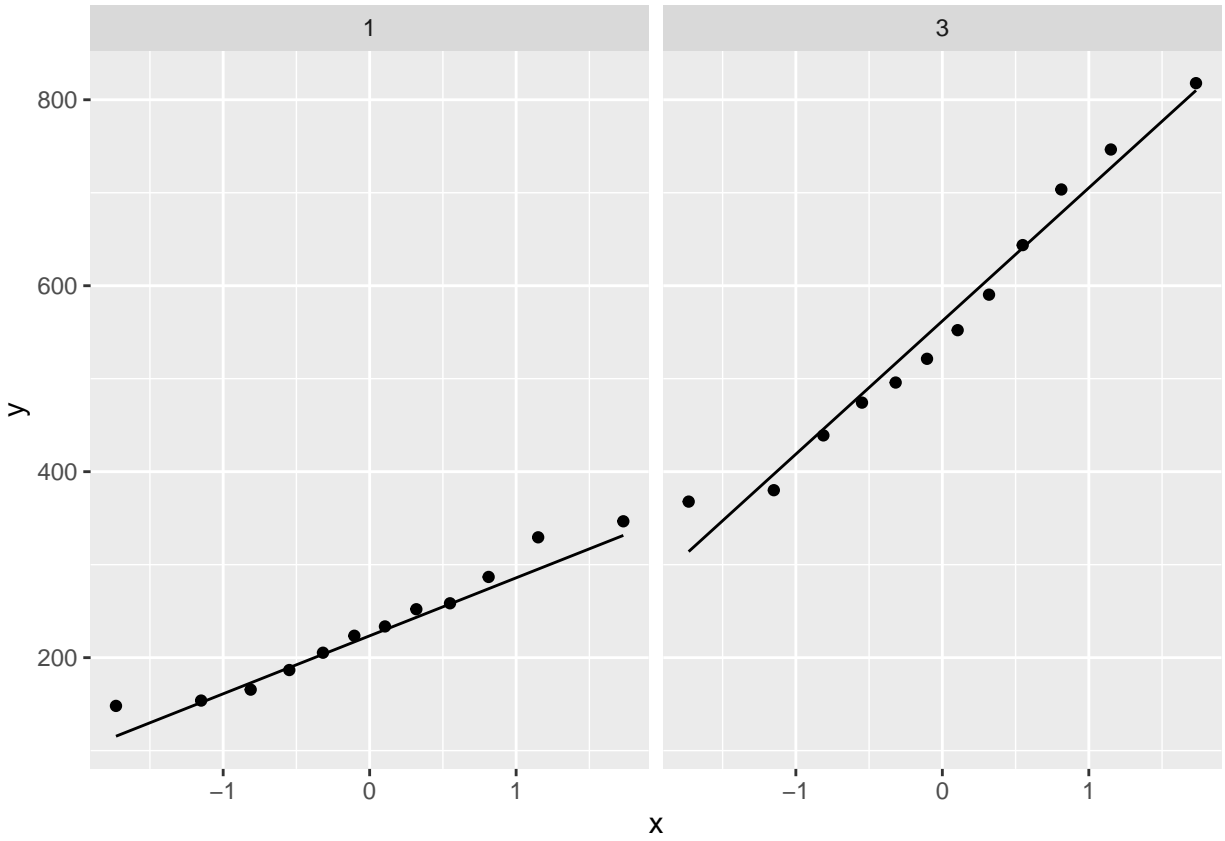


```
p2 <- gene %>%
  ggplot(aes(sample=gene)) +
  geom_qq() +
  geom_qq_line() +
  facet_wrap(~grade)
```

p1

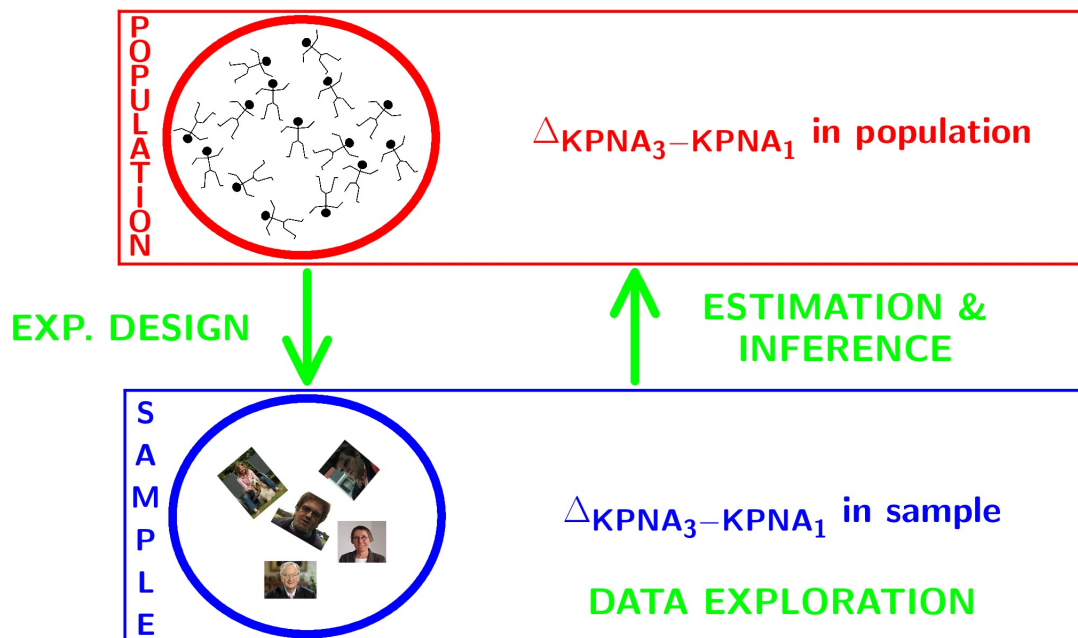


p2



## 2.4 Research questions

Researchers want to assess the association of the histological grade on KPNA2 gene expression



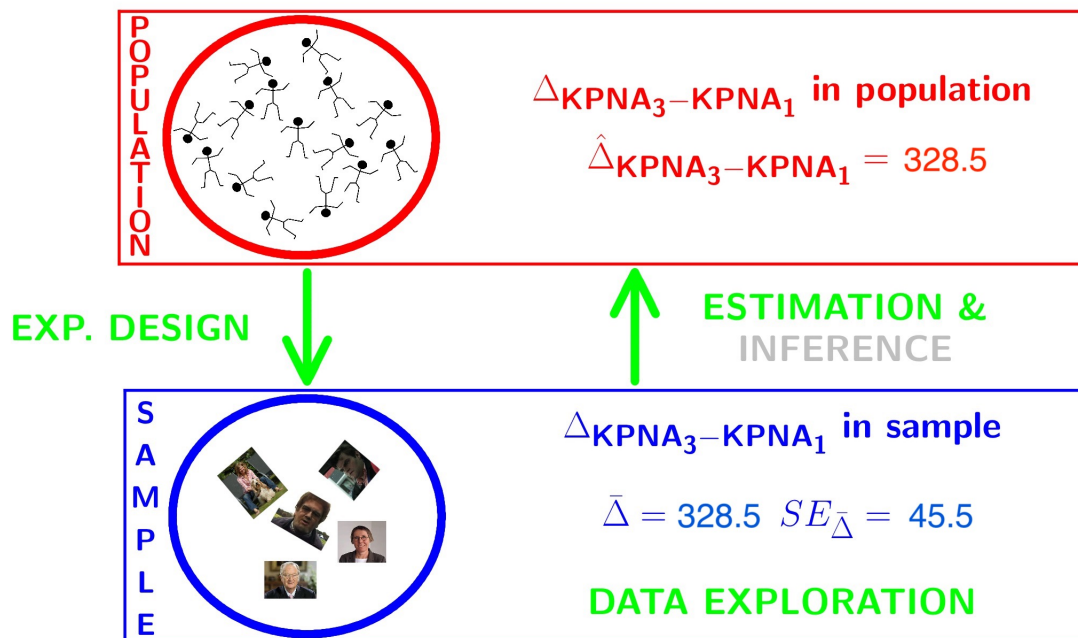
## 2.5 Estimation of effect size and standard error

```
effectSize <- tibble(
  delta = geneSum$mean[2] - geneSum$mean[1],
  seDelta = geneSum %>%
    pull(se) %>%
    .^2 %>%
    sum %>%
    sqrt
)
effectSize
```

```
## # A tibble: 1 x 2
##   delta seDelta
##   <dbl>   <dbl>
## 1  329.    45.5
```

## 3 Statistical Inference

- Researchers want to assess the association of histological grade on KPNA2 gene expression
- Inference?



