

Exercise 11. Two-sample tests/Interval estimates

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Overview of confidence intervals and hypothesis tests and their constructions

Two columns of data - pairs/independent

- Paired data indicates data that are taken as two measurements of the same entities -> data columns are dependent.
 - For paired data, we calculate the difference between the columns(or another function according to the input) and use one-sample tests for this difference.
- If there is no dependency between values in the two columns the data are independent.
 - Two-sample test is needed

Examples of paired data:

- measuring bulbs at two different temperatures(if each piece is measured twice - at temperature 1 and temperature 2)
- be careful here, it can happen that the tests are eg. destructive and it is not possible to measure twice the same entity(product). Then we would consider two independent selections, each for one type of measurement -> independent data columns -> two-sample tests
- measurement of the patient's blood values before and after drug administration
- again pay attention to, for example, drug testing in two groups(placebo/real drug) ->two independent groups -> two-sample tests

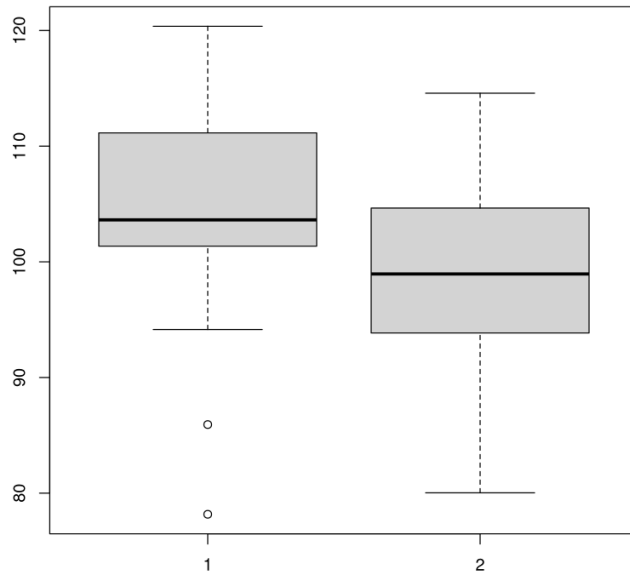
In general for two-sample tests/CI

- the test is always tied to the appropriate CI -> same conditions of use
- if the test has conditions of use(eg: normality of data, symmetry of data) then this condition must be met **for both data columns**, if at least one does not meet, we consider the assumption to be broken
- one of the very important assumptions is data independence
- eg: measurement of products of manufacturer A and products of manufacturer B - here it is reasonable to assume that the products of manufacturer A are separate entities from the products of manufacturer B

Two-sample tests/IO - difference of position measures

In [46]:

```
# we create test data
data1 = rnorm(n = 30, mean = 105, sd = 10)
data2 = rnorm(n = 30, mean = 100, sd = 10)
boxplot(data1,data2)
```



Two-sample Student's t-test

- Tests/estimates difference of means: $H_0 : \mu_1 - \mu_2 = a$
- requirements:
 - Data normality
 - Homoskedasticity(scatter matching)
 - independence of selections
- the function must have the parameter var.equal=TRUE

In [47]:

```
# H0: mu1 - mu2=2
# HA: mu1 - mu2!=2

t.test(x = data1, y = data2, mu = 2, alternative = "two.sided",
       var.equal = TRUE, conf.level = 0.95)
```

Two Sample t-test

```
data: data1 and data2
t = 1.2899, df = 58, p-value = 0.2022
alternative hypothesis: true difference in means is not equal to 2
95 percent confidence interval:
 0.462228 9.111616
sample estimates:
mean of x mean of y
104.26745 99.48053
```

In [48]:

```
# H0: mu1 - mu2=2
# HA: mu1 - mu2>2

t.test(x = data1, y = data2, mu = 2, alternative = "greater",
       var.equal = TRUE, conf.level = 0.95)
```

Two Sample t-test

```
data: data1 and data2
t = 1.2899, df = 58, p-value = 0.1011
alternative hypothesis: true difference in means is greater than 2
95 percent confidence interval:
 1.175546      Inf
sample estimates:
mean of x mean of y
104.26745 99.48053
```

In [49]:

```
# H0: mu1 - mu2=2
```

```
# HA:  $\mu_1 - \mu_2 < 2$ 
```

```
t.test(x = data1, y = data2, mu = 2, alternative = "less",  
       var.equal = TRUE, conf.level = 0.95)
```

