notebook

January 11, 2023

Note that this notebook was automatically generated from an RDocumentation page. It depends on the package and the example code whether this code will run without errors. You may need to edit the code to make things work.

pràctica 2

[3]:
```
##Llegim el dataset
data <- read.csv("heart.csv")


##Imprimim les primeres linies del data
head(data)

##Obtenim informació de rows i columns.

nombre_rows <- nrow(data)
nombre_columnes <- ncol(data)
cat("El nombre de files és de", nombre_rows, "i el nombre de columnes és de",␣
 ↪nombre_columnes)

##resum de les dades
summary(data)


##Llegim la tipologia de data de les variables

variables <- sapply(data,class)
kable(data.frame(variables=names(variables),clase=as.vector(variables)))
```

A data.frame: 6 × 14

	age <int>	sex <int>	cp <int>	trtbps <int>	chol <int>	fbs <int>	restecg <int>	thalachh <int>	exng <int>	oldpe <dbl
1	63	1	3	145	233	1	0	150	0	2.3
2	37	1	2	130	250	0	1	187	0	3.5
3	41	0	1	130	204	0	0	172	0	1.4
4	56	1	1	120	236	0	1	178	0	0.8
5	57	0	0	120	354	0	1	163	1	0.6
6	57	1	0	140	192	0	1	148	0	0.4

```
El nombre de files és de 303 i el nombre de columnes és de 14
```

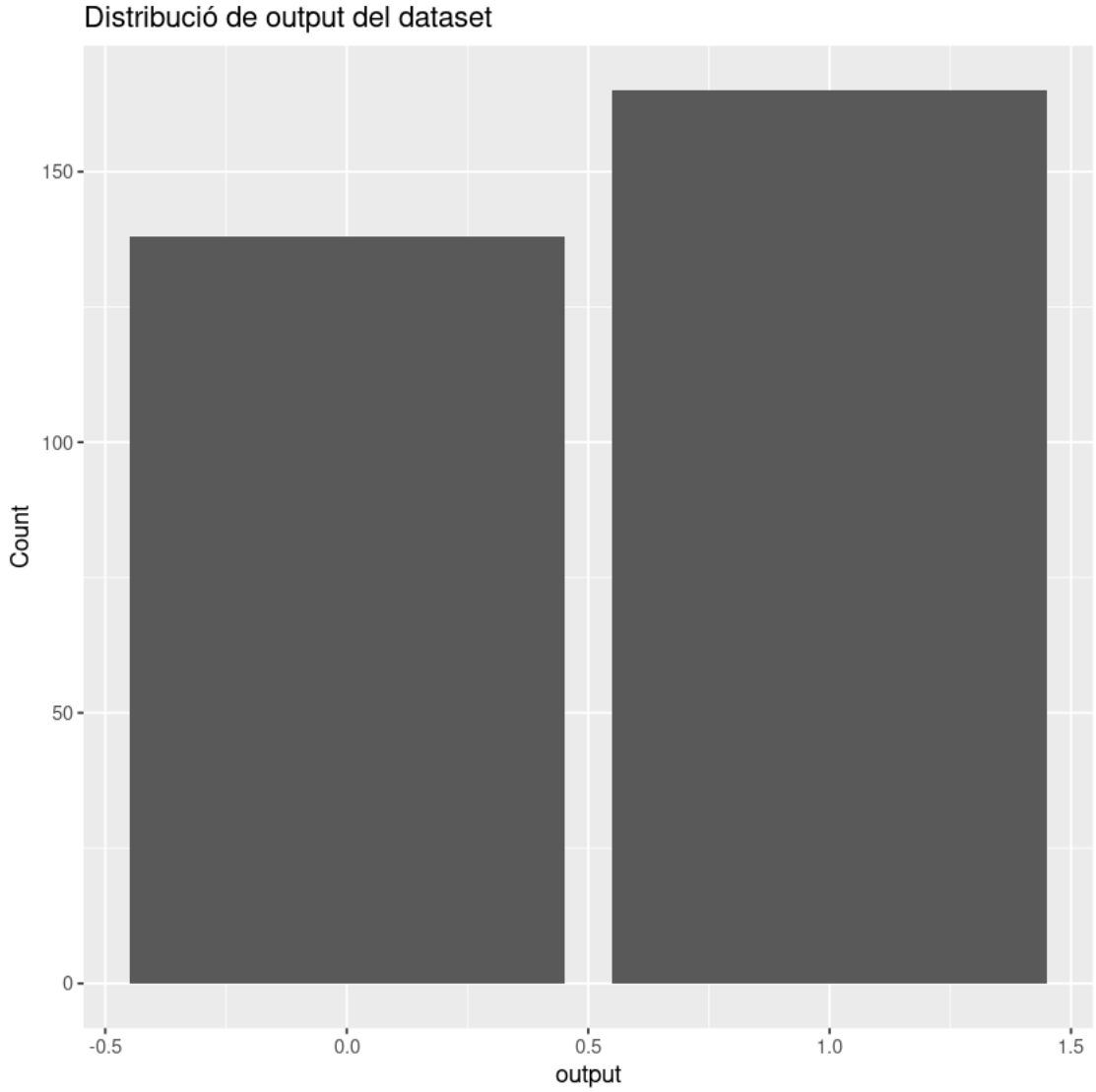
```
      age              sex               cp             trtbps      
 Min.   :29.00   Min.   :0.0000   Min.   :0.000   Min.   : 94.0  
 1st Qu.:47.50   1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:120.0  
 Median :55.00   Median :1.0000   Median :1.000   Median :130.0  
 Mean   :54.37   Mean   :0.6832   Mean   :0.967   Mean   :131.6  
 3rd Qu.:61.00   3rd Qu.:1.0000   3rd Qu.:2.000   3rd Qu.:140.0  
 Max.   :77.00   Max.   :1.0000   Max.   :3.000   Max.   :200.0  
      chol             fbs             restecg          thalachh     
 Min.   :126.0   Min.   :0.0000   Min.   :0.0000   Min.   : 71.0  
 1st Qu.:211.0   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:133.5  
 Median :240.0   Median :0.0000   Median :1.0000   Median :153.0  
 Mean   :246.3   Mean   :0.1485   Mean   :0.5281   Mean   :149.6  
 3rd Qu.:274.5   3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:166.0  
 Max.   :564.0   Max.   :1.0000   Max.   :2.0000   Max.   :202.0  
      exng           oldpeak          slp              caa        
 Min.   :0.0000   Min.   :0.00   Min.   :0.000   Min.   :0.0000  
 1st Qu.:0.0000   1st Qu.:0.00   1st Qu.:1.000   1st Qu.:0.0000  
 Median :0.0000   Median :0.80   Median :1.000   Median :0.0000  
 Mean   :0.3267   Mean   :1.04   Mean   :1.399   Mean   :0.7294  
 3rd Qu.:1.0000   3rd Qu.:1.60   3rd Qu.:2.000   3rd Qu.:1.0000  
 Max.   :1.0000   Max.   :6.20   Max.   :2.000   Max.   :4.0000  
     thall            output      
 Min.   :0.000   Min.   :0.0000  
 1st Qu.:2.000   1st Qu.:0.0000  
 Median :2.000   Median :1.0000  
 Mean   :2.314   Mean   :0.5446  
 3rd Qu.:3.000   3rd Qu.:1.0000  
 Max.   :3.000   Max.   :1.0000  
```

variables	clase
age	integer
sex	integer
cp	integer
trtbps	integer
chol	integer
fbs	integer
restecg	integer
thalachh	integer
exng	integer
oldpeak	numeric
slp	integer
caa	integer
thall	integer
output	integer

Visualització de les variables

Observem la distribució de la columna output

[4]:
```
output_plot <-ggplot(data,aes(output)) + geom_bar() + labs(x="output",␣
↪y="Count") + guides(fill=guide_legend(title="")) + ggtitle("Distribució de␣
↪output del dataset")
output_plot
```

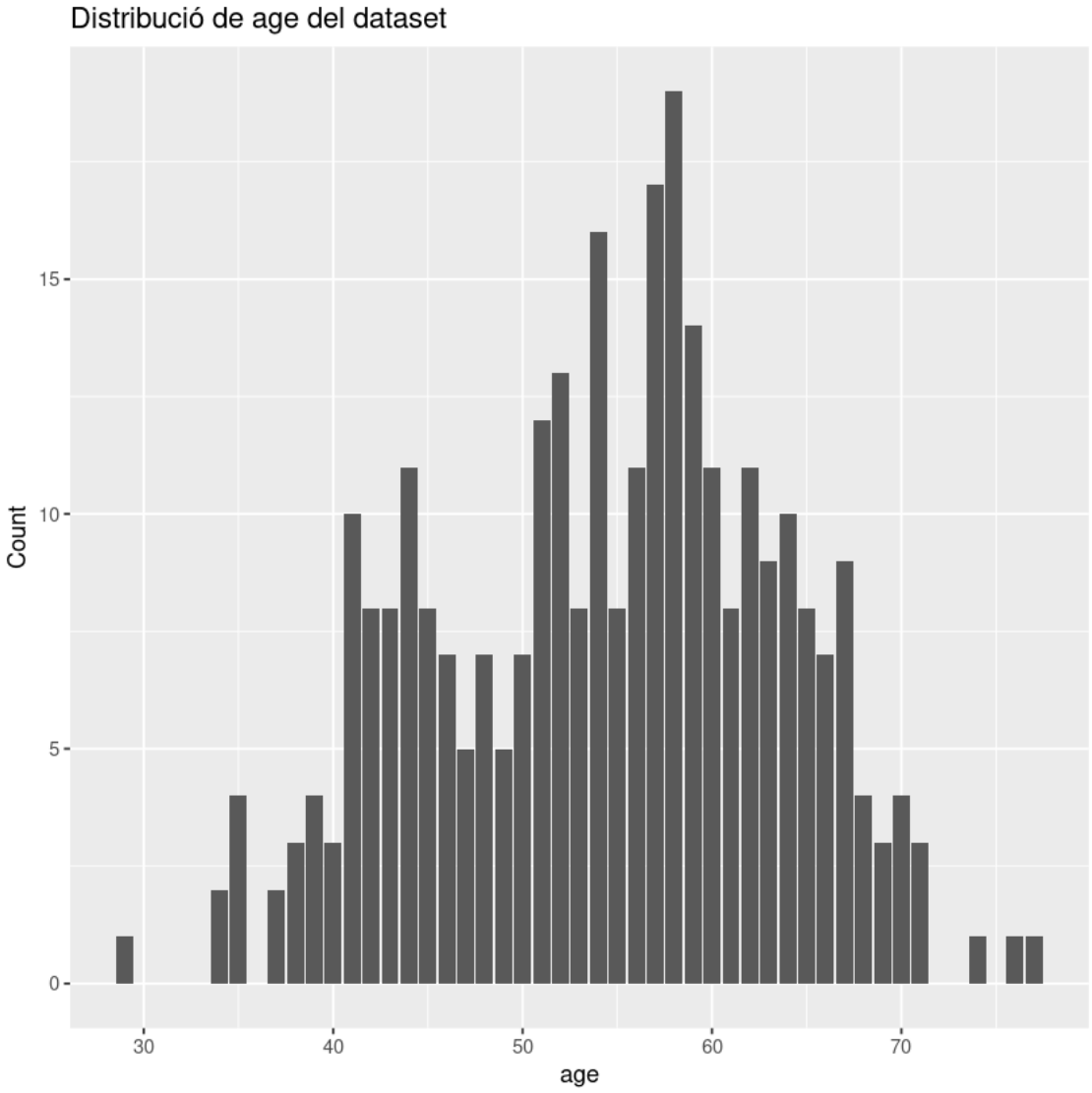


[5]:
```
output0 <- sum(data$output == 0)
output1 <- sum(data$output == 1)
percentatge_output0 = (output0/nombre_rows)*100
percentatge_output1 = (output1/nombre_rows)*100
```

```
cat("El percentatge de pacients amb output positiu és de", percentatge_output1,␣
 ↪"mentre que el percentatge de pacients amb output negatius és de",␣
 ↪percentatge_output0)
```

```
El percentatge de pacients amb output positiu és de 54.45545 mentre que el
percentatge de pacients amb output negatius és de 45.54455
```