- 
- Researchers want to assess the association of histological grade on KPNA2 gene expression
  - Inference?
  - testing + CI  $\rightarrow$  Assumptions

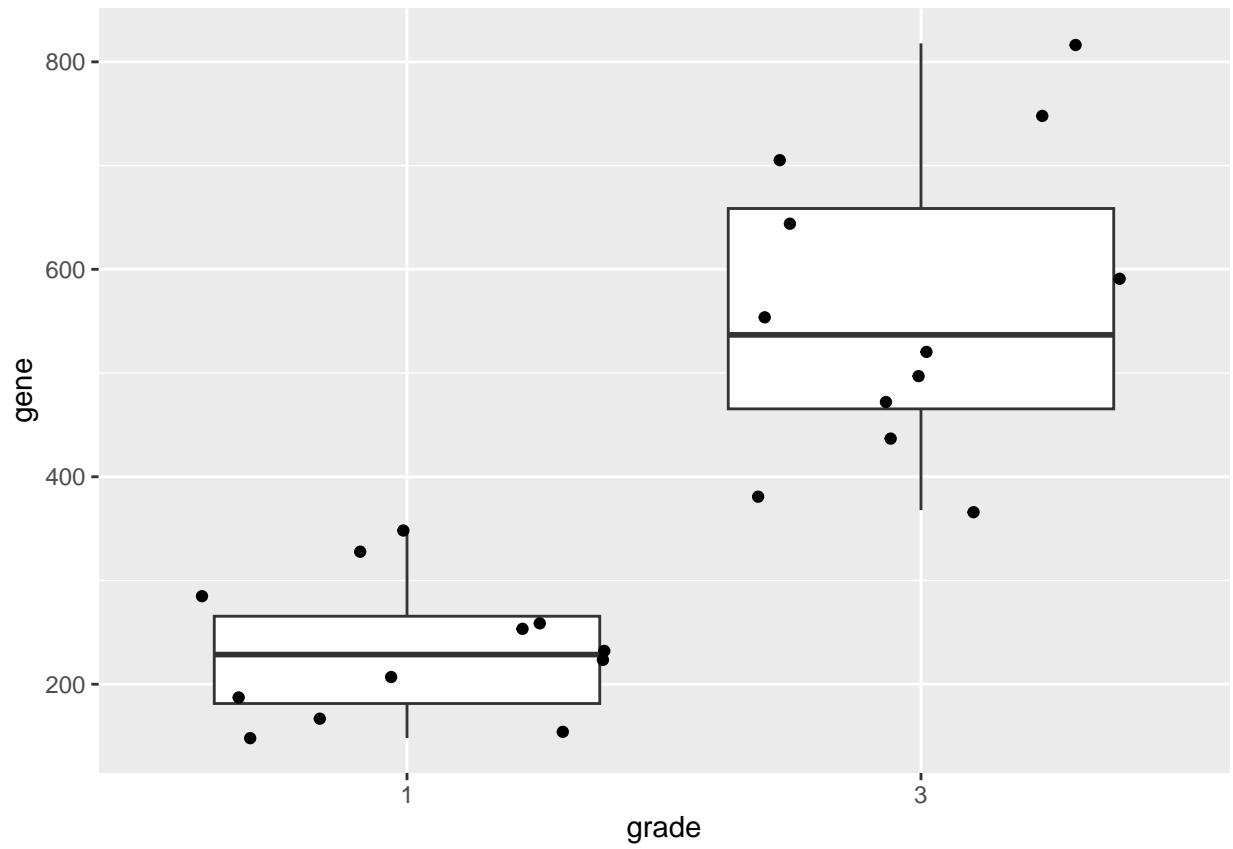
- 
- In general we start from **alternative hypothesis**  $H_A$ : we want to show an association
  - Gene expression of grade 1 and grade 3 patients is on average different
  - But, we will assess it by falsifying the opposite:
  - The average KPNA2 gene expression of grade 1 and grade 3 patients is equal

- 
- How likely is it to observe an equal or more extreme association 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**.
  - If the p-value is below a significance threshold  $\alpha$  we reject the null hypothesis

*We control the probability on a false positive result at the  $\alpha$ -level (type I error)*

- The p-value will only be calculated correctly if the underlying assumptions hold!

```
library(gridExtra)
p1
```



p2



```
t.test(gene~grade,data=gene)
```

```
##
## Welch Two Sample t-test
##
## data: gene by grade
## t = -7.2132, df = 15.384, p-value = 2.598e-06
## alternative hypothesis: true difference in means between group 1 and group 3 is not equal to 0
## 95 percent confidence interval:
## -425.4218 -231.6751
## sample estimates:
## mean in group 1 mean in group 3
## 232.5003 561.0487
```

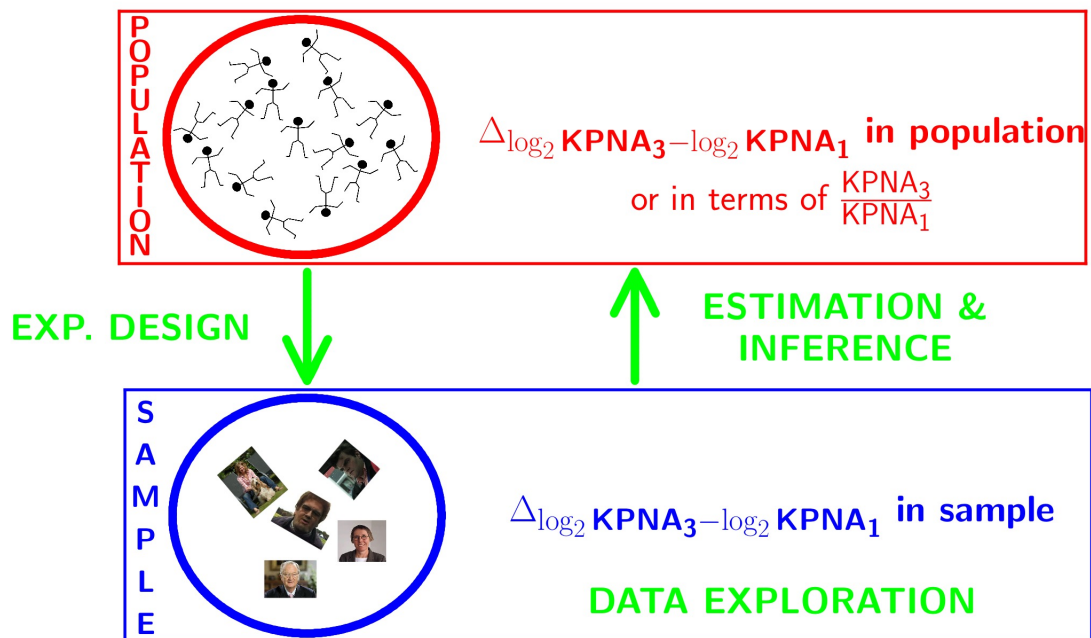
```
effectSize <- effectSize %>%
  mutate(t.stat=delta/seDelta) %>%
  mutate(p.value= pt(-abs(t.stat),21.352)*2)
```

```
effectSize
```

```
## # A tibble: 1 x 4
##   delta seDelta t.stat    p.value
##   <dbl>   <dbl>   <dbl>    <dbl>
## 1  329.    45.5    7.21 0.000000376
```

- Intensities are often not normally distributed and have a mean variance relation
- Commonly log2-transformed
- Differences on log scale:

$$\log_2(B) - \log_2(A) = \log_2 \frac{B}{A} = \log_2 FC_{\frac{B}{A}}$$



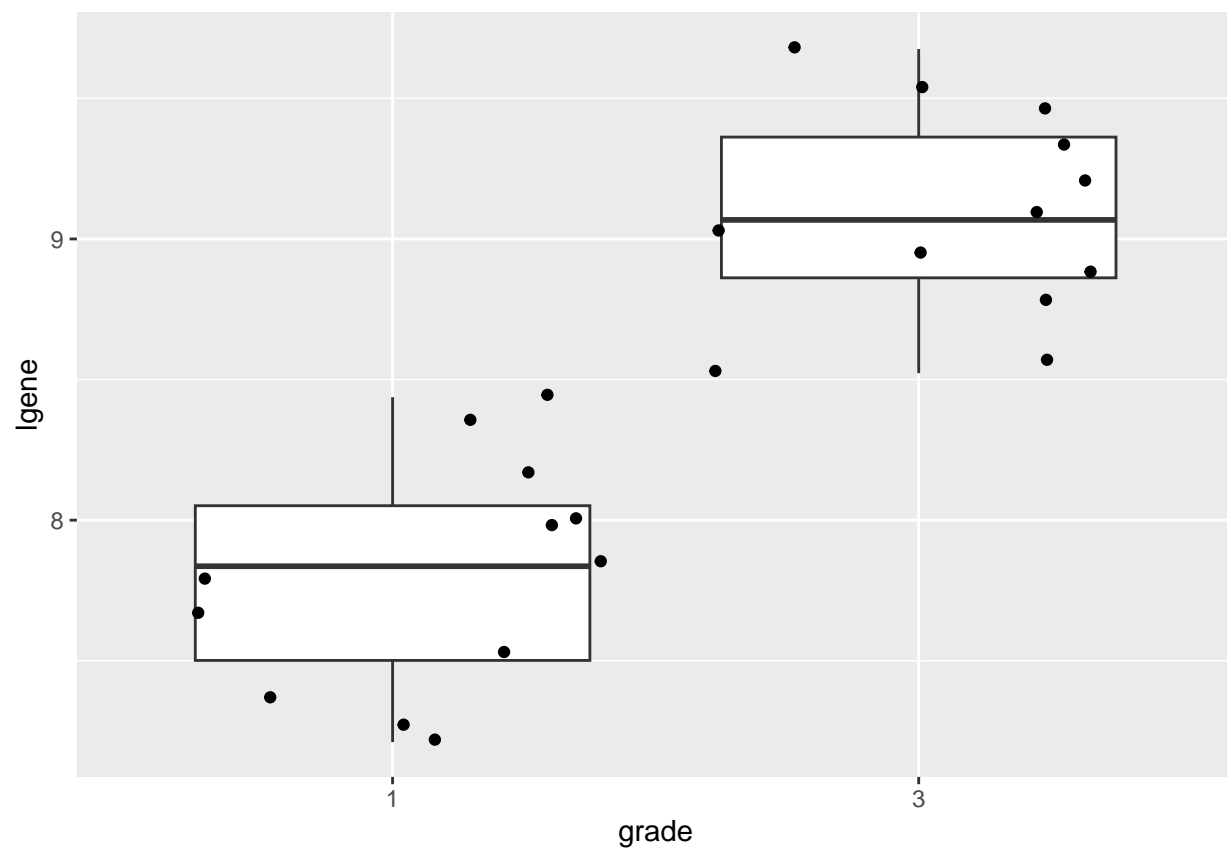
### 3.1 Log transformation

```
gene <- gene %>%
  mutate(lgene = log2(gene))

p1 <- gene %>%
  ggplot(aes(x=grade,y=lgene)) +
  geom_boxplot(outlier.shape=NA) +
  geom_jitter()

p2 <- gene %>%
  ggplot(aes(sample=lgene)) +
  geom_qq() +
  geom_qq_line() +
  facet_wrap(~grade)

p1
```