Two Sample t-test

```
data: data1 and data2  
t = 1.2899, df = 58, p-value = 0.8989  
alternative hypothesis: true difference in means is less than 2  
95 percent confidence interval:  
-Inf 8.398298  
sample estimates:  
mean of x mean of y  
104.26745 99.48053
```

Aspin-Welsh test

- Tests/estimates the difference of means: $H_0 : \mu_1 - \mu_2 = a$
- requirements:
 - Data normality
 - independence of selections
- the function must have the parameter var.equal=FALSE

In [50]:

```
# H0:  $\mu_1 - \mu_2 = 2$   
# HA:  $\mu_1 - \mu_2 \neq 2$ 
```

```
t.test(x = data1, y = data2, mu = 2, alternative = "two.sided",  
       var.equal = FALSE, conf.level = 0.95)
```

Welch Two Sample t-test

```
data: data1 and data2  
t = 1.2899, df = 56.406, p-value = 0.2023  
alternative hypothesis: true difference in means is not equal to 2  
95 percent confidence interval:  
0.4596243 9.1142201  
sample estimates:  
mean of x mean of y  
104.26745 99.48053
```

In [51]:

```
# H0:  $\mu_1 - \mu_2 = 2$   
# HA:  $\mu_1 - \mu_2 > 2$ 
```

```
t.test(x = data1, y = data2, mu = 0, alternative = "greater",  
       var.equal = FALSE, conf.level = 0.95)
```

Welch Two Sample t-test

```
data: data1 and data2  
t = 2.2157, df = 56.406, p-value = 0.01538  
alternative hypothesis: true difference in means is greater than 0  
95 percent confidence interval:  
1.173889 Inf  
sample estimates:  
mean of x mean of y  
104.26745 99.48053
```

In [52]:

```
# H0:  $\mu_1 - \mu_2 = 2$   
# HA:  $\mu_1 - \mu_2 < 2$ 
```

```
t.test(x = data1, y = data2, mu = 0, alternative = "less",  
       var.equal = FALSE, conf.level = 0.95)
```

Welch Two Sample t-test

```
data: data1 and data2  
t = 2.2157, df = 56.406, p-value = 0.9846  
alternative hypothesis: true difference in means is less than 0  
95 percent confidence interval:
```

```
-Inf 8.399956
sample estimates:
mean of x mean of y
104.26745  99.48053
```

Mann-Whitney test

- Tests/estimates difference of medians: $H_0 : X_{0.5,1} - X_{0.5,2} = a$
- requirements:
 - independence of selections
 - (same shape of the distribution)
- requires conf.int=TRUE, to calculate CI

In [53]:

```
# H0: X0.5,1 - X0.5,2=2
# HA: X0.5,1 - X0.5,2!=2

wilcox.test(x = data1, y = data2, mu = 2, alternative = "two.sided",
            conf.level=0.95, conf.int = TRUE)
```

Wilcoxon rank sum exact test

```
data: data1 and data2
W = 560, p-value = 0.1058
alternative hypothesis: true location shift is not equal to 2
95 percent confidence interval:
 1.356415 9.562378
sample estimates:
difference in location
      5.785621
```

In [54]:

```
# H0: X0.5,1 - X0.5,2=2
# HA: X0.5,1 - X0.5,2>2

wilcox.test(x = data1, y = data2, mu = 2, alternative = "greater",
            conf.level=0.95, conf.int = TRUE)
```

Wilcoxon rank sum exact test

```
data: data1 and data2
W = 560, p-value = 0.05291
alternative hypothesis: true location shift is greater than 2
95 percent confidence interval:
 1.983391      Inf
sample estimates:
difference in location
      5.785621
```

In [55]:

```
# H0: X0.5,1 - X0.5,2=2
# HA: X0.5,1 - X0.5,2<2

wilcox.test(x = data1, y = data2, mu = 2, alternative = "less",
            conf.level=0.95, conf.int = TRUE)
```

Wilcoxon rank sum exact test

```
data: data1 and data2
W = 560, p-value = 0.9487
alternative hypothesis: true location shift is less than 2
95 percent confidence interval:
 -Inf 8.880073
sample estimates:
difference in location
      5.785621
```