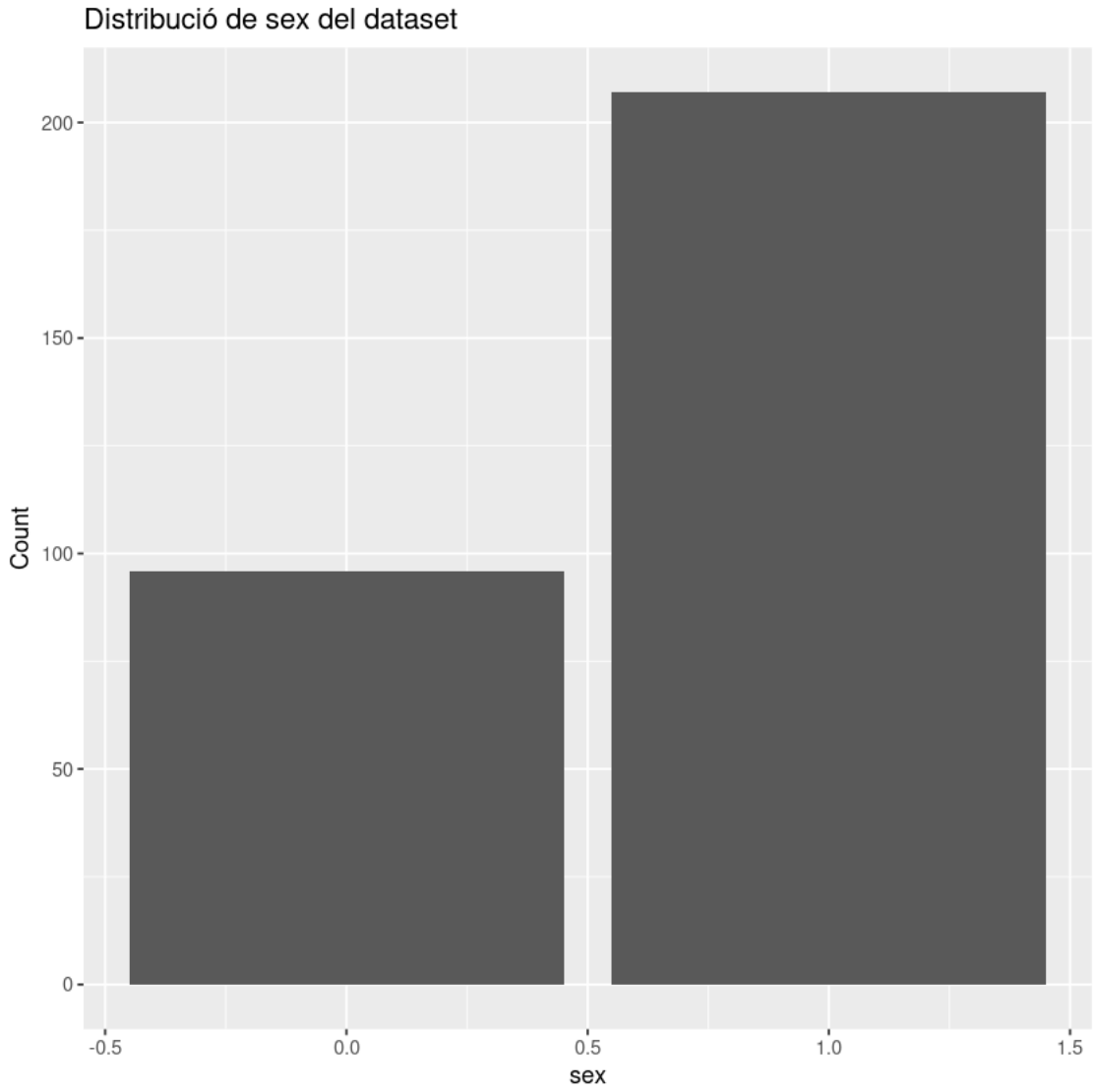
[6]:
```
age_plot <-ggplot(data,aes(age)) + geom_bar() + labs(x="age", y="Count") +␣
 ↪guides(fill=guide_legend(title="")) + ggtitle("Distribució de age del␣
 ↪dataset")
age_plot
```



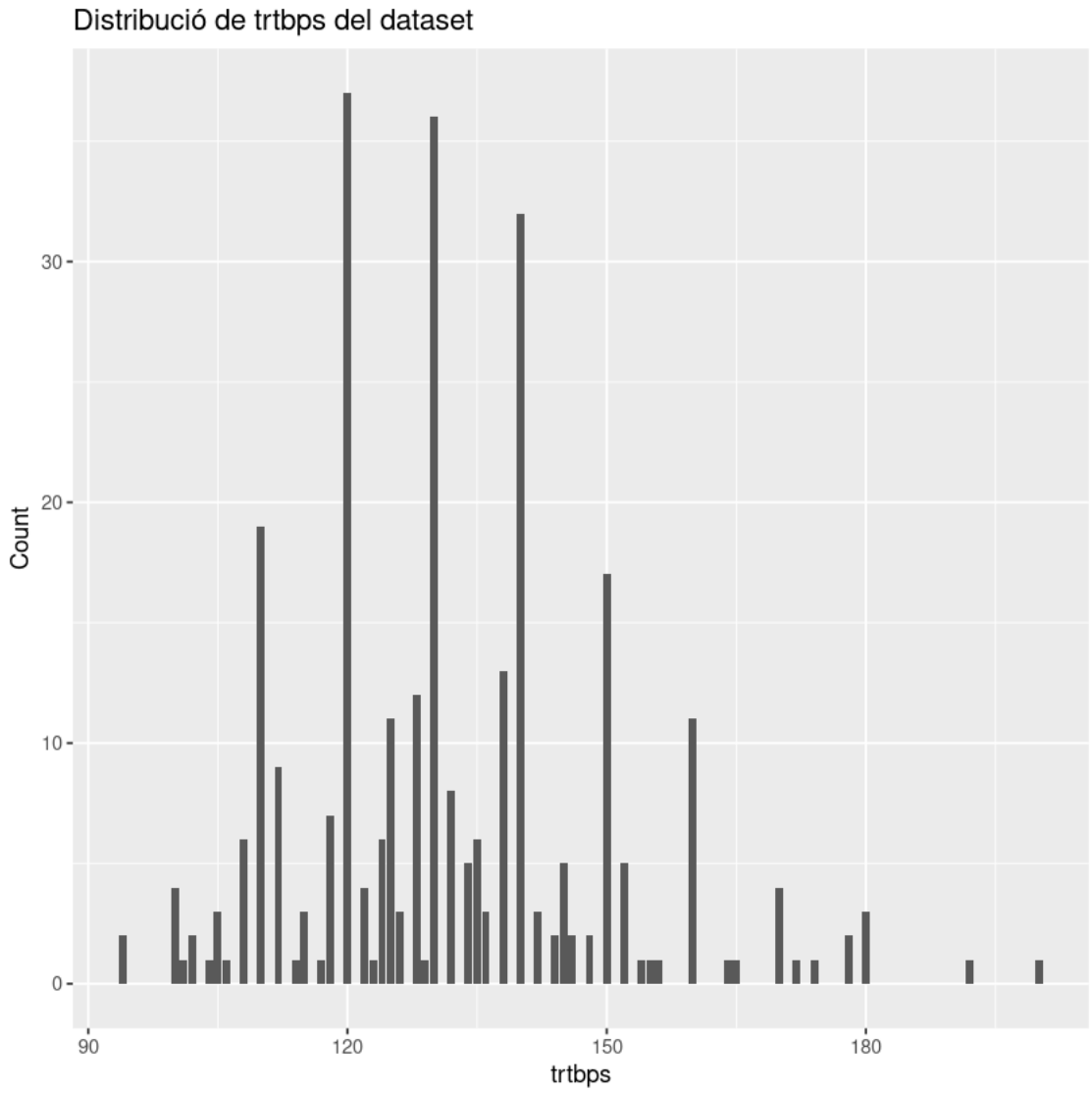
variable sexe

[7]:
```
sex_plot <-ggplot(data,aes(sex)) + geom_bar() + labs(x="sex", y="Count") +␣
 ↪guides(fill=guide_legend(title="")) + ggtitle("Distribució de sex del␣
 ↪dataset")
sex_plot

sex0 <- sum(data$sex == 0)
sex1 <- sum(data$sex == 1)
percentatge_sex0 = (sex0/nombre_rows)*100
percentatge_sex1 = (sex1/nombre_rows)*100
cat("El percentatge de pacients dones és de", percentatge_sex1, "mentre que el␣
 ↪percentatge de pacients amb output homes és de", percentatge_sex0)
```