p2





```
logtest <- t.test(lgene~grade,data=gene,var.equal=TRUE)
logtest
```

```
##
## Two Sample t-test
##
## data: lgene by grade
## t = -8.0455, df = 22, p-value = 5.372e-08
## alternative hypothesis: true difference in means between group 1 and group 3 is not equal to 0
## 95 percent confidence interval:
## -1.610148 -0.950178
## sample estimates:
## mean in group 1 mean in group 3
## 7.808478 9.088641
```

```
log2FC <- logtest$estimate[2]-logtest$estimate[1]
log2FC
```

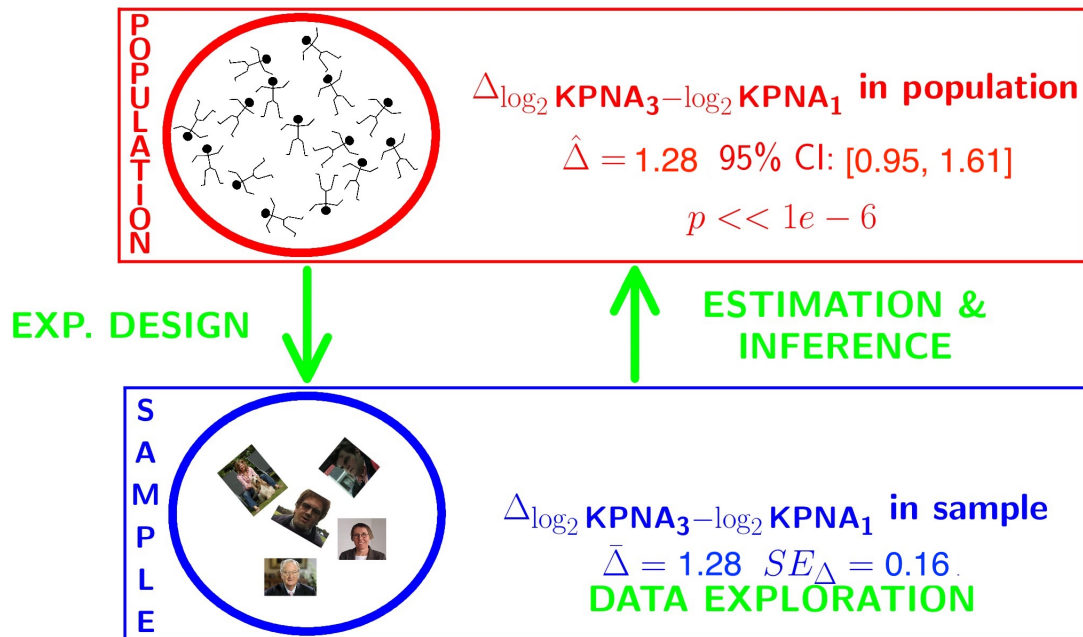
```
## mean in group 3
## 1.280163
```

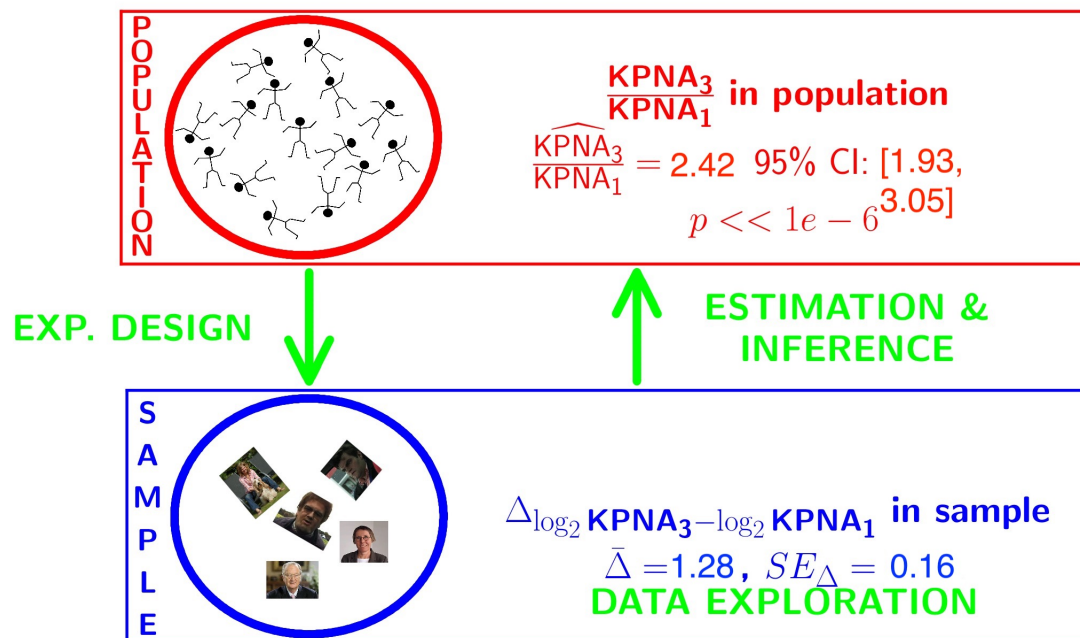
```
names(log2FC) <- "g3-g1"
2^log2FC
```

```
## g3-g1
## 2.428664
```

### 3.2 Conclusion

There is a extremely significant association of the histological grade on the gene expression in tumor tissue. On average, the gene expression for the grade 3 patients is 2.43 times higher than the gene expression in grade 1 patients (95% CI [1.93, 3.05],  $p < 0.001$ ).

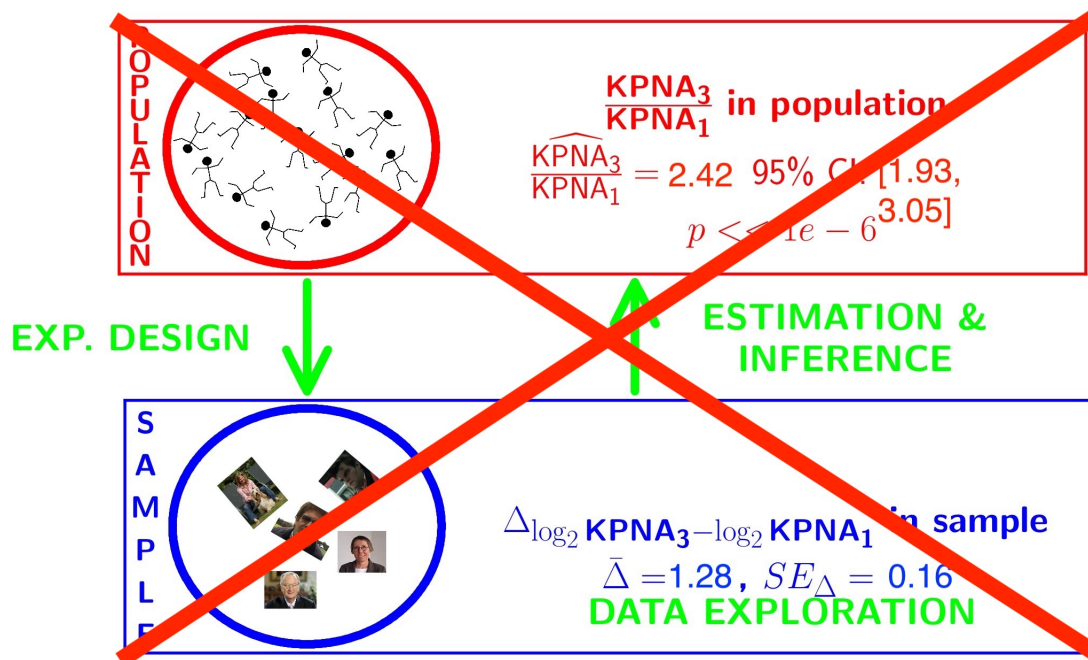





---

The patients also differ in the their lymph node status. Hence, we have a two factorial design: grade x lymph node status!!!