Two-sample tests/CI - proportion of variances

F-test

- Tests/estimates the ratio of variances: $H_0 : \sigma_1^2 / \sigma_2^2 = a$
- requirements:
 - data normality
 - independence of selections

In [56]:

```
# H0: sigma1 ^ 2/sigma2 ^ 2=1
# H0: sigma1 ^ 2/sigma2 ^ 2!=1

var.test(x = data1, y = data2, ratio = 1, alternative = "two.sided",
         conf.level = 0.95)
```

F test to compare two variances

```
data: data1 and data2
F = 1.4042, num df = 29, denom df = 29, p-value = 0.366
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.6683322 2.9501409
sample estimates:
ratio of variances
 1.404163
```

In [57]:

```
# H0: sigma1 ^ 2/sigma2 ^ 2=1
# H0: sigma1 ^ 2/sigma2 ^ 2>1

var.test(x = data1, y = data2, ratio = 1, alternative = "greater",
         conf.level = 0.95)
```

F test to compare two variances

```
data: data1 and data2
F = 1.4042, num df = 29, denom df = 29, p-value = 0.183
alternative hypothesis: true ratio of variances is greater than 1
95 percent confidence interval:
 0.7545972      Inf
sample estimates:
ratio of variances
 1.404163
```

In [58]:

```
# H0: sigma1 ^ 2/sigma2 ^ 2=1
# H0: sigma1 ^ 2/sigma2 ^ 2<1

var.test(x = data1, y = data2, ratio = 1, alternative = "less",
         conf.level = 0.95)
```

F test to compare two variances

```
data: data1 and data2
F = 1.4042, num df = 29, denom df = 29, p-value = 0.817
alternative hypothesis: true ratio of variances is less than 1
95 percent confidence interval:
 0.0000000 2.612883
sample estimates:
ratio of variances
 1.404163
```

Levene's test

- Tests equality of variances: $H_0 : \sigma_1^2 = \sigma_2^2$!
- requirements:
 - independence of selections
- requires data in standard data format
- leveneTest function in the car package

In [59]:

```
# we produce data in a standard data format

data1.df = as.data.frame(data1)
data1.df$typ = "d1"
```

```
colnames(data1.df) = c("data", "typ")

data2.df = as.data.frame(data2)
data2.df$typ = "d2"
colnames(data2.df) = c("data", "typ")

data = rbind(data1.df, data2.df)
data$typ = as.factor(data$typ)

head(data)
```

A data.frame: 6 × 2

	data	typ
	<dbl>	<fct>
1	118.68545	d1
2	111.25032	d1
3	103.14060	d1
4	112.95088	d1
5	78.17256	d1
6	103.84503	d1

In [60]:

```
# install.packages("car")

# H0: sigma1 ^ 2=sigma2 ^ 2
# HA: sigma1 ^ 2!=Sigma2 ^ 2

car::leveneTest(data$data ~ data$typ)
```

A anova: 2 × 3

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	0.2097549	0.6486708
	58	NA	NA

Two-sample tests/CI - difference of probabilities

Test of parameter of two binomial distributions

- Tests if the probability matches: $H_0 : \pi_1 - \pi_2 = 0$
- requirements:
 - sufficient selection size: $n_i > \frac{9}{p_i(1-p_i)}$
 - independence of selections

In [61]:

```
# we will produce suitable data
pi1 = 0.4
pi2 = 0.3

dp1 = runif(n = 100, min = 0, max = 1) < pi1
dp2 = runif(n = 130, min = 0, max = 1) < pi2

x1 = sum(dp1)
n1 = length(dp1)

x2 = sum(dp2)
n2 = length(dp2)

x1
n1
x2
n2
```

41

100

47

```
In [62]: # H0: pi1 - pi2=0
# HA: pi1 - pi2!=0

prop.test(x = c(x1, x2), n = c(n1, n2), alternative="two.sided",
          conf.level=0.95)
```

2-sample test for equality of proportions with continuity correction

```
data: c(x1, x2) out of c(n1, n2)
X-squared = 0.37552, df = 1, p-value = 0.54
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.08732316  0.18424624
sample estimates:
 prop 1      prop 2 
0.4100000 0.3615385
```

```
In [63]: # H0: pi1 - pi2=0
# HA: pi1 - pi2>0

prop.test(x = c(x1, x2), n = c(n1, n2), alternative="greater",
          conf.level=0.95)
```