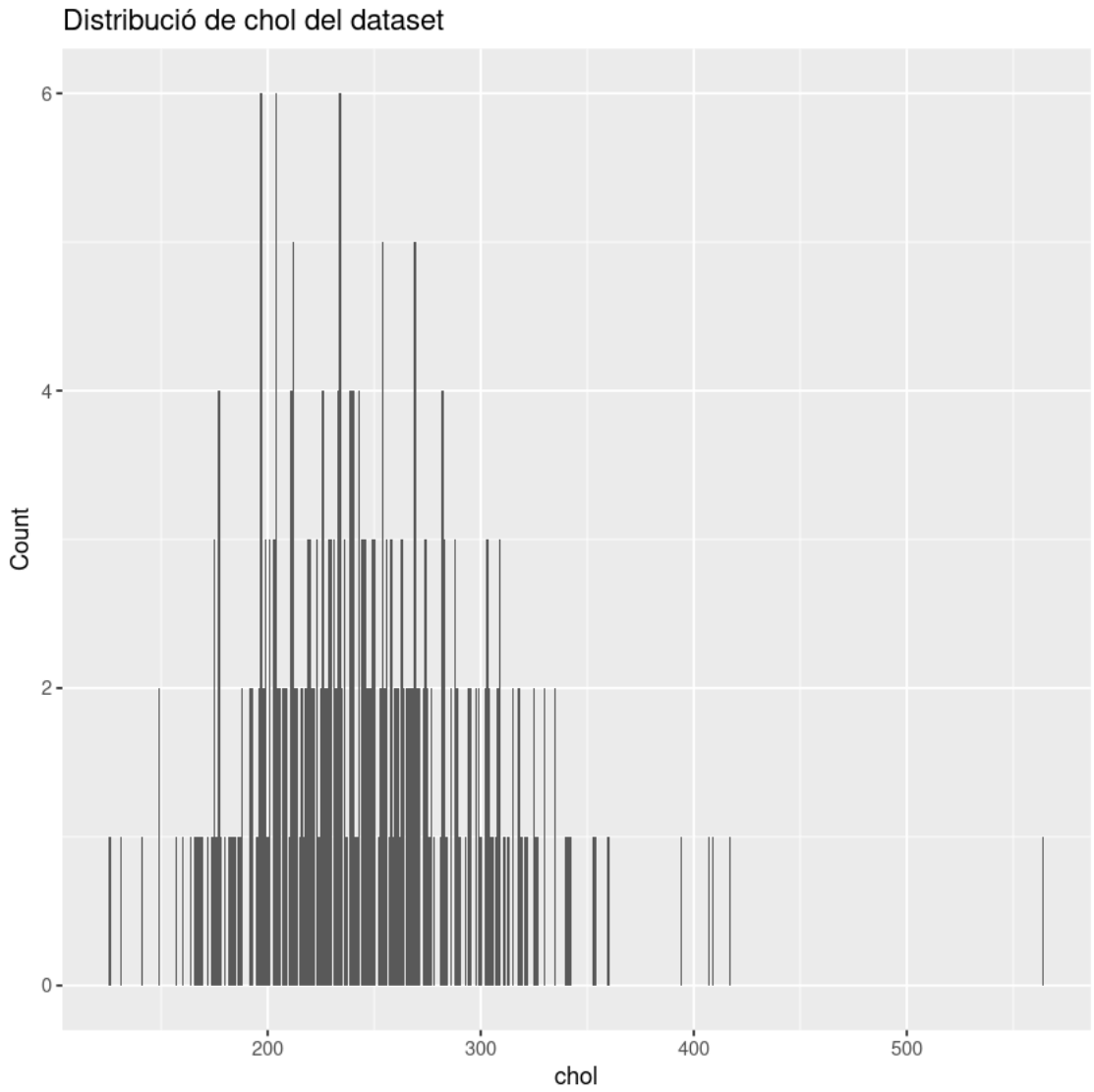
```
El percentatge de pacients dones és de 68.31683 mentre que el percentatge de
pacients amb output homes és de 31.68317
```



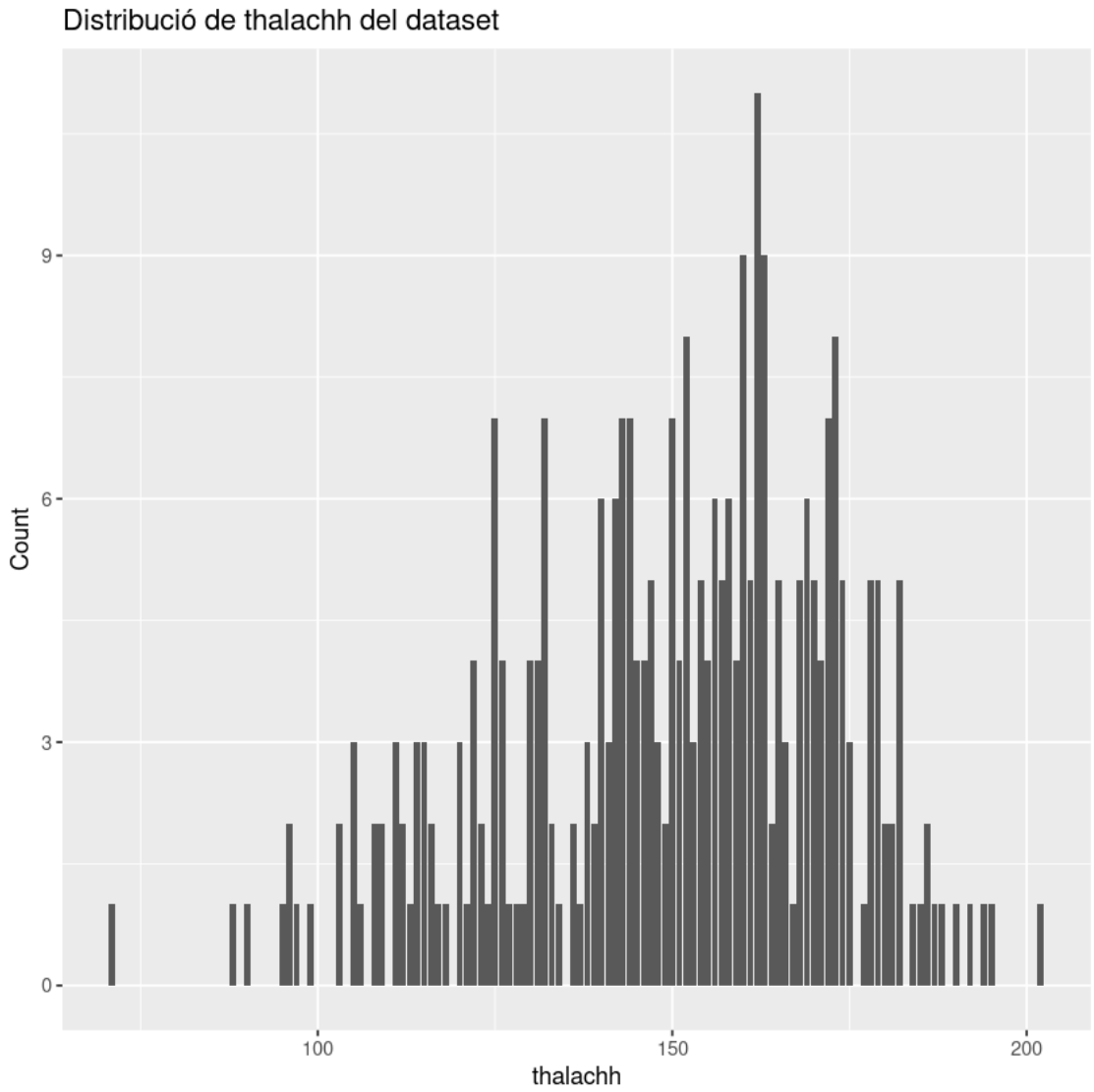
[8]:
```
trtbps_plot <-ggplot(data,aes(trtbps)) + geom_bar() + labs(x="trtbps",␣
↪y="Count") + guides(fill=guide_legend(title="")) + ggtitle("Distribució de␣
↪trtbps del dataset")
trtbps_plot
```



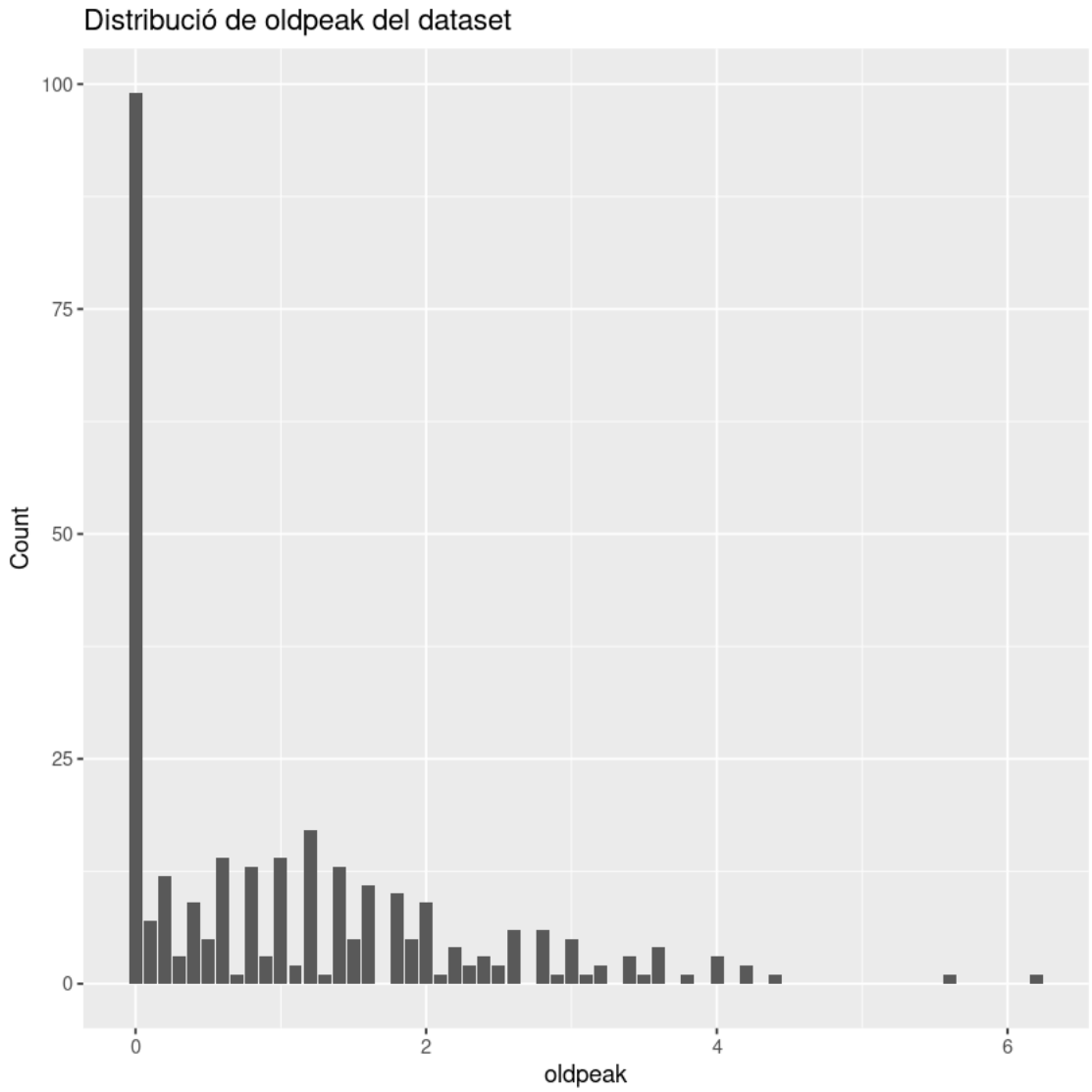
[9]:
```
chol_plot <-ggplot(data,aes(chol)) + geom_bar() + labs(x="chol", y="Count") +␣
↪guides(fill=guide_legend(title="")) + ggtitle("Distribució de chol del␣
↪dataset")
chol_plot
```



[10]:
```
thalachh_plot <-ggplot(data,aes(thalachh)) + geom_bar() + labs(x="thalachh",␣
 ↪y="Count") + guides(fill=guide_legend(title="")) + ggtitle("Distribució de␣
 ↪thalachh del dataset")
thalachh_plot
```



[11]:
```
oldpeak_plot <-ggplot(data,aes(oldpeak)) + geom_bar() + labs(x="oldpeak",␣
↪y="Count") + guides(fill=guide_legend(title="")) + ggtitle("Distribució de␣
↪oldpeak del dataset")
oldpeak_plot
```