Solution??



## 4 General Linear Model

How can we integrate multiple factors and continuous covariates in linear model.

$$y_i = \beta_0 + \beta_1 x_{i,1} + \beta_2 x_{i,2} + \beta_{12} x_{i,1} x_{i,2} + \epsilon_i,$$

with

- $x_{i,1}$  a dummy variable for histological grade:  $x_{i,1} = \begin{cases} 0 & \text{grade 1} \\ 1 & \text{grade 3} \end{cases}$
- $x_{i,2}$  a dummy variable for :  $x_{i,2} = \begin{cases} 0 & \text{lymph nodes were not removed} \\ 1 & \text{lymph nodes were removed} \end{cases}$
- $\epsilon_i$ ?

### 4.1 Implementation in R

```
lm1 <- lm(gene~grade*node,data=gene)
summary(lm1)
```

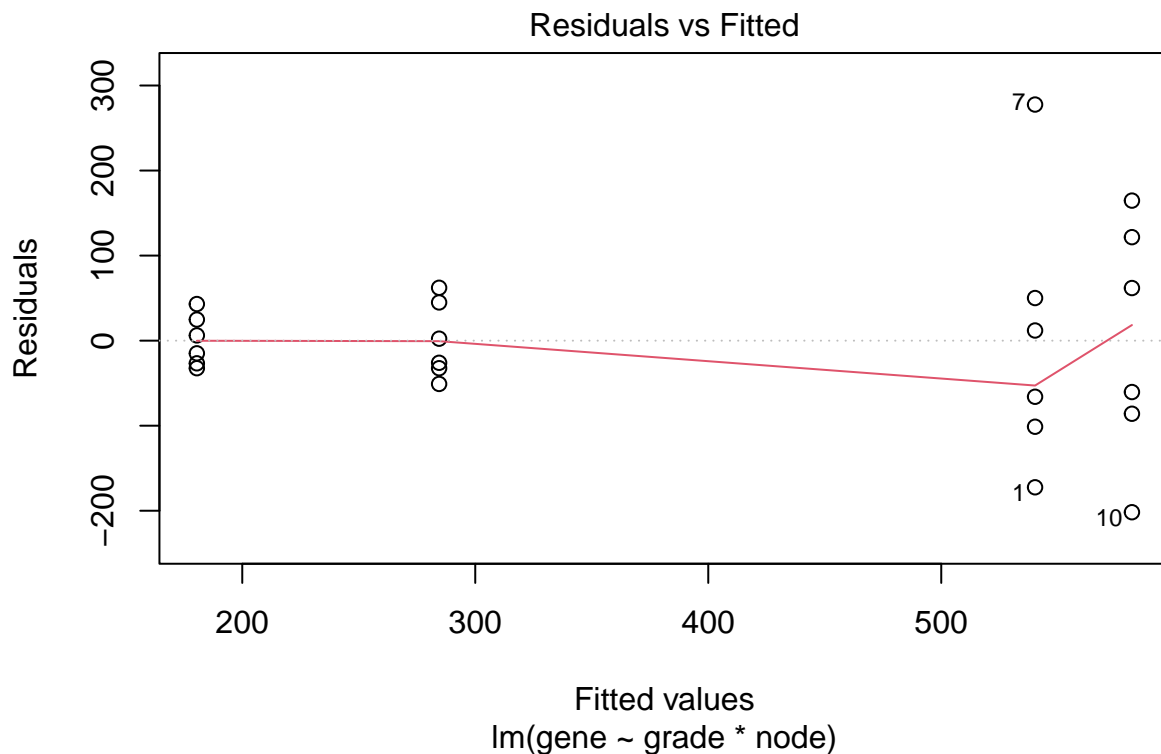
```
##
## Call:
```

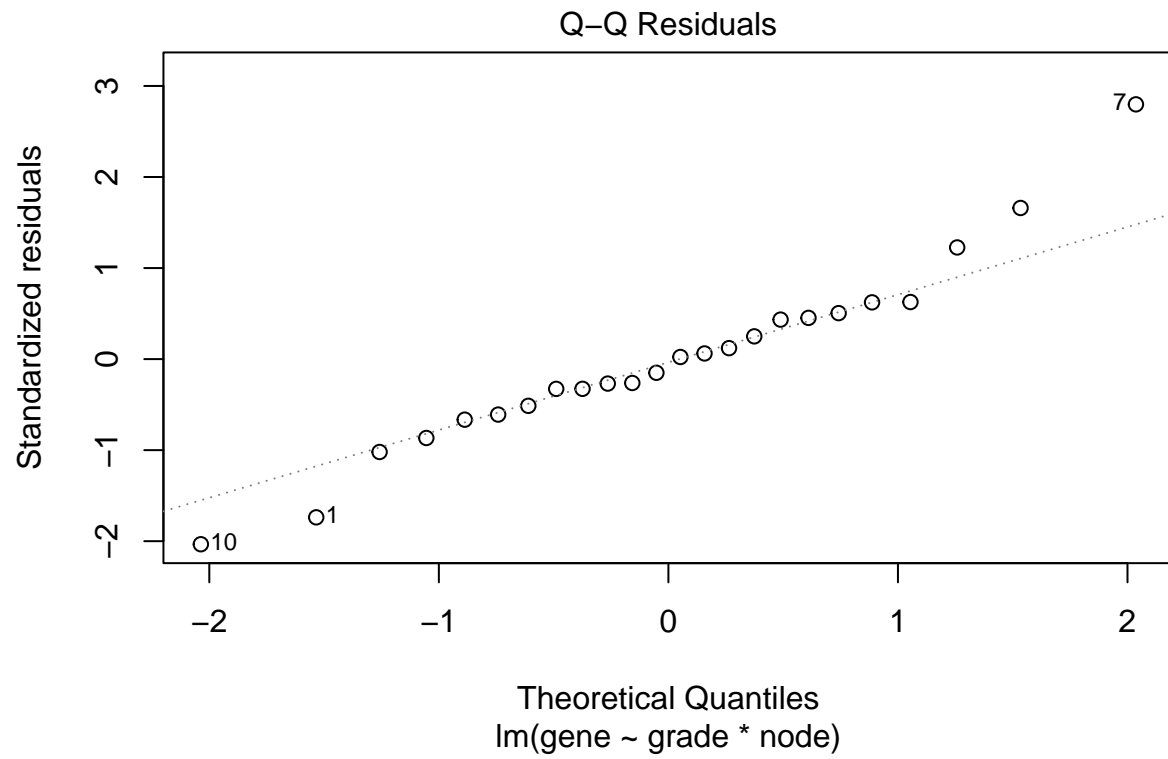
```
## lm(formula = gene ~ grade * node, data = gene)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -201.748  -53.294   -6.308   46.216  277.601
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    180.51     44.37   4.068  0.0006 ***
## grade3         401.33     62.75   6.396 3.07e-06 ***
## node1          103.98     62.75   1.657  0.1131
## grade3:node1  -145.57     88.74  -1.640  0.1166
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 108.7 on 20 degrees of freedom
## Multiple R-squared:  0.7437, Adjusted R-squared:  0.7052
## F-statistic: 19.34 on 3 and 20 DF,  p-value: 3.971e-06
```