2-sample test for equality of proportions with continuity correction

```
data: c(x1, x2) out of c(n1, n2)
X-squared = 0.37552, df = 1, p-value = 0.27
alternative hypothesis: greater
95 percent confidence interval:
 -0.0669148  1.0000000
sample estimates:
 prop 1      prop 2 
0.4100000 0.3615385
```

```
In [64]: # H0: pi1 - pi2=0
# HA: pi1 - pi2<0

prop.test(x = c(x1, x2), n = c(n1, n2), alternative="less",
          conf.level=0.95)
```

2-sample test for equality of proportions with continuity correction

```
data: c(x1, x2) out of c(n1, n2)
X-squared = 0.37552, df = 1, p-value = 0.73
alternative hypothesis: less
95 percent confidence interval:
 -1.0000000  0.1638379
sample estimates:
 prop 1      prop 2 
0.4100000 0.3615385
```

Examples

```
In [65]: library(dplyr)
library(rstatix)
```

Example 1.

Data in the cholesterol2.xls file indicate the blood cholesterol level of men of two different age groups(20-30 years and 40-50 years). Verify at the significance level 0.05 the hypothesis that the cholesterol level in the blood of older men does not differ from the cholesterol level in the blood of younger men.

```
In [66]: # Load data
chol = readxl::read_excel("data/testy_dvouvyberove.xlsx",
                          sheet = "cholesterol2",
```

```

      skip = 1)
colnames(chol)=c("young", "old")
head(chol)

```

A tibble: 6 × 2

young	old
<dbl>	<dbl>
4.573	4.593
4.565	4.589
4.624	4.864
4.720	4.603
4.604	5.090
4.662	5.472

In [67]:

```

# Convert to standard data format
chol.s = stack(chol)
chol.s = na.omit(chol.s)
colnames(chol.s) = c("values", "group")
head(chol.s)

```

A data.frame: 6 × 2

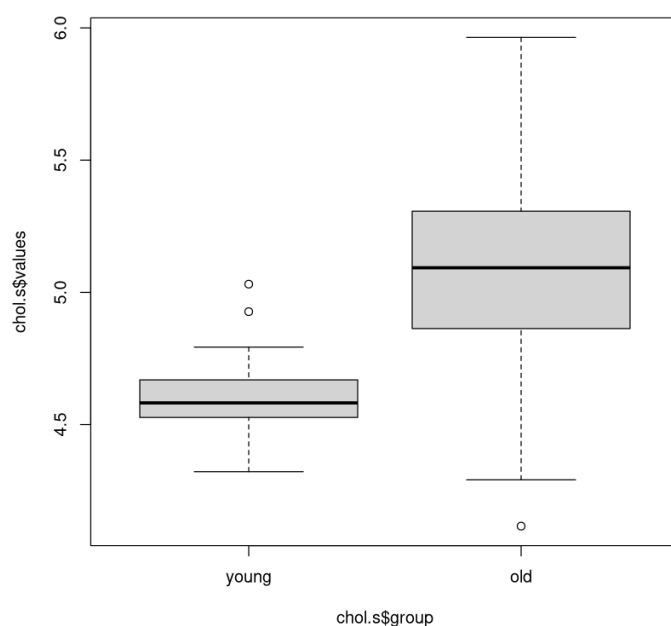
	values	group
	<dbl>	<fct>
1	4.573	young
2	4.565	young
3	4.624	young
4	4.720	young
5	4.604	young
6	4.662	young

In [68]:

```

# Exploratory analysis
boxplot(chol.s$values ~ chol.s$group)

```



In [69]:

```

# Elimination of outliers:
chol.s$id = seq(1,length(chol.s$values))

outliers = chol.s %>% group_by(group) %>% identify_outliers(values)
outliers