[12]:
```
sum(is.na(data))
```

0

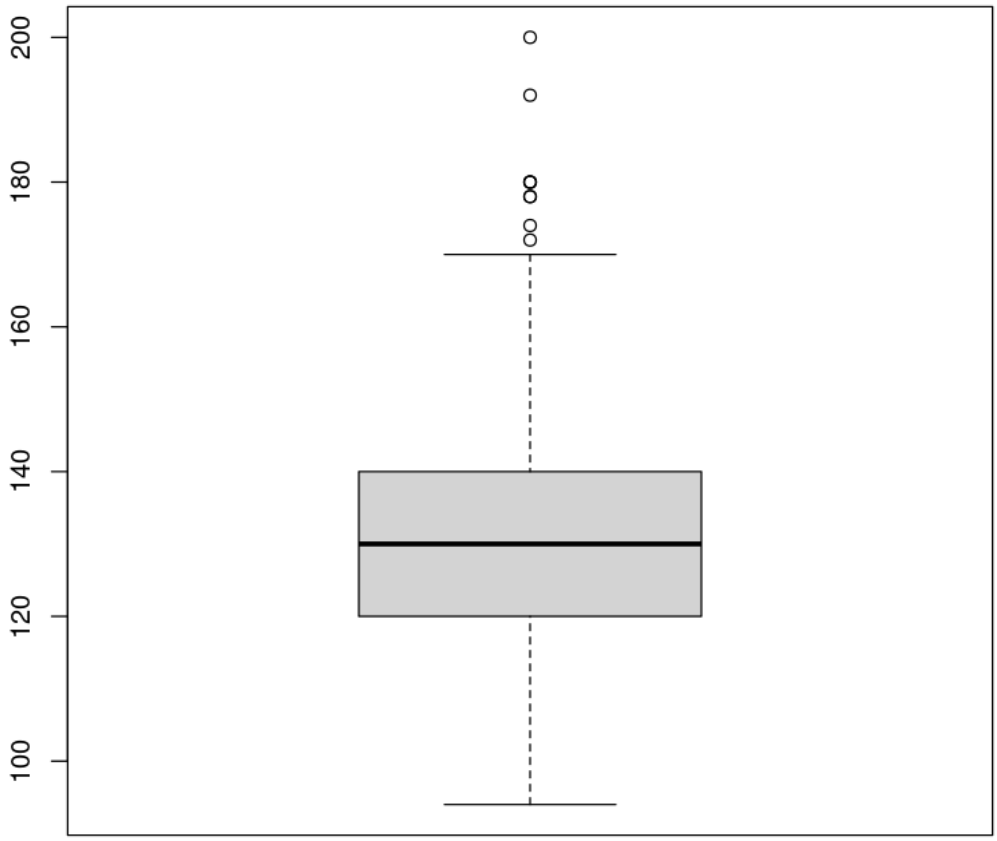
[13]:
```
data <- unique(data)
```

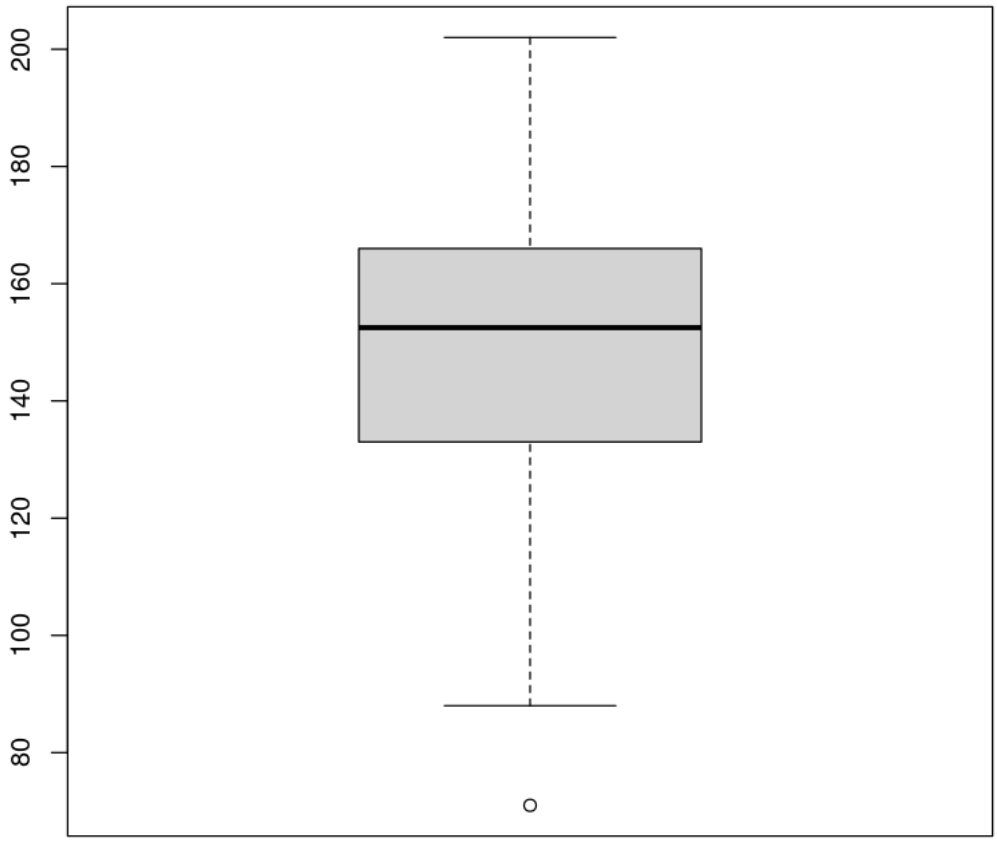
[14]:
```
duplicats <- duplicated(data)
print(sum(duplicats))
```

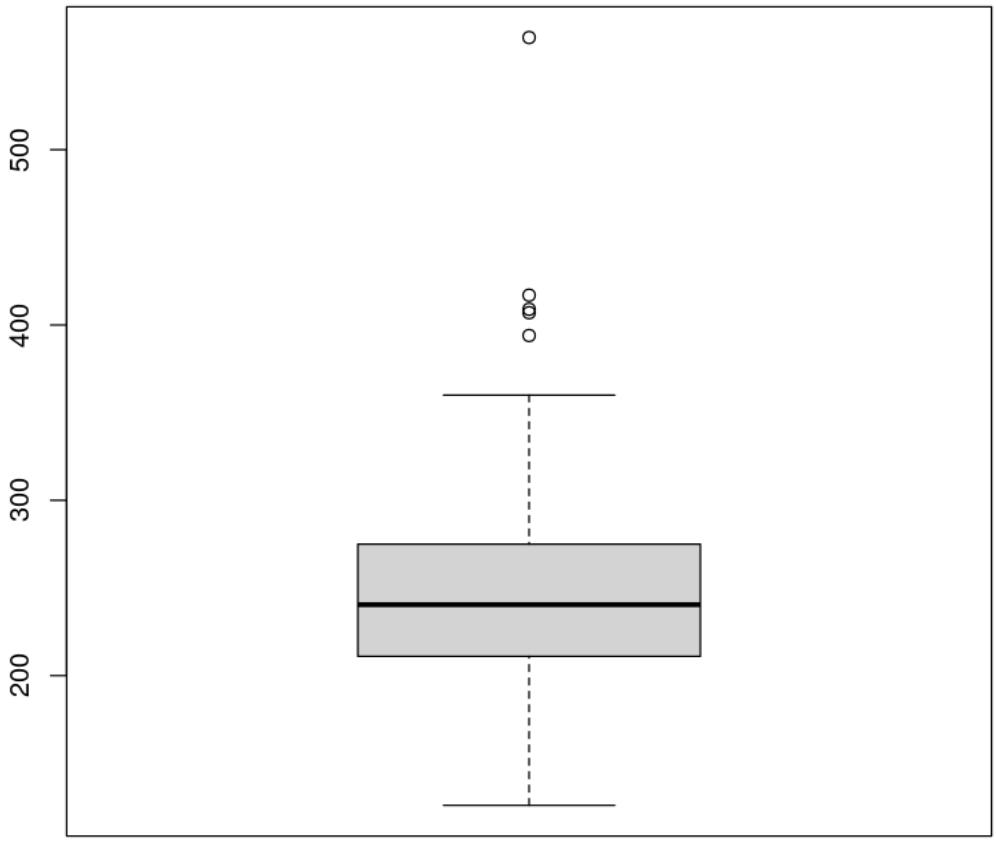
```
[1] 0
```

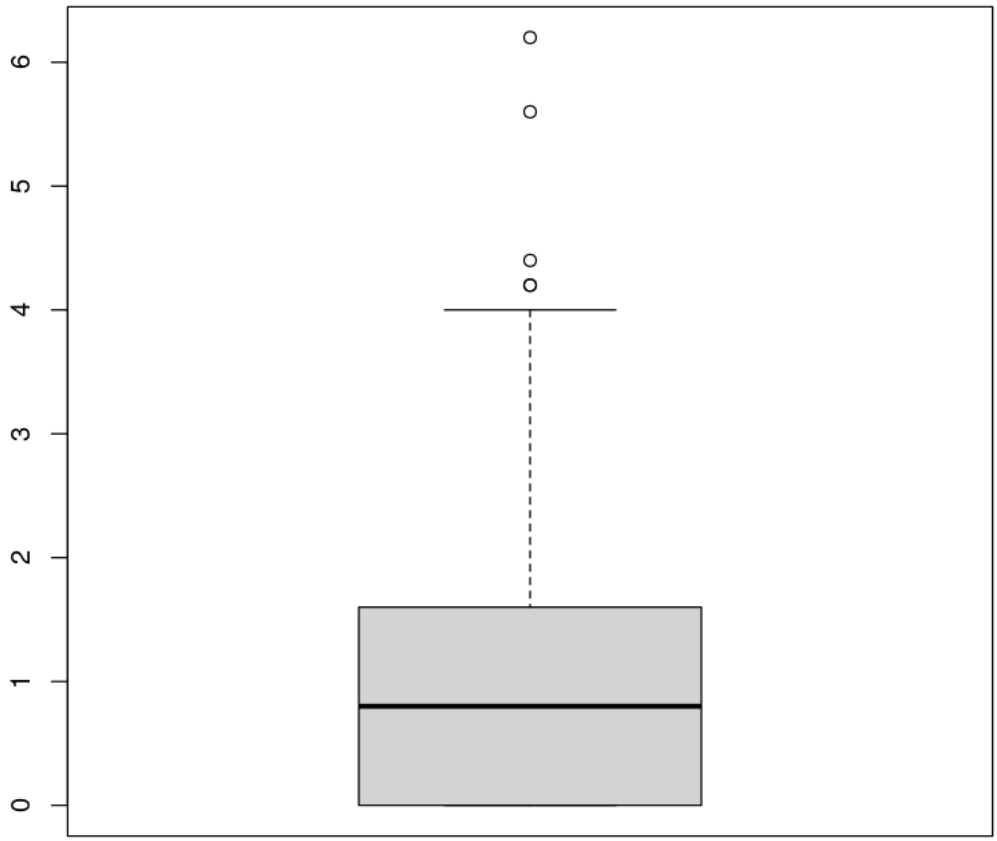
[15]:
```
trtbps <- boxplot(data$trtbps)
thalachh <- boxplot(data$thalachh)
```

```
chol <- boxplot(data$chol)
oldpeak <- boxplot(data$oldpeak)
```