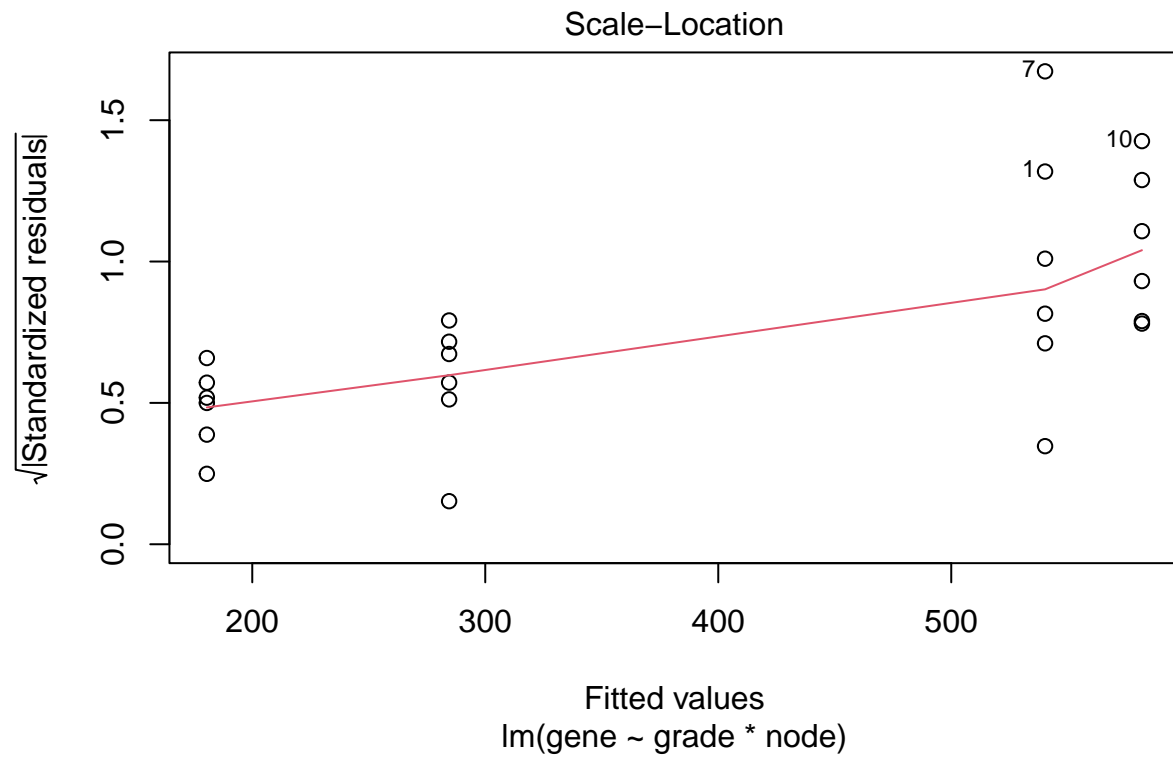
---

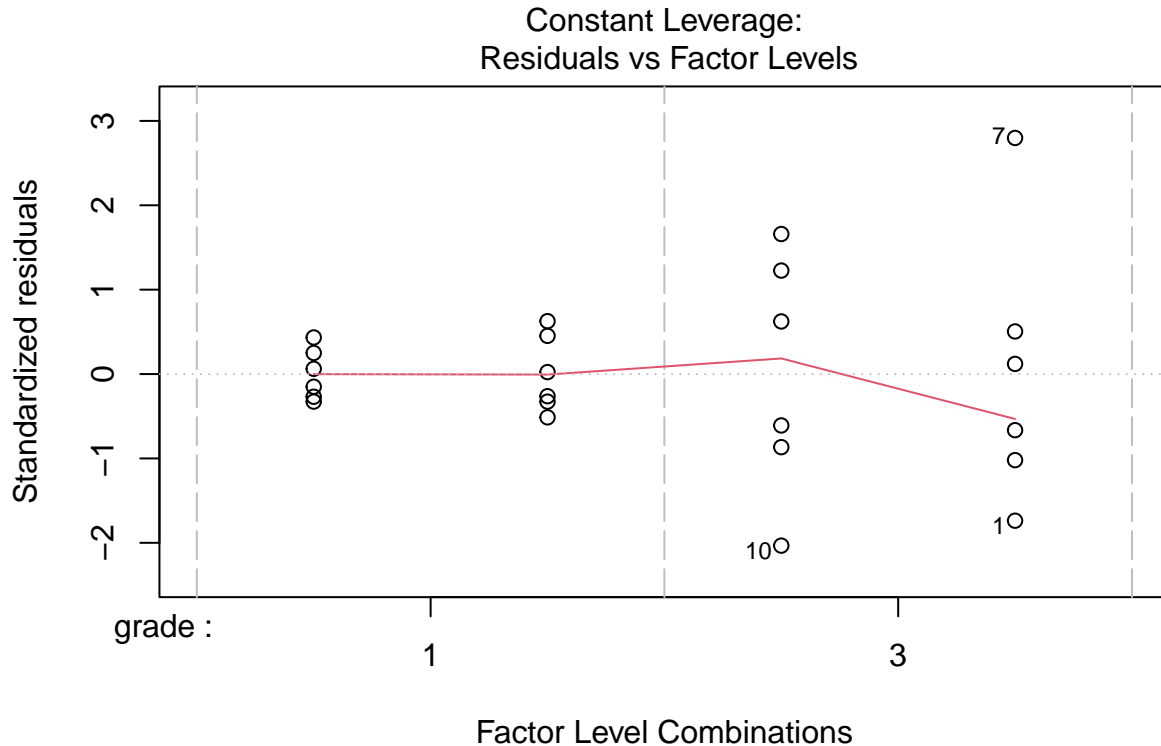
## 4.2 Assumptions

```
plot(lm1)
```









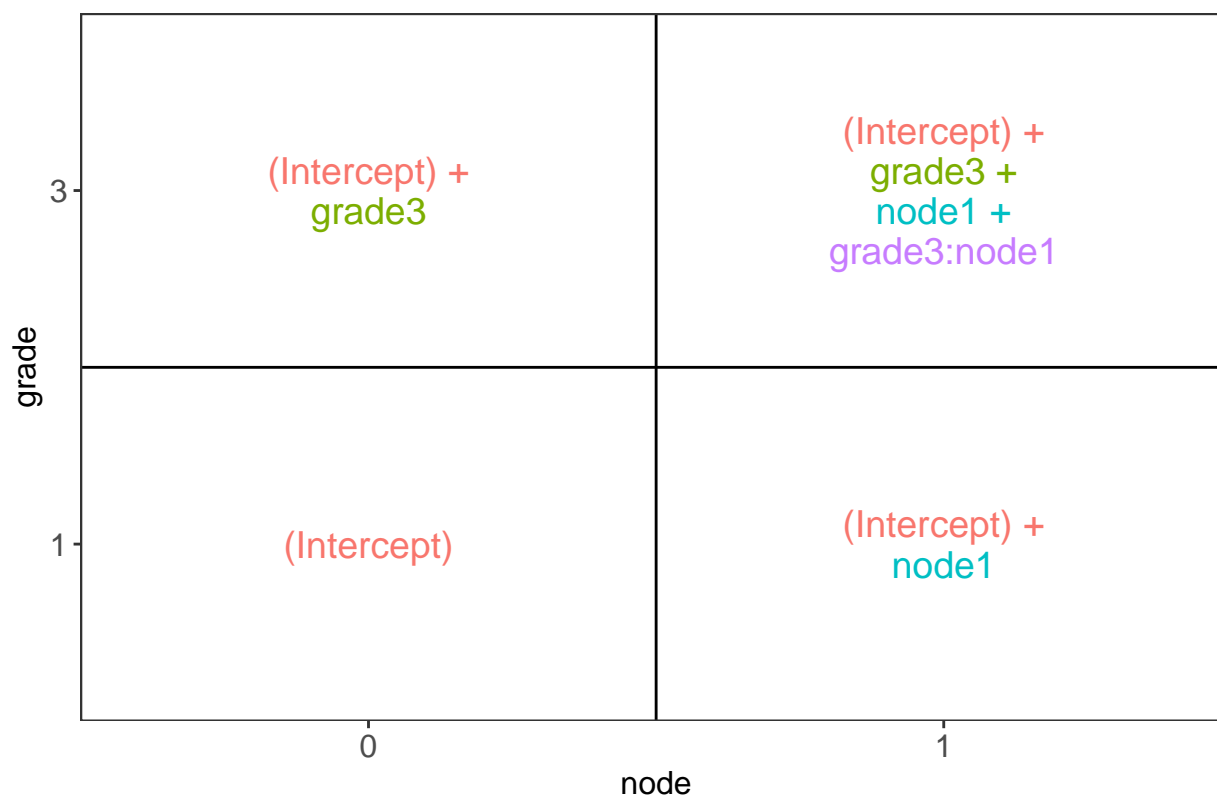
### 4.3 Breast cancer example

- Paper: <https://doi.org/10.1093/jnci/djj052>
- Histologic grade in breast cancer provides clinically important prognostic information. Two factors have to be considered: Histologic grade (grade 1 and grade 3) and lymph node status (0 vs 1). The researchers assessed gene expression of the KPNA2 gene a protein-coding gene associated with breast cancer and are mainly interested in the association of histological grade. Note, that the gene variable consists of background corrected normalized intensities obtained with a microarray platform. Upon log-transformation, they are known to be a good proxy for the log transformed concentration of gene expression product of the KPNA2 gene.
- Research questions and translate them towards model parameters (contrasts)?
- Make an R markdown file to answer the research questions

```
library(ExploreModelMatrix)
explMx <- VisualizeDesign(gene, designFormula = ~grade*node)
explMx$plotlist
```

```
## [[1]]
```





You can also explore the model matrix interactively:

```
ExploreModelMatrix(gene, designFormula = ~grade*node)
```

## 5 Linear regression in matrix form

### 5.1 Scalar form

- Consider a vector of predictors  $\mathbf{x} = (x_1, \dots, x_p)^T$  and
- a real-valued response  $Y$
- then the linear regression model can be written as

$$Y = f(\mathbf{x}) + \epsilon = \beta_0 + \sum_{j=1}^p x_j \beta_j + \epsilon$$

with i.i.d.  $\epsilon \sim N(0, \sigma^2)$

### 5.2 Matrix form

- $n$  observations  $(\mathbf{x}_1, y_1) \dots (\mathbf{x}_n, y_n)$
- Regression in matrix notation

$$\mathbf{Y} = \mathbf{X} \boldsymbol{\beta} + \boldsymbol{\epsilon}$$

with  $\mathbf{Y} = \begin{bmatrix} y_1 \\ \vdots \\ y_n \end{bmatrix}$ ,  $\mathbf{X} = \begin{bmatrix} 1 & x_{11} & \dots & x_{1p} \\ \vdots & \vdots & & \vdots \\ 1 & x_{n1} & \dots & x_{np} \end{bmatrix}$ ,  $\boldsymbol{\beta} = \begin{bmatrix} \beta_0 \\ \vdots \\ \beta_p \end{bmatrix}$  and  $\boldsymbol{\epsilon} = \begin{bmatrix} \epsilon_1 \\ \vdots \\ \epsilon_n \end{bmatrix}$