```

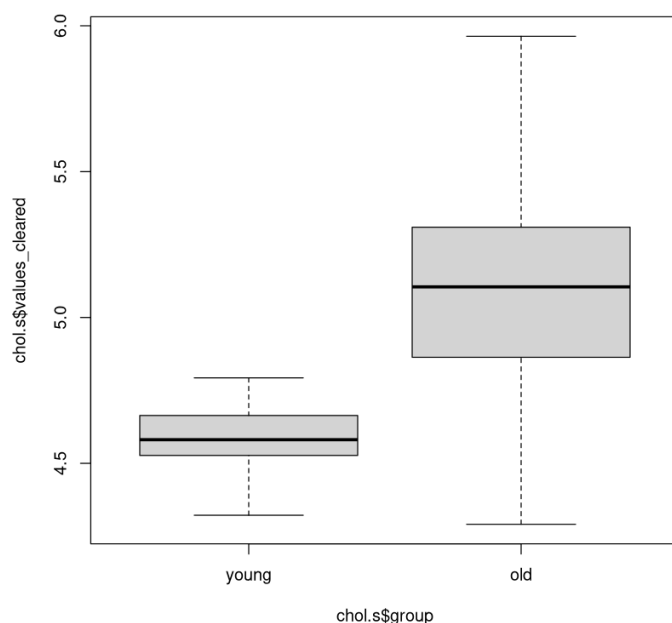

A tibble: 3 × 5

group	values	id	is.outlier	is.extreme
<fct>	<dbl>	<int>	<lgl>	<lgl>
young	5.031	44	TRUE	FALSE
young	4.927	73	TRUE	FALSE
old	4.116	151	TRUE	FALSE

```
In [70]: chol.s$values_cleared = ifelse(chol.s$id %in% outliers$id, NA, chol.s$values)
```

```
In [71]: boxplot(chol.s$values_cleared~chol.s$group)

# be careful in the data we have NA
# eg for length determination
```



```
In [72]: chol.s %>% group_by(group) %>%
  summarise(count = sum(!is.na(values_cleared)),
            mean = mean(values_cleared, na.rm = TRUE),
            std = sd(values_cleared, na.rm = TRUE))

# rounding ->3 valid digits ->according to sd to thousands
```

A tibble: 2 × 4

group	count	mean	std
<fct>	<int>	<dbl>	<dbl>
young	97	4.588918	0.1014021
old	84	5.113012	0.3541456

Difference of Mean/median test

```
In [73]: # Verification of normality
chol.s %>% group_by(group) %>%
  summarise(norm.pval = shapiro.test(values_cleared)$p.value)

# normality at significance 0.05 OK
```

A tibble: 2 × 2

group	norm.pval
<fct>	<dbl>
young	0.4639368

group norm.pval

<fct> <dbl>

old 0.9394985

In [74]:

```
# Exactly by F-test

# H0: sigma.old=sigma.young
# Ha: sigma.old<>sigma.young

# I select the required data
young = chol.s$values_cleared[chol.s$group == "young"]
old = chol.s$values_cleared[chol.s$group == "old"]

var.test(x = young, y = old, ratio = 1, conf.level=0.95)

# at. significance 0.05 we reject the assumption of same variances
# The observed discrepancy between the variances is significant at the significance level of 0.05
# Mark as statistically significant.
```

F test to compare two variances

data: young and old
F = 0.081984, num df = 96, denom df = 83, p-value < 2.2e-16
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
0.05379533 0.12414422
sample estimates:
ratio of variances
0.08198425

In [75]:

```
# Verification of same mean values(Aspin-Welch test)

# H0: mu.old - mu.young=0
# Ha: mu.old - mu.young!=0

t.test(x = old, y = young, mu = 0,
       alternative = "two.sided", var.equal=FALSE, conf.level=0.95)

# in hl. significance 0.05 we reject H0->there is a stat. significant difference.
```

Welch Two Sample t-test

data: old and young
t = 13.106, df = 94.791, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
0.4447047 0.6034840
sample estimates:
mean of x mean of y
5.113012 4.588918

In [76]:

```
# H0: mu.old=mu.young
# Ha: mu.old>mu.young

t.test(x = old, y = young, mu = 0, alternative = "greater",
       var.equal = FALSE, conf.level = 0.95)
```

Welch Two Sample t-test

data: old and young
t = 13.106, df = 94.791, p-value < 2.2e-16
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
0.4576698 Inf
sample estimates:
mean of x mean of y
5.113012 4.588918

Example 2.

The data in the depression.xls file represent the length of remission in days from a simple random selection of two different groups of patients(patients with endogenous depression and patients with neurotic depression). Verify that the observed difference in mean remission length in these two groups of patients is statistically significant.