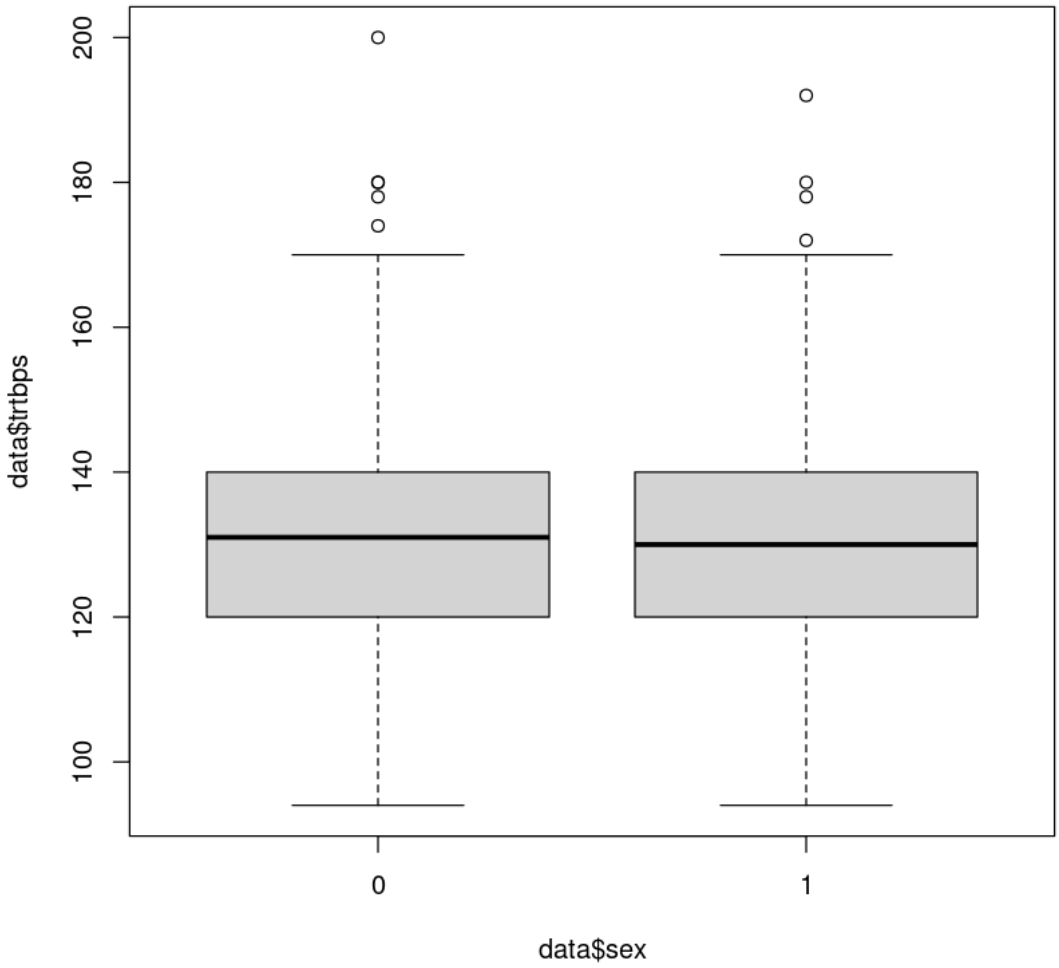


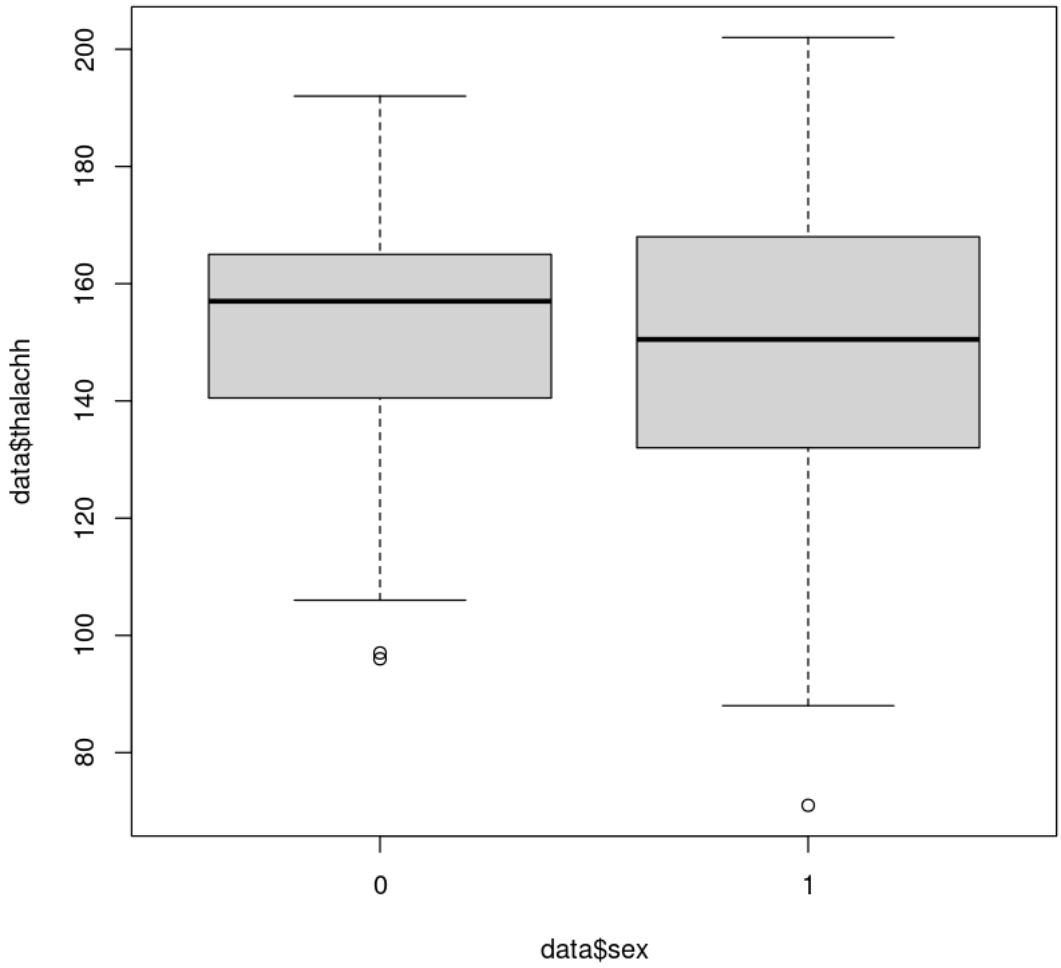

200
180
160
140
120
100
80

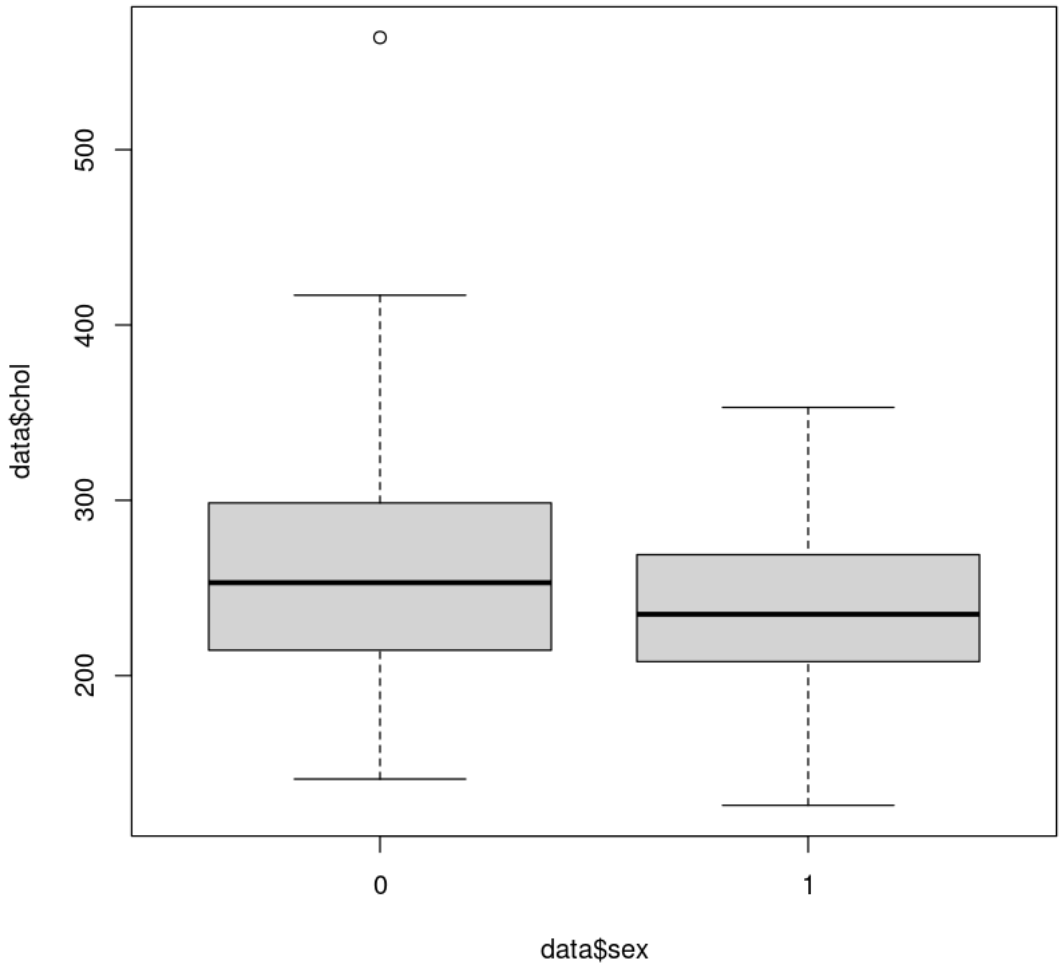

500
400
300
200

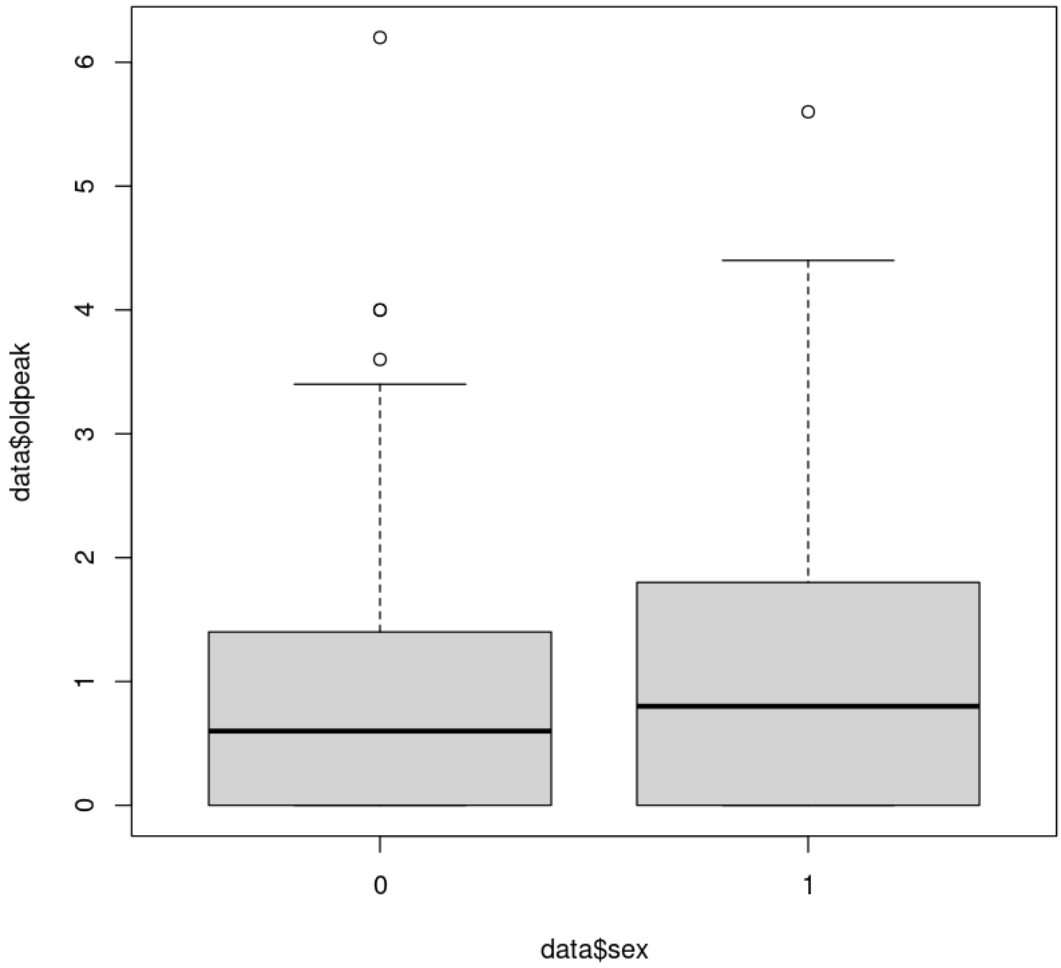


[16]:
```
trtbps <- boxplot(data$trtbps ~ data$sex)
thalachh <- boxplot(data$thalachh ~ data$sex)
chol <- boxplot(data$chol ~ data$sex)
oldpeak <- boxplot(data$oldpeak ~ data$sex)
```