## 5.3 Least Squares (LS)

- Minimize the residual sum of squares

$$\begin{aligned}RSS(\beta) &= \sum_{i=1}^n e_i^2 \\&= \sum_{i=1}^n \left( y_i - \beta_0 - \sum_{j=1}^p x_{ij} \beta_j \right)^2\end{aligned}$$

- or in matrix notation

$$\begin{aligned}RSS(\beta) &= (\mathbf{Y} - \mathbf{X}\beta)^T (\mathbf{Y} - \mathbf{X}\beta) \\&= \|\mathbf{Y} - \mathbf{X}\beta\|_2^2\end{aligned}$$

with the  $L_2$ -norm of a  $p$ -dim. vector  $\mathbf{v}$   $\|\mathbf{v}\| = \sqrt{v_1^2 + \dots + v_p^2} \rightarrow \hat{\beta} = \operatorname{argmin}_{\beta} \|\mathbf{Y} - \mathbf{X}\beta\|_2^2$

---

### 5.3.1 Minimize RSS

$$\begin{aligned}\frac{\partial RSS}{\partial \beta} &= \mathbf{0} \\ \frac{\partial (\mathbf{Y} - \mathbf{X}\beta)^T (\mathbf{Y} - \mathbf{X}\beta)}{\partial \beta} &= \mathbf{0} \\ -2\mathbf{X}^T (\mathbf{Y} - \mathbf{X}\beta) &= \mathbf{0} \\ \mathbf{X}^T \mathbf{X} \beta &= \mathbf{X}^T \mathbf{Y} \\ \hat{\beta} &= (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{Y}\end{aligned}$$

---

### 5.3.2 Geometric Interpretation

**5.3.2.1 Toy dataset** We will illustrate this on a toy dataset

```
library(tidyverse)
data <- data.frame(x=1:3, y=c(1,2,2))
data
```

```
##   x y
## 1 1 1
## 2 2 2
## 3 3 2
```

**5.3.2.2 Matrix form for toy dataset** We can also write this in matrix form

$$\mathbf{Y} = \mathbf{X}\beta + \epsilon$$

with

$$\mathbf{Y} = \begin{bmatrix} 1 \\ 2 \\ 2 \end{bmatrix}, \quad \mathbf{X} = \begin{bmatrix} 1 & 1 \\ 1 & 2 \\ 1 & 3 \end{bmatrix}, \quad \beta = \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix} \quad \text{and} \quad \epsilon = \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \end{bmatrix}$$

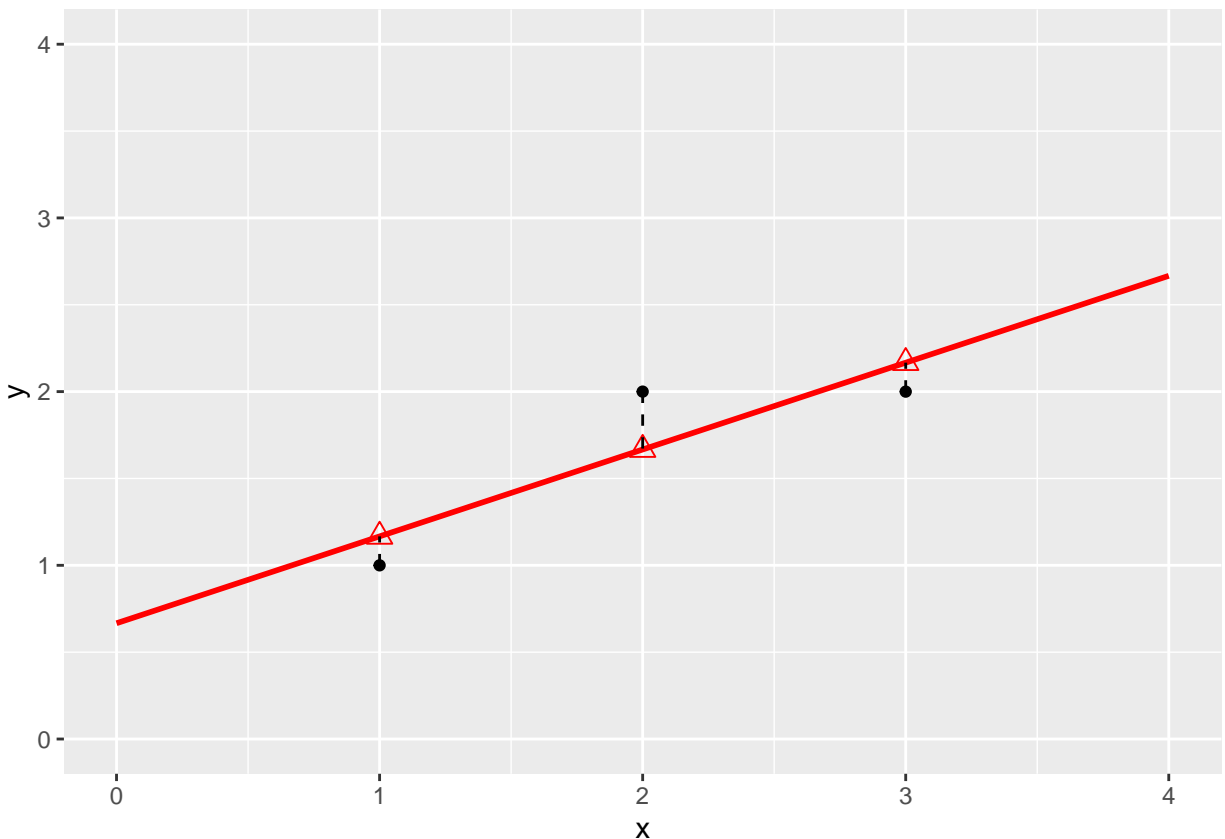
### 5.3.2.3 Classical interpretation Model fit and predictions based on the toy dataset

```
lm1 <- lm(y~x,data)
data$yhat <- lm1$fitted
```

```
data %>%
  ggplot(aes(x,y)) +
  geom_point() +
  ylim(0,4) +
  xlim(0,4) +
  stat_smooth(method = "lm", color = "red", fullrange = TRUE) +
  geom_point(aes(x=x, y =yhat), pch = 2, size = 3, color = "red") +
  geom_segment(data = data, aes(x = x, xend = x, y = y, yend = yhat), lty = 2 )
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning
## -Inf
```



### 5.3.3 Projection

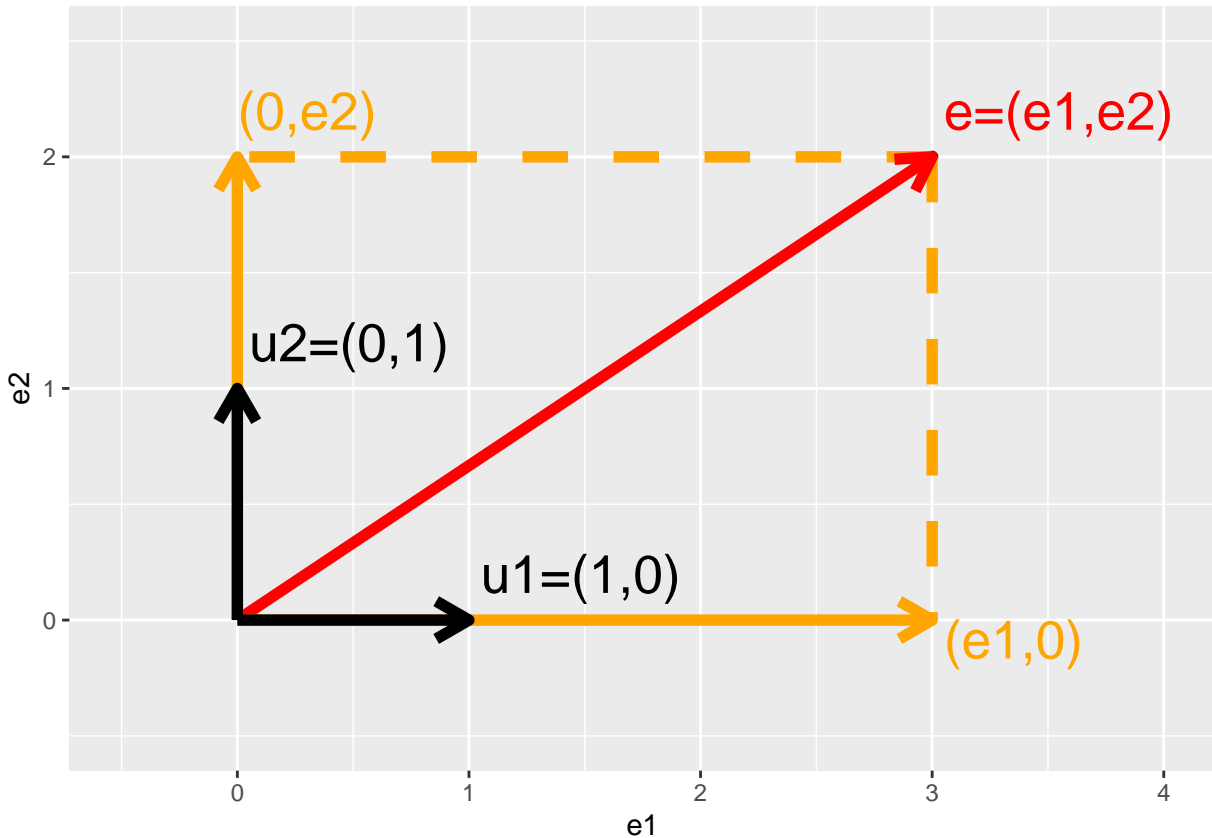
There is also another picture to regression:

- Instead of plotting each observation  $i = 1 \dots n$  as a data-point in  $\mathbb{R}^p$  with dimensions  $1 \dots p$  for every variable/feature that is recorded for each observation
- We can also plot  $\mathbf{Y}$ ,  $\hat{\mathbf{Y}}$  and each column of  $\mathbf{X}$ :  $\mathbf{X}_j$  with  $j = 1 \dots p$  as a vector in  $\mathbb{R}^n$  with dimensions  $1 \dots n$  for every observation.