In [77]:

```
# Read data from xlsx file(using readxl package)
deprese = readxl::read_excel("data/testy_dvouvyberove.xlsx",
                             sheet = "deprese")
colnames(deprese)=c("endo", "neuro")

head(deprese)
```

A tibble: 6 × 2

endo	neuro
<dbl>	<dbl>
247	472
384	454
285	479
141	588
381	309
336	315

In [78]:

```
# Conversion to standard data format
deprese.s = stack(deprese)
deprese.s = na.omit(deprese.s)
colnames(deprese.s) = c("values", "group")

head(deprese.s)
```

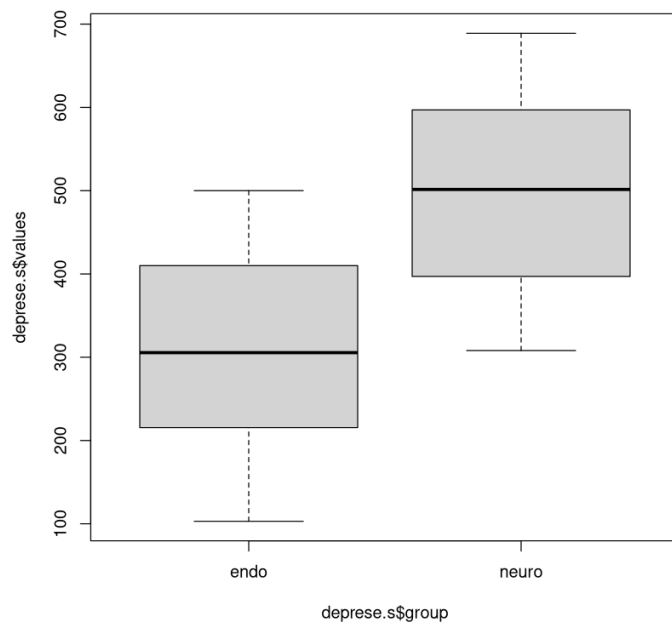
A data.frame: 6 × 2

	values	group
	<dbl>	<fct>
1	247	endo
2	384	endo
3	285	endo
4	141	endo
5	381	endo
6	336	endo

In [79]:

```
# Exploratory analysis
boxplot(deprese.s$values~deprese.s$group)

# Data does not contain outliers
```



```
In [80]: library(dplyr)

deprese.s %>% group_by(group) %>%
  summarise(count = length(values),
            mean = mean(values),
            std = sd(values))

# rounding ->3 valid digits ->according to sd
```

A tibble: 2 × 4

group	count	mean	std
<fct>	<int>	<dbl>	<dbl>
endo	140	306.9429	115.2301
neuro	134	498.6866	111.5799

Diference of Mean/median test

```
In [81]: # Normality verification
# We assume the assumption of normality by the Shapir - Wilk test.
deprese.s %>% group_by(group) %>%
  summarise(norm.pval = shapiro.test(values)$p.value)

# at significance 0.05, we reject the assumption of normality
```

A tibble: 2 × 2

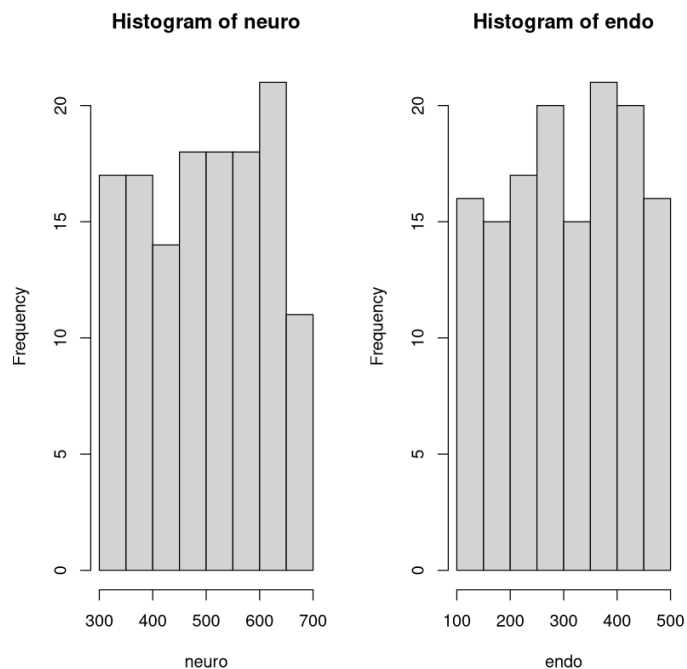
group	norm.pval
<fct>	<dbl>
endo	2.786054e-04
neuro	9.480001e-05

```
In [82]: # at least as a guide, we check the similarity of the distribution

# we choose data for easier processing

neuro = deprese.s$values[deprese.s$group == "neuro"]
endo = deprese.s$values[deprese.s$group == "endo"]

par(mfrow = c(1,2))
hist(neuro)
hist(endo)
```



```
In [83]: # Difference of median (Mann-Whitney test)

# According to the histograms, we assume that the data have the same type of distribution.

# H0: med.neuro=med.endo (med.neuro - med.endo=0)
# Ha: med.neuro!=med.endo (med.neuro - med.endo!=0)

wilcox.test(x = neuro, y = endo, mu = 0, alternative = "two.sided",
            conf.level=0.95, conf.int = TRUE)

# at significance 0.05 we reject H0->there is a stat. significant difference
```