data$trtbps
100
120
140
160
180
200
0
1
data$sex


data$thalachh
80
100
120
140
160
180
200
0
1
data$sex


data$chol
500
400
300
200
0
1
data$sex



[17]:
```
nombre_rows <- nrow(data)
nombre_columnes <- ncol(data)
cat("El nombre de files és de", nombre_rows, "i el nombre de columnes és de",␣
 ↪nombre_columnes)
```

```
El nombre de files és de 302 i el nombre de columnes és de 14
```

[18]:
```
trtbps170 <- sum(data$trtbps >= 170)
thalachh90 <- sum(data$thalachh <= 90)
chol350 <- sum(data$chol >= 350)
oldpeak_4 <- sum(data$oldpeak >= 4)
cat("La suma de files amb outliers a la columna trtbps és de", trtbps170, "\n")
```

```
cat("La suma de les files amb outliers a la columna thalachh és de",␣
 ↪thalachh90, "\n")
cat("La suma de les files amb outliers a la columna chol és de", chol350, "\n")
cat("La suma de les files amb outliers a la columna oldpeak és de", oldpeak_4,␣
 ↪"\n")
```

```
La suma de files amb outliers a la columna trtbps és de 13
La suma de les files amb outliers a la columna thalachh és de 3
La suma de les files amb outliers a la columna chol és de 8
La suma de les files amb outliers a la columna oldpeak és de 8
```

[41]:
```
data <- subset(data, trtbps <= 170)
data <- subset(data, thalachh >= 90)
data <- subset(data, chol <= 350)
data <- subset(data, oldpeak <= 4)
```

[20]:
```
nombre_rows <- nrow(data)
nombre_columnes <- ncol(data)
cat("El nombre de files és de", nombre_rows, "i el nombre de columnes és de",␣
 ↪nombre_columnes)
```

```
El nombre de files és de 279 i el nombre de columnes és de 14
```

[21]:
```
taula_correlacions <- round(cor(data), 2)
print(taula_correlacions)
```

```
           age   sex    cp trtbps  chol   fbs restecg thalachh  exng oldpeak
age       1.00 -0.06 -0.06   0.28  0.16  0.11   -0.11    -0.42  0.09    0.21
sex      -0.06  1.00 -0.09   0.01 -0.11  0.06   -0.09    -0.03  0.18    0.16
cp       -0.06 -0.09  1.00   0.08 -0.07  0.08    0.10     0.28 -0.38   -0.12
trtbps    0.28  0.01  0.08   1.00  0.10  0.13   -0.14    -0.06  0.00    0.15
chol      0.16 -0.11 -0.07   0.10  1.00  0.03   -0.16    -0.01  0.06   -0.01
fbs       0.11  0.06  0.08   0.13  0.03  1.00   -0.08    -0.03  0.01    0.02
restecg  -0.11 -0.09  0.10  -0.14 -0.16 -0.08    1.00     0.10 -0.12   -0.09
thalachh -0.42 -0.03  0.28  -0.06 -0.01 -0.03    0.10     1.00 -0.38   -0.34
exng      0.09  0.18 -0.38   0.00  0.06  0.01   -0.12    -0.38  1.00    0.32
oldpeak   0.21  0.16 -0.12   0.15 -0.01  0.02   -0.09    -0.34  0.32    1.00
slp      -0.15 -0.05  0.09  -0.08  0.03 -0.07    0.12     0.37 -0.26   -0.53
caa       0.33  0.14 -0.17   0.11  0.09  0.16   -0.09    -0.25  0.13    0.18
thall     0.06  0.24 -0.17  -0.02  0.09 -0.06    0.03    -0.10  0.20    0.19
output   -0.23 -0.31  0.41  -0.12 -0.11 -0.03    0.18     0.42 -0.43   -0.43
           slp   caa thall output
age      -0.15  0.33  0.06  -0.23
sex      -0.05  0.14  0.24  -0.31
cp        0.09 -0.17 -0.17   0.41
trtbps   -0.08  0.11 -0.02  -0.12
chol      0.03  0.09  0.09  -0.11
fbs      -0.07  0.16 -0.06  -0.03
```

```
restecg   0.12 -0.09  0.03   0.18
thalachh  0.37 -0.25 -0.10   0.42
exng     -0.26  0.13  0.20  -0.43
oldpeak  -0.53  0.18  0.19  -0.43
slp       1.00 -0.05 -0.08   0.32
caa      -0.05  1.00  0.15  -0.39
thall    -0.08  0.15  1.00  -0.34
output    0.32 -0.39 -0.34   1.00
```

[22]:
```r
shapiro_age <- shapiro.test(data$age)
shapiro_trtbps <- shapiro.test(data$trtbps)
shapiro_chol <- shapiro.test(data$chol)
shapiro_thalachh <- shapiro.test(data$thalachh)
shapiro_oldpeak <- shapiro.test(data$oldpeak)
print(shapiro_age)
print(shapiro_trtbps)
print(shapiro_chol)
print(shapiro_thalachh)
print(shapiro_oldpeak)
taula <- matrix(c("0.0203", "0.003591", "0.1485", "7.648e-05", "1.
 ↪42e-15"),ncol=5,byrow=TRUE)
colnames(taula) <- c("age","trtbps", "chol", "thalachh", "oldpeak")
rownames(taula) <- c("pvalue")
taula <- as.table(taula)
taula <- kable(taula)
taula
```

```
        Shapiro-Wilk normality test

data:  data$age
W = 0.98799, p-value = 0.0203


        Shapiro-Wilk normality test

data:  data$trtbps
W = 0.9842, p-value = 0.003591


        Shapiro-Wilk normality test

data:  data$chol
W = 0.99218, p-value = 0.1485


        Shapiro-Wilk normality test
```

```
data:  data$thalachh
W = 0.97474, p-value = 7.648e-05


        Shapiro-Wilk normality test

data:  data$oldpeak
W = 0.85352, p-value = 1.42e-15
```

	age	trtbps	chol	thalachh	oldpeak
pvalue	0.0203	0.003591	0.1485	7.648e-05	1.42e-15

[42]:
```
ntrain <- nrow(data)*0.8
ntest <- nrow(data)*0.2
set.seed(1)
index_train<-sample(1:nrow(data),size = ntrain)
train<-data[index_train,]
test<-data[-index_train,]
model <- lm(output ~ age + sex + cp + trtbps + chol + fbs + restecg + thalachh␣
 ↪+ exng + oldpeak + slp + caa + thall, data=train)
summary(model)
## Ens quedem només amb les que tenen coeficients significatius
model1 <- lm(output ~ sex + cp + thalachh + exng + oldpeak + caa + thall,␣
 ↪data=train)
summary(model1)
```

```
Call:
lm(formula = output ~ age + sex + cp + trtbps + chol + fbs +
    restecg + thalachh + exng + oldpeak + slp + caa + thall,
    data = train)

Residuals:
     Min       1Q   Median       3Q      Max
-0.83129 -0.21817  0.04336  0.24405  0.90542

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.007e+00  3.632e-01   2.772 0.006068 **
age          7.806e-06  3.085e-03   0.003 0.997983
sex         -1.874e-01  5.595e-02  -3.349 0.000961 ***
cp           1.017e-01  2.679e-02   3.797 0.000192 ***
trtbps      -2.015e-03  1.654e-03  -1.218 0.224448
chol        -7.377e-04  5.607e-04  -1.316 0.189681
```

```
fbs          2.349e-02  6.551e-02   0.359 0.720271
restecg      2.510e-02  4.778e-02   0.525 0.599895
thalachh     2.555e-03  1.356e-03   1.884 0.060890 .
exng        -1.399e-01  6.156e-02  -2.273 0.024069 *
oldpeak     -8.203e-02  2.926e-02  -2.803 0.005537 **
slp          7.814e-02  4.810e-02   1.624 0.105780
caa         -1.160e-01  2.612e-02  -4.443 1.44e-05 ***
thall       -1.242e-01  4.219e-02  -2.944 0.003602 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3519 on 209 degrees of freedom
Multiple R-squared:  0.5308,        Adjusted R-squared:  0.5016
F-statistic: 18.18 on 13 and 209 DF,  p-value: < 2.2e-16



Call:
lm(formula = output ~ sex + cp + thalachh + exng + oldpeak +
    caa + thall, data = train)

Residuals:
     Min       1Q   Median       3Q      Max
-0.91006 -0.21219  0.05871  0.22471  0.88323

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.638746   0.211677   3.018 0.002856 **
sex         -0.183931   0.054568  -3.371 0.000889 ***
cp           0.099021   0.026376   3.754 0.000224 ***
thalachh     0.003082   0.001225   2.516 0.012610 *
exng        -0.153394   0.061046  -2.513 0.012714 *
oldpeak     -0.105318   0.026046  -4.044 7.34e-05 ***
caa         -0.117385   0.024945  -4.706 4.53e-06 ***
thall       -0.123255   0.041806  -2.948 0.003549 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3529 on 215 degrees of freedom
Multiple R-squared:  0.5147,        Adjusted R-squared:  0.4989
F-statistic: 32.57 on 7 and 215 DF,  p-value: < 2.2e-16
```

[24]:
```
str(data)
```

```
'data.frame':   279 obs. of  14 variables:
 $ age     : int  63 37 41 56 57 56 44 57 54 48 …
 $ sex     : int  1 1 0 1 1 0 1 1 1 0 …
```

```
$ cp      : int  3 2 1 1 0 1 1 2 0 2 …
$ trtbps  : int  145 130 130 120 140 140 120 150 140 130 …
$ chol    : int  233 250 204 236 192 294 263 168 239 275 …
$ fbs     : int  1 0 0 0 0 0 0 0 0 0 …
$ restecg : int  0 1 0 1 1 0 1 1 1 1 …
$ thalachh: int  150 187 172 178 148 153 173 174 160 139 …
$ exng    : int  0 0 0 0 0 0 0 0 0 0 …
$ oldpeak : num  2.3 3.5 1.4 0.8 0.4 1.3 0 1.6 1.2 0.2 …
$ slp     : int  0 0 2 2 1 1 2 2 2 2 …
$ caa     : int  0 0 0 0 0 0 0 0 0 0 …
$ thall   : int  1 2 2 2 1 2 3 2 2 2 …
$ output  : int  1 1 1 1 1 1 1 1 1 1 …
```