- In this representation linear regression can be interpreted as a projection of the vector  $\mathbf{Y}$  onto the subspace of  $\mathbb{R}^n$  that is spanned by the vectors for the predictors  $\mathbf{X}_1 \dots \mathbf{X}_p$ .
- The space  $\mathbf{X}_1 \dots \mathbf{X}_p$  is also referred to as the column space of  $\mathbf{X}$ , the space that consists of all linear combinations of the vectors of the predictors or columns  $\mathbf{X}_1 \dots \mathbf{X}_p$ .

### 5.3.3.1 Intermezzo: Projection of vector on X and Y axis

$$\mathbf{e} = \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}, \mathbf{u}_1 = \begin{bmatrix} 1 \\ 0 \end{bmatrix}, \mathbf{u}_2 = \begin{bmatrix} 0 \\ 1 \end{bmatrix}$$



1. Projection of error on x-axis

$$\begin{aligned} \mathbf{u}_1^T \mathbf{e} &= \|\mathbf{u}_1\|_2 \|\mathbf{e}_1\|_2 \cos \angle \mathbf{u}_1, \mathbf{e}_1 > \\ &= \begin{bmatrix} 1 & 0 \end{bmatrix} \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \\ &= 1 \times e_1 + 0 \times e_2 \\ &= e_1 \end{aligned}$$

2. Projection of error on y-axis

$$\begin{aligned}
\mathbf{u}_2^T \mathbf{e} &= \begin{bmatrix} 1 & 0 \end{bmatrix} \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \\
&= 0 \times e_1 + 1 \times e_2 \\
&= e_2
\end{aligned}$$

3. Projection of error on itself

$$\begin{aligned}
\mathbf{e}^T \mathbf{e} &= \begin{bmatrix} e_1 & e_2 \end{bmatrix} \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \\
&= e_1^2 + e_2^2 \\
&= \|\mathbf{e}\|_2^2 \rightarrow \text{Pythagorean theorem}
\end{aligned}$$


---

**5.3.3.2 Interpretation of least squares as a projection** Fitted values:

$$\begin{aligned}
\hat{\mathbf{Y}} &= \mathbf{X}\hat{\beta} \\
&= \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y} \\
&= \mathbf{H}\mathbf{Y}
\end{aligned}$$

with  $\mathbf{H}$  the projection matrix also referred to as the hat matrix.

```
X <- model.matrix(~x,data)
X
```

```
##      (Intercept) x
## 1             1  1
## 2             1  2
## 3             1  3
## attr(,"assign")
## [1] 0 1
```

```
XtX <- t(X)%*%X
XtX
```

```
##              (Intercept)  x
## (Intercept)           3  6
## x                   6 14
```

```
XtXinv <- solve(t(X)%*%X)
XtXinv
```

```
##              (Intercept)  x
## (Intercept)  2.333333 -1.0
## x          -1.000000  0.5
```

```
H <- X %*% XtXinv %*% t(X)
H
```

```
##              1          2          3
## 1  0.8333333 0.3333333 -0.1666667
## 2  0.3333333 0.3333333  0.3333333
## 3 -0.1666667 0.3333333  0.8333333
```

```
Y <- data$y
Yhat <- H%*%Y
Yhat
```

```
##      [,1]
## 1 1.166667
## 2 1.666667
## 3 2.166667
```

- We can also interpret the fit as the projection of the  $n \times 1$  vector  $\mathbf{Y}$  on the column space of the matrix  $\mathbf{X}$ .
- So each column in  $\mathbf{X}$  is also an  $n \times 1$  vector.
- For the toy example  $n=3$  and  $p=2$ . The other picture to linear regression is to consider  $X_0$ ,  $X_1$  and  $Y$  as vectors in the space of the data  $\mathbb{R}^n$ , here  $\mathbb{R}^3$  because we have three data points. So the column space of  $\mathbf{X}$  is a plane in the three dimensional space.

$$\hat{\mathbf{Y}} = \mathbf{X}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{Y}$$

1. Plane spanned by column space:

```
originRn <- data.frame(X1=0,X2=0,X3=0)
data$x0 <- 1
dataRn <- data.frame(t(data))

library(plotly)

p1 <- plot_ly(
  originRn,
  x = ~ X1,
  y = ~ X2,
  z = ~ X3, name="origin") %>%
add_markers(type="scatter3d") %>%
layout(
  scene = list(
    aspectmode="cube",
    xaxis = list(range=c(-4,4)), yaxis = list(range=c(-4,4)), zaxis = list(range=c(-4,4))
  )
)
p1 <- p1 %>%
add_trace(
  x = c(0,1),
  y = c(0,0),
  z = c(0,0),
  mode = "lines",
  line = list(width = 5, color = "grey"),
  type="scatter3d",
  name = "obs1") %>%
add_trace(
  x = c(0,0),
  y = c(0,1),
  z = c(0,0),
  mode = "lines",
  line = list(width = 5, color = "grey"),
  type="scatter3d",
```

```

    name = "obs2") %>%
add_trace(
  x = c(0,0),
  y = c(0,0),
  z = c(0,1),
  mode = "lines",
  line = list(width = 5, color = "grey"),
  type="scatter3d",
  name = "obs3") %>%
add_trace(
  x = c(0,1),
  y = c(0,1),
  z = c(0,1),
  mode = "lines",
  line = list(width = 5, color = "black"),
  type="scatter3d",
  name = "X1") %>%
add_trace(
  x = c(0,1),
  y = c(0,2),
  z = c(0,3),
  mode = "lines",
  line = list(width = 5, color = "black"),
  type="scatter3d",
  name = "X2")
p1

```

2. Vector of Y:

Actual values of  $\mathbf{Y}$ :

```
data$y
```

```
## [1] 1 2 2
```

$$\mathbf{Y} = \begin{bmatrix} 1 \\ 2 \\ 2 \end{bmatrix}$$

```

p2 <- p1 %>%
add_trace(
  x = c(0,Y[1]),
  y = c(0,Y[2]),
  z = c(0,Y[3]),
  mode = "lines",
  line = list(width = 5, color = "red"),
  type="scatter3d",
  name = "Y")
p2

```

3. Projection of Y onto column space

Actual values of fitted values  $\hat{\mathbf{Y}}$ :

```
data$yhat
```

```
## [1] 1.166667 1.666667 2.166667
```

$$\mathbf{Y} = \begin{bmatrix} 1.166667 \\ 1.666667 \\ 2.166667 \end{bmatrix}$$

```
p2 <- p2 %>%
  add_trace(
    x = c(0,Yhat[1]),
    y = c(0,Yhat[2]),
    z = c(0,Yhat[3]),
    mode = "lines",
    line = list(width = 5, color = "orange"),
    type="scatter3d",
    name="Yhat") %>%
  add_trace(
    x = c(Y[1],Yhat[1]),
    y = c(Y[2],Yhat[2]),
    z = c(Y[3],Yhat[3]),
    mode = "lines",
    line = list(width = 5, color = "red", dash="dash"),
    type="scatter3d",
    name="Y -> Yhat"
  )
p2
```

$\mathbf{Y}$  is projected in the column space of  $\mathbf{X}$ ! spanned by the columns.