Wilcoxon rank sum test with continuity correction

```
data: neuro and endo
W = 16366, p-value < 2.2e-16
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 163 220
sample estimates:
difference in location
 191.0001
```

```
In [84]: # H0: med.neuro=med.endo (med.neuro - med.endo=0)
# Ha: med.neuro>med.endo (med.neuro - med.endo>0)

wilcox.test(x = neuro, y = endo, mu = 0, alternative = "greater",
            conf.level=0.95, conf.int = TRUE)
```

Wilcoxon rank sum test with continuity correction

```
data: neuro and endo
W = 16366, p-value < 2.2e-16
alternative hypothesis: true location shift is greater than 0
95 percent confidence interval:
 168 Inf
sample estimates:
difference in location
 191.0001
```

Example 3.

We monitor urine osmolality at the patient station at 08:00 and 11:00 for 16 men. Based on the results in the osmolality.xls file, verify that the osmolality has increased statistically significantly.

```
In [85]:
```

```
# Load data
osmolalita = readxl::read_excel("data/testy_dvouvyberove.xlsx",
                                sheet = "osmolalita", skip = 1)
osmolalita = osmolalita[,c(2,3)]
colnames(osmolalita)=c("o8", "o11")
head(osmolalita)
```

New names:

```
* `` -> ...1
```

A tibble: 6 × 2

	o8	o11
<dbl>	<dbl>	
364	421	
349	369	
349	284	
387	366	
295	376	
357	376	

In [86]:

```
# Calculation of osmolality increase
osmolalita$increase = osmolalita$o11 - osmolalita$o8

# Exploratory analysis
par(mfrow = c(1,1))
boxplot(osmolalita$increase)

# Data contains outliers
```



In [87]:

```
# Elimination of outliers:
osmolalita$id = seq(1,length(osmolalita$increase))

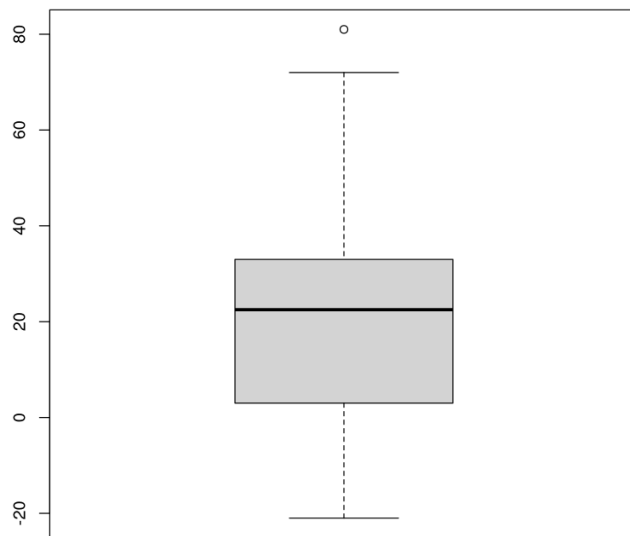
outliers = osmolalita %>% identify_outliers(increase)
outliers
osmolalita$increase_cleared = ifelse(osmolalita$id %in% outliers$id, NA, osmolalita$increase)

boxplot(osmolalita$increase_cleared)
```