[25]:
```
table(data$output, data$sex)
summary(table(data$output, data$sex))
```

```
    0   1
0  17 106
1  66  90
```

```
Number of cases in table: 279
Number of factors: 2
Test for independence of all factors:
        Chisq = 26.704, df = 1, p-value = 2.371e-07
```

[26]:
```
table(data$fbs, data$sex)
summary(table(data$fbs, data$sex))
```

```
    0   1
0  74 165
1   9  31
```

```
Number of cases in table: 279
Number of factors: 2
Test for independence of all factors:
        Chisq = 1.1741, df = 1, p-value = 0.2786
```

[27]:
```
table(data$cp, data$sex)
summary(table(data$cp, data$sex))
```

```
   0  1
0 29 98
1 18 31
2 32 49
3  4 18
```

```
Number of cases in table: 279
Number of factors: 2
Test for independence of all factors:
        Chisq = 9.148, df = 3, p-value = 0.02739
```

[28]:
```
table(data$restecg  , data$sex)
summary(table(data$restecg, data$sex))

test <- fisher.test(table(data$restecg , data$sex))
test
```

```
     0   1
  0  36 100
  1  45  96
  2   2   0
Number of cases in table: 279
Number of factors: 2
Test for independence of all factors:
        Chisq = 5.739, df = 2, p-value = 0.05673
        Chi-squared approximation may be incorrect


        Fisher's Exact Test for Count Data

data:  table(data$restecg, data$sex)
p-value = 0.06927
alternative hypothesis: two.sided
```

[29]:
```
table(data$slp , data$sex)
summary(table(data$slp, data$sex))

test <- fisher.test(table(data$slp , data$sex))
test
```

```
    0  1
  0  3 13
  1 38 90
  2 42 93
Number of cases in table: 279
Number of factors: 2
Test for independence of all factors:
        Chisq = 1.0463, df = 2, p-value = 0.5927
        Chi-squared approximation may be incorrect
```

```
        Fisher's Exact Test for Count Data

data:  table(data$slp, data$sex)
p-value = 0.6523
alternative hypothesis: two.sided
```

[30]:
```
table(data$thall  , data$sex)
summary(table(data$thall, data$sex))
test <- fisher.test(table(data$thall , data$sex))
test
```

```
    0  1
  0  1  1
  1  1 16
  2 72 85
  3  9 94
Number of cases in table: 279
Number of factors: 2
Test for independence of all factors:
        Chisq = 46.28, df = 3, p-value = 4.939e-10
        Chi-squared approximation may be incorrect


        Fisher's Exact Test for Count Data

data:  table(data$thall, data$sex)
p-value = 1.143e-11
alternative hypothesis: two.sided
```

[31]:
```
table(data$exng , data$sex)
summary(table(data$exng, data$sex))
```

```
     0   1
  0  68 124
  1  15  72
Number of cases in table: 279
Number of factors: 2
Test for independence of all factors:
        Chisq = 9.464, df = 1, p-value = 0.002096
```

[32]:
```
aggregate(chol~sex, data = data, FUN = var)
```

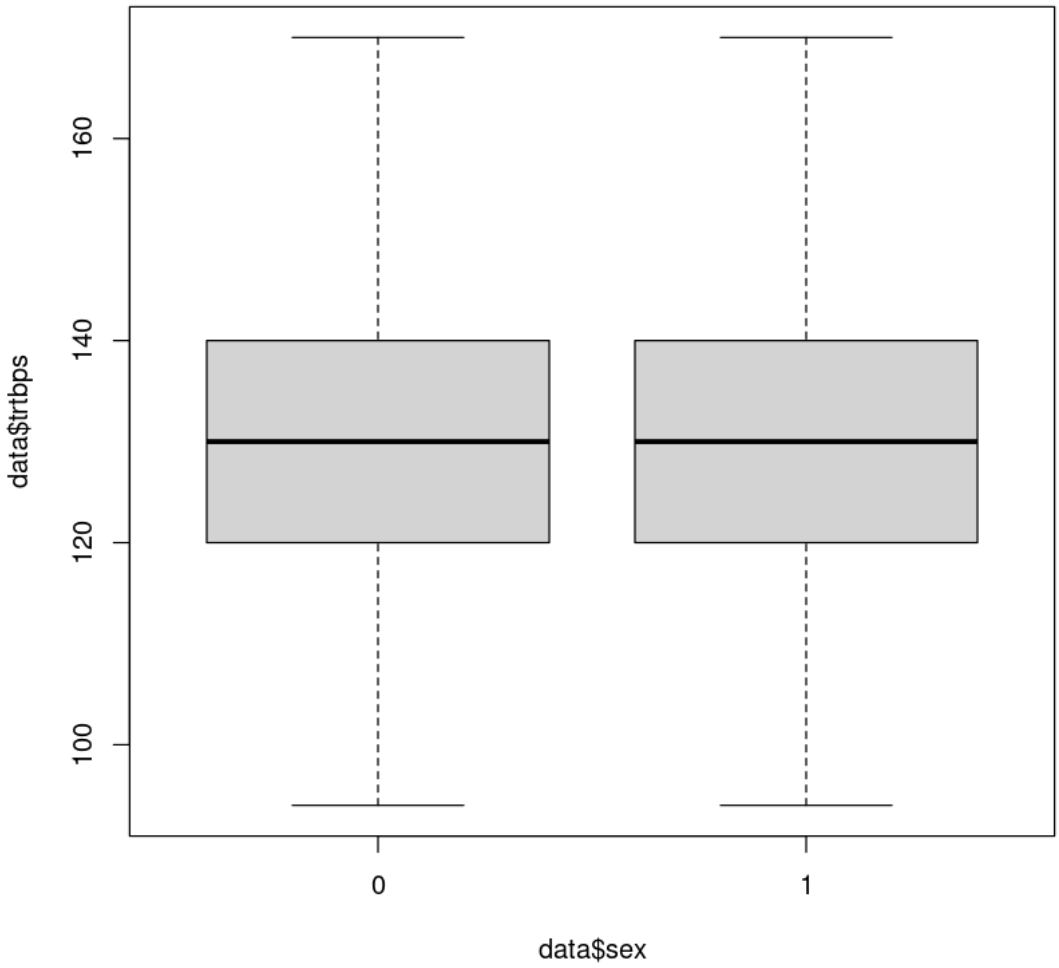
```
var.test(x = data[data$sex == 0, "chol"],
         y = data[data$sex == 1, "chol"] )
```

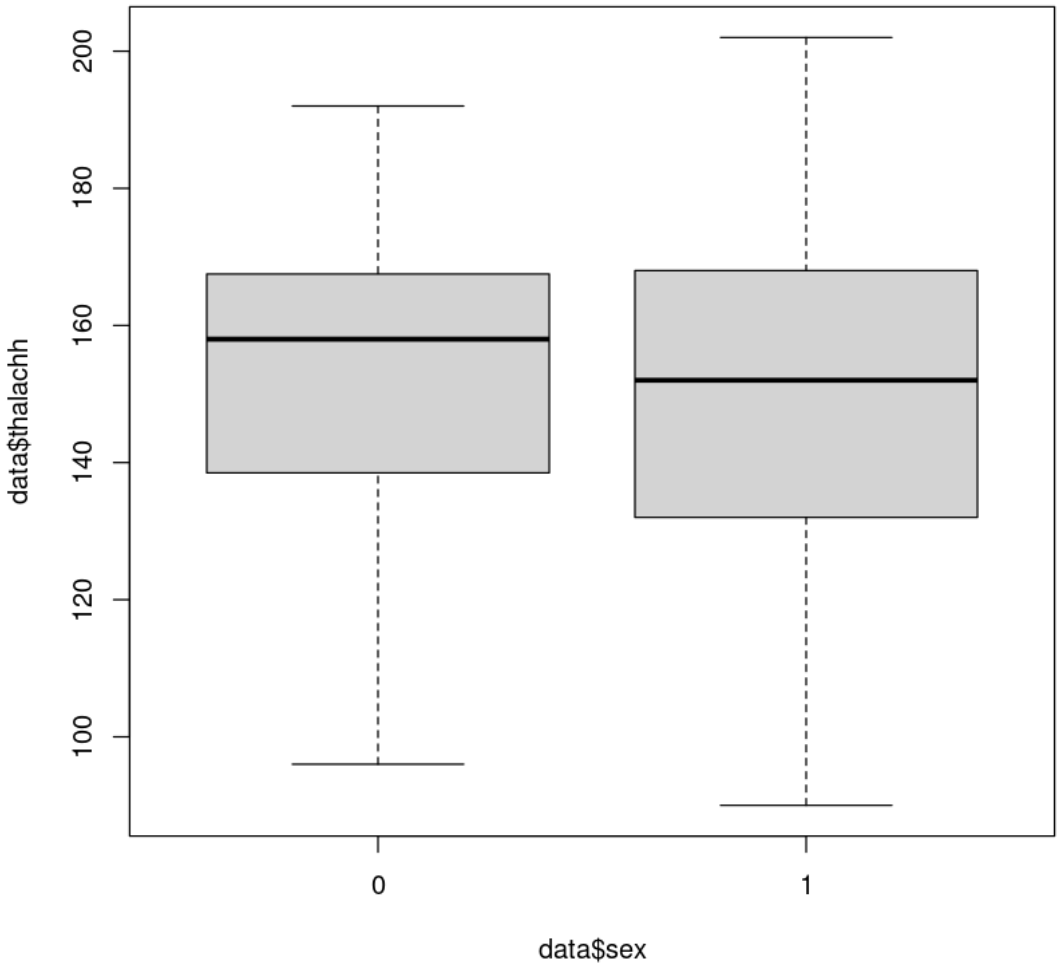
A data.frame: 2 × 2

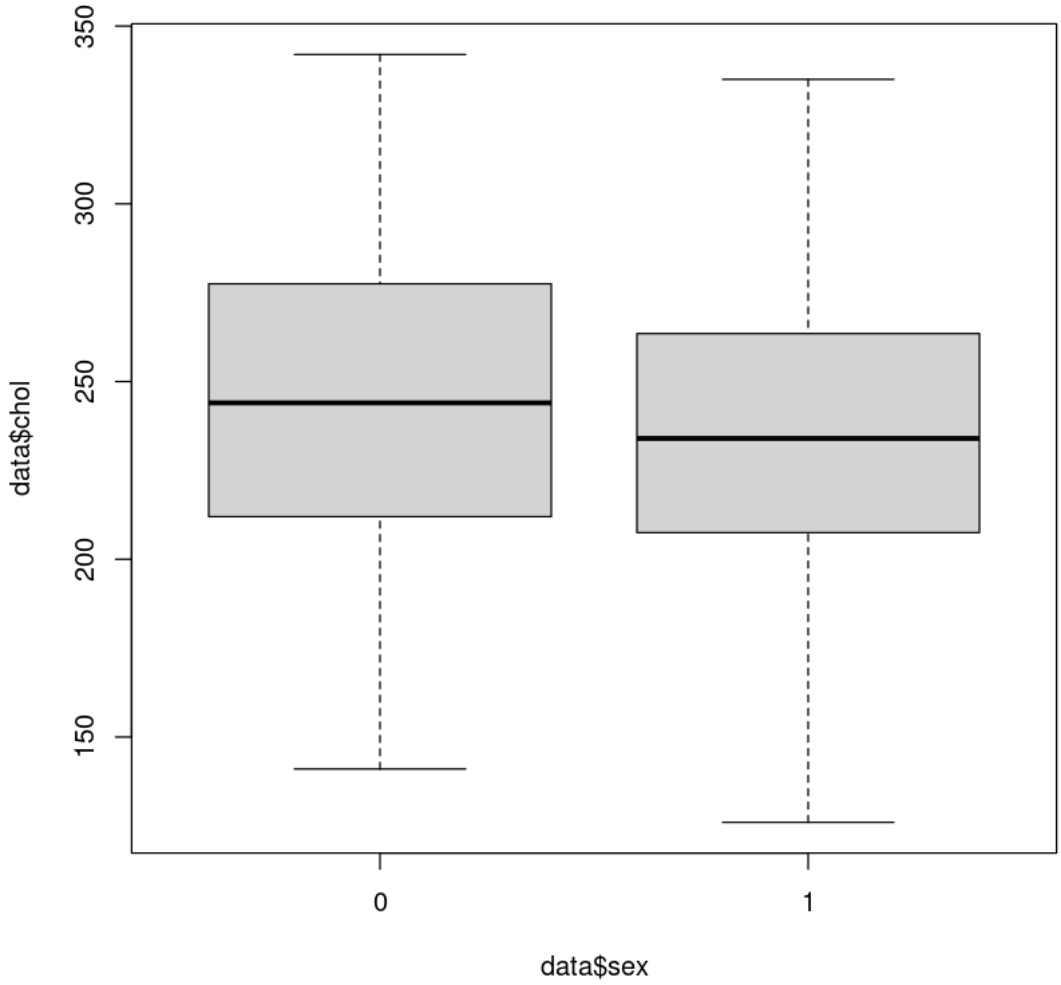
sex	chol
<int>	<dbl>
0	2116.052
1	1756.893

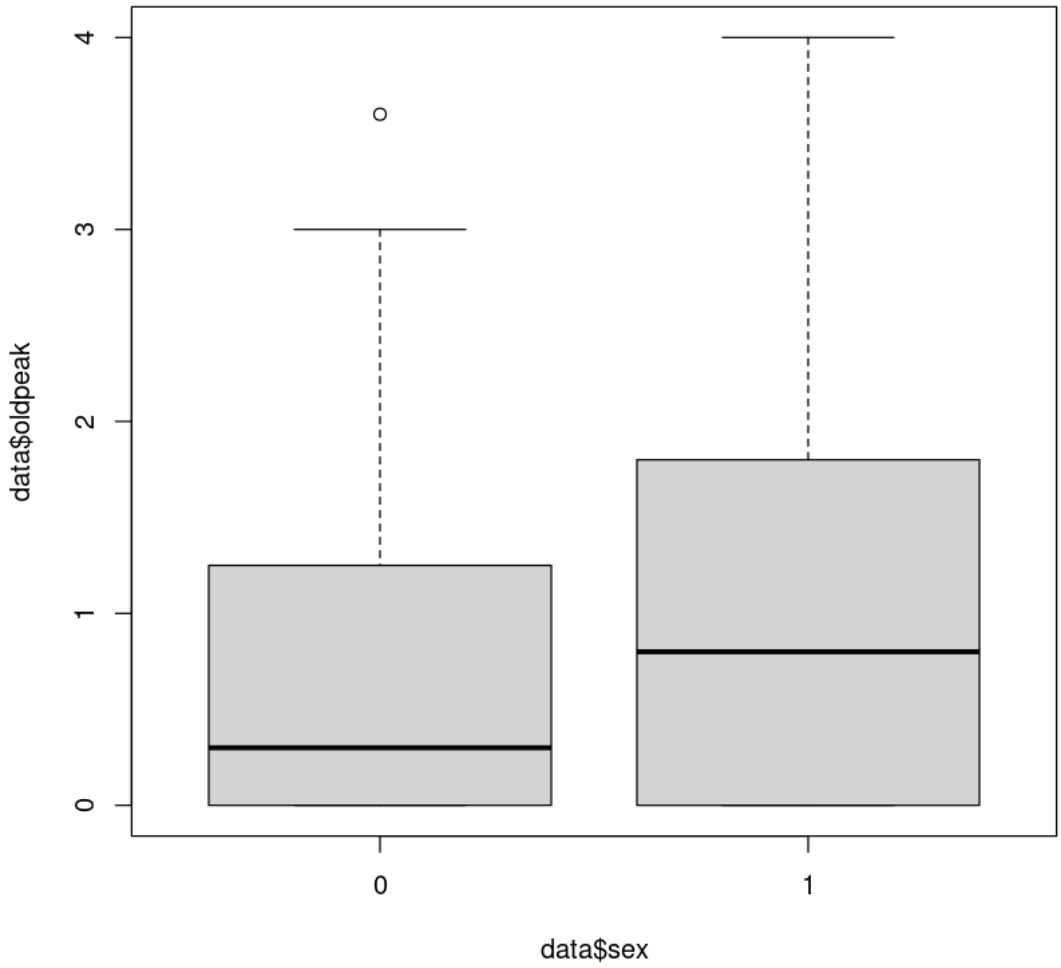
```
        F test to compare two variances

data:  data[data$sex == 0, "chol"] and data[data$sex == 1, "chol"]
F = 1.2044, num df = 82, denom df = 195, p-value = 0.3008
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.8462295 1.7624922
sample estimates:
ratio of variances
          1.204429
```

[33]:
```
trtbps <- boxplot(data$trtbps ~ data$sex)
thalachh <- boxplot(data$thalachh ~ data$sex)
chol <- boxplot(data$chol ~ data$sex)
oldpeak <- boxplot(data$oldpeak ~ data$sex)
```


data$trtbps
100
120
140
160
0
1
data$sex


data$thalachh
100
120
140
160
180
200
0
1
data$sex


350
300
250
200
150
data$chol
0
1
data$sex



[34]:
```
cor.test(data$output,data$oldpeak, method="spearman")
```

```
Warning message in cor.test.default(data$output, data$oldpeak, method =
"spearman"):
"Cannot compute exact p-value with ties"


        Spearman's rank correlation rho

data:  data$output and data$oldpeak
S = 5120405, p-value = 5.099e-13
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
```

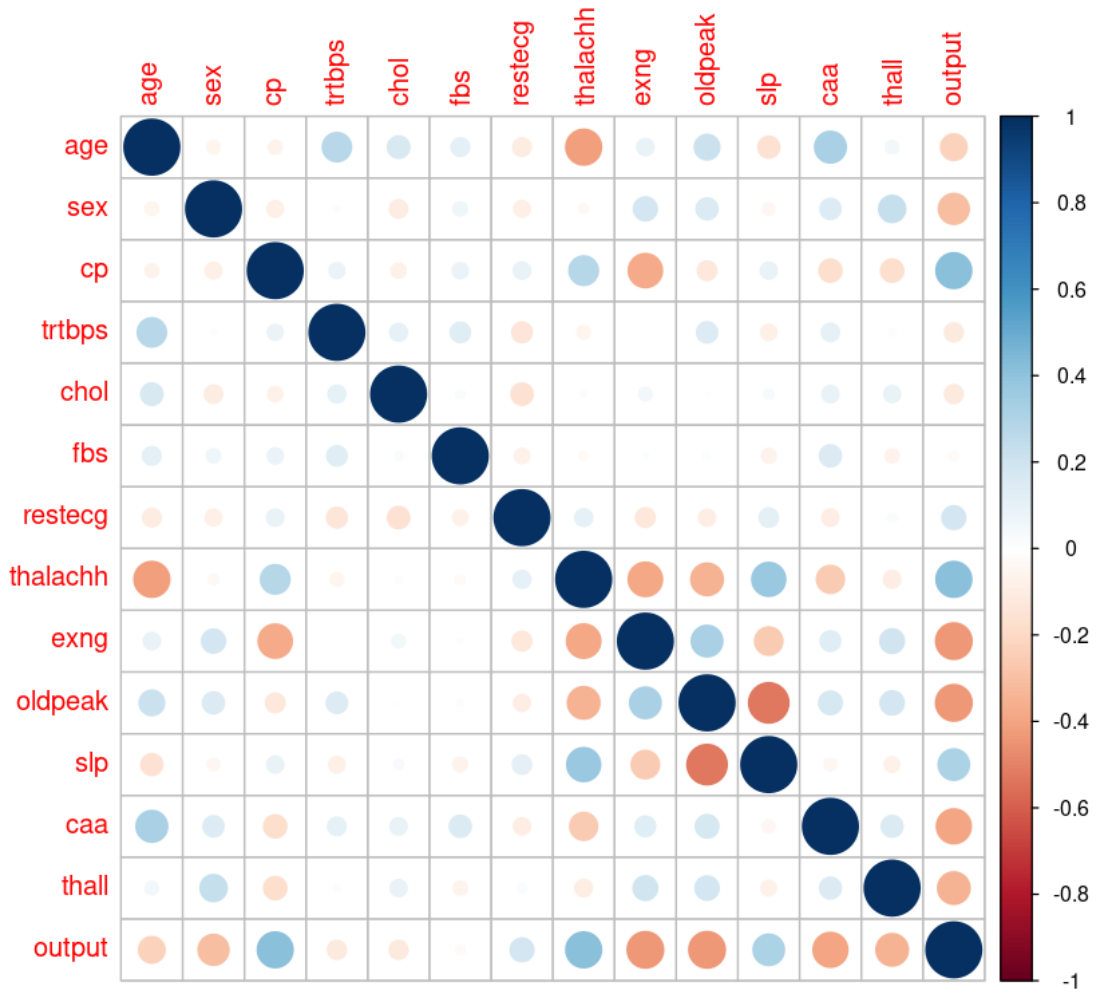
```
-0.4146483
```

[35]:
```
cor.test(data$cp,data$thalachh, method="spearman")
```

```
Warning message in cor.test.default(data$cp, data$thalachh, method =
"spearman"):
"Cannot compute exact p-value with ties"


        Spearman's rank correlation rho

data:  data$cp and data$thalachh
S = 2504543, p-value = 1.516e-07
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.3080531
```

[36]:
```
if(!require('corrplot')) {
    install.packages('corrplot')
    library('corrplot')
}



corr.res<-cor(data)
corrplot(corr.res,method="circle")
```

```
Loading required package: corrplot

Warning message in library(package, lib.loc = lib.loc, character.only = TRUE,
logical.return = TRUE, :
"there is no package called ‘corrplot’"
Retrieving 'https://packagemanager.rstudio.com/all/__linux__/focal/latest/src/co
ntrib/corrplot_0.92.tar.gz' …
        OK [downloaded 3.7 Mb in 0.1 secs]
Installing corrplot [0.92] …
        OK [installed binary]
Moving corrplot [0.92] into the cache …
        OK [moved to cache in 0.42 milliseconds]

corrplot 0.92 loaded
```


age
sex
cp
trtbps
chol
fbs
restecg
thalachh
exng
oldpeak
slp
caa
thall
output
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1