### 5.3.3.3 How does this projection works?

$$\begin{aligned}\hat{\mathbf{Y}} &= \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y} \\ &= \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1/2}(\mathbf{X}^T\mathbf{X})^{-1/2}\mathbf{X}^T\mathbf{Y} \\ &= \mathbf{U}\mathbf{U}^T\mathbf{Y}\end{aligned}$$

- $\mathbf{U}$  is a new orthonormal basis in  $\mathbb{R}^2$ , a subspace of  $\mathbb{R}^3$
- The space spanned by  $\mathbf{U}$  and  $\mathbf{X}$  is the column space of  $\mathbf{X}$ , e.g. it contains all possible linear combinations of  $\mathbf{X}$ .  $\mathbf{U}^t\mathbf{Y}$  is the projection of  $\mathbf{Y}$  on this new orthonormal basis

```
eigenXtX <- eigen(XtX)
XtXinvSqrt <- eigenXtX$vectors %*%diag(1/eigenXtX$values^.5)%*%t(eigenXtX$vectors)
U <- X %*% XtXinvSqrt
```

- $\mathbf{U}$  orthonormal basis

$\mathbf{U}$

```
##           [,1]           [,2]
## 1  0.9116067 -0.04802616
## 2  0.3881706  0.42738380
## 3 -0.1352655  0.90279376
```

$\mathbf{t}(\mathbf{U})\mathbf{U}$

```
##           [,1]           [,2]
## [1,] 1.000000e+00 2.915205e-16
## [2,] 2.915205e-16 1.000000e+00
```



- $UU^T$  equals projection matrix

```
U%*%t(U)
```

```
##           1           2           3
## 1  0.8333333 0.3333333 -0.1666667
## 2  0.3333333 0.3333333  0.3333333
## 3 -0.1666667 0.3333333  0.8333333
```

```
H
```

```
##           1           2           3
## 1  0.8333333 0.3333333 -0.1666667
## 2  0.3333333 0.3333333  0.3333333
## 3 -0.1666667 0.3333333  0.8333333
```

```
p3 <- p1 %>%
  add_trace(
    x = c(0,U[1,1]),
    y = c(0,U[2,1]),
    z = c(0,U[3,1]),
    mode = "lines",
    line = list(width = 5, color = "blue"),
    type="scatter3d",
    name = "U1") %>%
  add_trace(
    x = c(0,U[1,2]),
    y = c(0,U[2,2]),
    z = c(0,U[3,2]),
    mode = "lines",
    line = list(width = 5, color = "blue"),
    type="scatter3d",
    name = "U2")
```

```
p3
```

- $U^T Y$  is the projection of  $Y$  in the space spanned by  $U$ .
- Indeed  $U_1^T Y$

```
p4 <- p3 %>%
  add_trace(
    x = c(0,Y[1]),
    y = c(0,Y[2]),
    z = c(0,Y[3]),
    mode = "lines",
    line = list(width = 5, color = "red"),
    type="scatter3d",
    name = "Y") %>%
  add_trace(
    x = c(0,U[1,1]*(U[,1]%*%Y)),
    y = c(0,U[2,1]*(U[,1]%*%Y)),
    z = c(0,U[3,1]*(U[,1]%*%Y)),
    mode = "lines",
    line = list(width = 5, color = "red",dash="dash"),
    type="scatter3d",
    name="Y -> U1") %>% add_trace(
    x = c(Y[1],U[1,1]*(U[,1]%*%Y)),
```

```

y = c(Y[2],U[2,1]*(U[,1]**%Y)),
z = c(Y[3],U[3,1]*(U[,1]**%Y)),
mode = "lines",
line = list(width = 5, color = "red", dash="dash"),
type="scatter3d",
name="Y -> U1")

```

p4

- and  $U_2^T Y$

```

p5 <- p4 %>%
add_trace(
  x = c(0,U[1,2]*(U[,2]**%Y)),
  y = c(0,U[2,2]*(U[,2]**%Y)),
  z = c(0,U[3,2]*(U[,2]**%Y)),
  mode = "lines",
  line = list(width = 5, color = "red",dash="dash"),
  type="scatter3d",
  name="Y -> U2") %>% add_trace(
  x = c(Y[1],U[1,2]*(U[,2]**%Y)),
  y = c(Y[2],U[2,2]*(U[,2]**%Y)),
  z = c(Y[3],U[3,2]*(U[,2]**%Y)),
  mode = "lines",
  line = list(width = 5, color = "red", dash="dash"),
  type="scatter3d",
  name="Y -> U2")

```

p5

- $\hat{Y}$  is the resulting vector that lies in the plane spanned by  $U_1$  and  $U_2$  and thus also in the column space of  $X$ .

```

p6 <- p5 %>%
add_trace(
  x = c(0,Yhat[1]),
  y = c(0,Yhat[2]),
  z = c(0,Yhat[3]),
  mode = "lines",
  line = list(width = 5, color = "orange"),
  type="scatter3d",
  name = "Yhat") %>%
add_trace(
  x = c(Y[1],Yhat[1]),
  y = c(Y[2],Yhat[2]),
  z = c(Y[3],Yhat[3]),
  mode = "lines",
  line = list(width = 5, color = "maroon2"),
  type="scatter3d",
  name = "e") %>%
add_trace(
  x = c(U[1,1]*(U[,1]**%Y),Yhat[1]),
  y = c(U[2,1]*(U[,1]**%Y),Yhat[2]),
  z = c(U[3,1]*(U[,1]**%Y),Yhat[3]),
  mode = "lines",
  line = list(width = 5, color = "orange", dash="dash"),
  type="scatter3d",

```

```

    name = "Y -> U")  %>%
add_trace(
  x = c(U[1,2]*(U[,2]**Y), Yhat[1]),
  y = c(U[2,2]*(U[,2]**Y), Yhat[2]),
  z = c(U[3,2]*(U[,2]**Y), Yhat[3]),
  mode = "lines",
  line = list(width = 5, color = "orange", dash="dash"),
  type="scatter3d",
  name = "Y -> U")

```

p6

### 5.3.4 Error

Note, that it is also clear from the equation in the derivation of the least squares solution that the residual is orthogonal on the column space:

$$-2\mathbf{X}^T(\mathbf{Y} - \mathbf{X}\beta) = 0$$


---

## 5.4 Variance Estimator?

$$\begin{aligned}
 \hat{\Sigma} &= \text{var}[(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y}] \\
 &= (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\text{var}[\mathbf{Y}]\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1} \\
 &= (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T(\mathbf{I}\sigma^2)\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1} \\
 &= (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{I}\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\sigma^2 \\
 &= (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\sigma^2 \\
 &= (\mathbf{X}^T\mathbf{X})^{-1}\sigma^2
 \end{aligned}$$


---

## 5.5 Contrasts

Hypotheses often involve linear combinations of the model parameters!

e.g.

- $H_0 : \log_2 FC_{g3n1-g1n1} = \beta_{g3} + \hat{\beta}_{g3n1} = 0 \rightarrow \text{"grade3+grade3:node1 = 0"}$
- Let

$$\beta = \begin{bmatrix} \beta_0 \\ \beta_{g3} \\ \beta_{n1} \\ \beta_{g3:n1} \end{bmatrix}$$

- we can write that contrast using a contrast matrix:

$$\mathbf{L} = \begin{bmatrix} 0 \\ 1 \\ 0 \\ 1 \end{bmatrix} \rightarrow \mathbf{L}^T\beta$$

- Then the variance becomes:

$$\text{var}_{\mathbf{L}^T \hat{\beta}} = \mathbf{L}^T \Sigma_{\hat{\beta}} \mathbf{L}$$


---

## 6 Homework: Adopt the gene analysis on log scale in matrix form!

1. Study the solution of the exercise to understand the analysis in R
  2. Calculate
    - model parameters and contrasts of interest
    - standard errors, standard errors on contrasts
    - t-test statistics on the model parameters and contrasts of interest
  3. Compare your results with the output of the `lm(.)` function
- 

### 6.1 Inspiration

Tip: details on the implementation can be found in the book of Faraway (chapter 2). <https://people.bath.ac.uk/jjf23/book/>

- Design matrix

```
X <- model.matrix(~grade*node,data=gene)
```

- Transpose of a matrix: use function `t(.)`

```
t(X)
```

```
##           1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
## (Intercept) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## grade3      1 1 0 0 0 1 1 0 1 1 0 1 0 0 0 1 0 1 0 1 0 1 1 0
## node1       1 1 1 1 0 0 1 1 0 0 0 0 0 0 0 1 1 0 1 1 1 0 1 0
## grade3:node1 1 1 0 0 0 0 1 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 1 0
## attr("assign")
## [1] 0 1 2 3
## attr("contrasts")
## attr("contrasts")$grade
## [1] "contr.treatment"
##
## attr("contrasts")$node
## [1] "contr.treatment"
```

- Matrix product `%*%` operator

```
t(X)%*%X
```

```
##           (Intercept) grade3 node1 grade3:node1
## (Intercept)         24      12      12          6
## grade3              12      12       6          6
## node1               12       6      12          6
## grade3:node1         6       6       6          6
```

- Degrees of freedom of a model?

$$df = n - p$$

```
summary(lm1)
```

```
##
## Call:
## lm(formula = y ~ x, data = data)
##
## Residuals:
##      1      2      3
## -0.1667  0.3333 -0.1667
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.6667     0.6236   1.069   0.479
## x             0.5000     0.2887   1.732   0.333
##
## Residual standard error: 0.4082 on 1 degrees of freedom
## Multiple R-squared:  0.75, Adjusted R-squared:  0.5
## F-statistic:      3 on 1 and 1 DF,  p-value: 0.3333
```

```
dfRes <- (nrow(X)-ncol(X))
```

```
dfRes
```

```
## [1] 20
```

- Variance estimator: MSE

$$\hat{\sigma}^2 = \frac{\sum_{i=1}^n \epsilon_i^2}{n-p}$$

- Invert matrix: use function solve(.)
- Diagonal elements of a matrix: use function diag(.)

```
t(X)%*%X
```

```
##              (Intercept) grade3 node1 grade3:node1
## (Intercept)           24      12      12           6
## grade3                12      12       6           6
## node1                  12       6      12           6
## grade3:node1           6       6       6           6
```

```
diag(t(X)%*%X)
```

```
## (Intercept)      grade3      node1 grade3:node1
##           24           12           12           6
```