A tibble: 2 × 6

	o8	o11	increase	id	is.outlier	is.extreme
<dbl>	<dbl>	<dbl>	<int>	<dbl>	<lg1>	<lg1>
349	284	-65	3	TRUE	FALSE	

o8	o11	increase	id	is.outlier	is.extreme
<dbl>	<dbl>	<dbl>	<int>	<lgl>	<lgl>
352	502	150	10	TRUE	TRUE



```
In [88]: # Exploratory analysis for data without outliers
library(dplyr)

osmolalita %>% summarise(count = sum(!is.na(increase_cleared)),
                        mean = mean(increase_cleared, na.rm = TRUE),
                        std = sd(increase_cleared, na.rm = TRUE))

# rounding ->2 valid digits ->according to sd per unit
```

A tibble: 1 × 3

count	mean	std
<int>	<dbl>	<dbl>
14	24.28571	29.77978

```
In [89]: # Verification of normality
# The presumption of normality is verified by the Shapir - Wilk test.
shapiro.test(osmolalita$increase_cleared)
```

Shapiro-Wilk normality test

data: osmolalita\$increase_cleared
W = 0.94899, p-value = 0.5452

```
In [90]: # Paired t-test
# H0: mu.increase=0 mm
# Ha: mu.increase>0 mm

t.test(osmolalita$increase_cleared, mu = 0, alternative = "greater")
```

One Sample t-test

data: osmolalita\$increase_cleared
t = 3.0514, df = 13, p-value = 0.004638
alternative hypothesis: true mean is greater than 0
95 percent confidence interval:
10.19089 Inf
sample estimates:
mean of x
24.28571

Example 4.

Semiconductor components of two manufacturers - MM and PP - were tested. MM claims that its products have a lower percentage of defective pieces. To verify this claim, 200 components were randomly selected from MM production, of which 14 were defective. A similar experiment was performed at PP with the result of 10 defective out of 100 randomly selected components.

a)

Test MM's claim with a clean significance test.

```
In [91]: x.MM = 14
n.MM = 200
p.MM = x.MM/n.MM
p.MM

x.PP = 10
n.PP = 100
p.PP = x.PP/n.PP
p.PP
```

0.07

0.1

```
In [92]: # Verification of assumptions
9/(p.MM*(1-p.MM))
9/(p.PP*(1-p.PP))
```

138.248847926267

100

```
In [93]: # Pearson's X2 test
# H0: pi.PP=pi.MM
# Ha: pi.PP>pi.MM

prop.test(x = c(x.PP,x.MM),n = c(n.PP,n.MM), alternative = "greater",
          conf.level = 0.95)

# at significance 0.05 we do not reject H0 - ie assumption.
# identical error rates. Therefore, it cannot be said that MM has better production.
```

2-sample test for equality of proportions with continuity correction

```
data: c(x.PP, x.MM) out of c(n.PP, n.MM)
X-squared = 0.45856, df = 1, p-value = 0.2491
alternative hypothesis: greater
95 percent confidence interval:
 -0.03508162  1.00000000
sample estimates:
prop 1 prop 2
 0.10  0.07
```

```
In [94]: # Pearson's X2 test
# H0: pi.PP=pi.MM
# Ha: pi.PP!=pi.MM

prop.test(x = c(x.PP,x.MM),n = c(n.PP,n.MM), alternative = "two.sided",
          conf.level = 0.95)
```

2-sample test for equality of proportions with continuity correction

```
data: c(x.PP, x.MM) out of c(n.PP, n.MM)
X-squared = 0.45856, df = 1, p-value = 0.4983
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.04611274  0.10611274
sample estimates:
```



```
prop 1 prop 2
0.10    0.07
```

b)

Test MM's statement using an interval estimate of a significance level of 0.05.

In [95]:

```
# Based on 95% Clopper - Pearson right - hand interval estimation
# -0.036; 1,000) the observed difference in production quality can be described as
# not statistically significant. We can reach the same conclusions on the basis of
# Pearson's right-hand test
prop.test(x = c(x.PP,x.MM),n = c(n.PP,n.MM), alternative = "two.sided",
          conf.level = 0.95)
```

2-sample test for equality of proportions with continuity correction

```
data:  c(x.PP, x.MM) out of c(n.PP, n.MM)
X-squared = 0.45856, df = 1, p-value = 0.4983
alternative hypothesis: two.sided
95 percent confidence interval:
-0.04611274  0.10611274
sample estimates:
prop 1 prop 2
0.10    0.07
```

In []: