R version 3.6.1 (2019-07-05) -- "Action of the Toes"

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Platform: x86\_64-w64-mingw32/x64 (64-bit)

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> vino<-read.csv("winequality-red.csv", header = TRUE)

Error in file(file, "rt") : no se puede abrir la conexión

Además: Warning message:

In file(file, "rt") :

no fue posible abrir el archivo 'winequality-red.csv': No such file or directory

> vino<-read.csv("~PRA2\_Datos/winequality-red.csv", header = TRUE)

Error in file(file, "rt") : no se puede abrir la conexión

Además: Warning message:

In file(file, "rt") :

no fue posible abrir el archivo '~PRA2\_Datos/winequality-red.csv': No such file or directory

> vino<-read.csv("~PRA2\_Datos/winequality-red.csv", header = TRUE)

Error in file(file, "rt") : no se puede abrir la conexión

Además: Warning message:

In file(file, "rt") :

no fue posible abrir el archivo '~PRA2\_Datos/winequality-red.csv': No such file or directory

> vino<-read.csv("~/PRA2\_Datos/winequality-red.csv", header = TRUE)

> head(vino[,1:5])

fixed.acidity volatile.acidity citric.acid residual.sugar chlorides

1 7.4 0.70 0.00 1.9 0.076

2 7.8 0.88 0.00 2.6 0.098

3 7.8 0.76 0.04 2.3 0.092

4 11.2 0.28 0.56 1.9 0.075

5 7.4 0.70 0.00 1.9 0.076

6 7.4 0.66 0.00 1.8 0.075

> str(vino)

'data.frame': 1599 obs. of 12 variables:

$ fixed.acidity : num 7.4 7.8 7.8 11.2 7.4 7.4 7.9 7.3 7.8 7.5 ...

$ volatile.acidity : num 0.7 0.88 0.76 0.28 0.7 0.66 0.6 0.65 0.58 0.5 ...

$ citric.acid : num 0 0 0.04 0.56 0 0 0.06 0 0.02 0.36 ...

$ residual.sugar : num 1.9 2.6 2.3 1.9 1.9 1.8 1.6 1.2 2 6.1 ...

$ chlorides : num 0.076 0.098 0.092 0.075 0.076 0.075 0.069 0.065 0.073 0.071 ...

$ free.sulfur.dioxide : num 11 25 15 17 11 13 15 15 9 17 ...

$ total.sulfur.dioxide: num 34 67 54 60 34 40 59 21 18 102 ...

$ density : num 0.998 0.997 0.997 0.998 0.998 ...

$ pH : num 3.51 3.2 3.26 3.16 3.51 3.51 3.3 3.39 3.36 3.35 ...

$ sulphates : num 0.56 0.68 0.65 0.58 0.56 0.56 0.46 0.47 0.57 0.8 ...

$ alcohol : num 9.4 9.8 9.8 9.8 9.4 9.4 9.4 10 9.5 10.5 ...

$ quality : int 5 5 5 6 5 5 5 7 7 5 ...

> summary(vino)

fixed.acidity volatile.acidity citric.acid residual.sugar

Min. : 4.60 Min. :0.1200 Min. :0.000 Min. : 0.900

1st Qu.: 7.10 1st Qu.:0.3900 1st Qu.:0.090 1st Qu.: 1.900

Median : 7.90 Median :0.5200 Median :0.260 Median : 2.200

Mean : 8.32 Mean :0.5278 Mean :0.271 Mean : 2.539

3rd Qu.: 9.20 3rd Qu.:0.6400 3rd Qu.:0.420 3rd Qu.: 2.600

Max. :15.90 Max. :1.5800 Max. :1.000 Max. :15.500

chlorides free.sulfur.dioxide total.sulfur.dioxide density

Min. :0.01200 Min. : 1.00 Min. : 6.00 Min. :0.9901

1st Qu.:0.07000 1st Qu.: 7.00 1st Qu.: 22.00 1st Qu.:0.9956

Median :0.07900 Median :14.00 Median : 38.00 Median :0.9968

Mean :0.08747 Mean :15.87 Mean : 46.47 Mean :0.9967

3rd Qu.:0.09000 3rd Qu.:21.00 3rd Qu.: 62.00 3rd Qu.:0.9978

Max. :0.61100 Max. :72.00 Max. :289.00 Max. :1.0037

pH sulphates alcohol quality

Min. :2.740 Min. :0.3300 Min. : 8.40 Min. :3.000

1st Qu.:3.210 1st Qu.:0.5500 1st Qu.: 9.50 1st Qu.:5.000

Median :3.310 Median :0.6200 Median :10.20 Median :6.000

Mean :3.311 Mean :0.6581 Mean :10.42 Mean :5.636

3rd Qu.:3.400 3rd Qu.:0.7300 3rd Qu.:11.10 3rd Qu.:6.000

Max. :4.010 Max. :2.0000 Max. :14.90 Max. :8.000

> sapply(vino, function(x) sum(is.na(x)))

fixed.acidity volatile.acidity citric.acid residual.sugar

0 0 0 0

chlorides free.sulfur.dioxide total.sulfur.dioxide density

0 0 0 0

pH sulphates alcohol quality

0 0 0 0

> boxplot.matrix(vino)

Error in sort.int(x, na.last = na.last, decreasing = decreasing, ...) :

'x' must be atomic

Además: Warning message:

In split.default(c(x), rep.int(1L:ncol(x), rep.int(nrow(x), ncol(x)))) :

largo de datos no es múltiplo de la variable de separación

> boxplot(vino)

> boxplot(vino$fixed.acidity)

> boxplots.stats(vino$fixed.acidity)

Error in boxplots.stats(vino$fixed.acidity) :

no se pudo encontrar la función "boxplots.stats"

> boxplot.stats(vino$fixed.acidity)

$stats

[1] 4.6 7.1 7.9 9.2 12.3

$n

[1] 1599

$conf

[1] 7.817024 7.982976

$out

[1] 12.8 12.8 15.0 15.0 12.5 13.3 13.4 12.4 12.5 13.8 13.5 12.6 12.5 12.8 12.8 14.0

[17] 13.7 13.7 12.7 12.5 12.8 12.6 15.6 12.5 13.0 12.5 13.3 12.4 12.5 12.9 14.3 12.4

[33] 15.5 15.5 15.6 13.0 12.7 13.0 12.7 12.4 12.7 13.2 13.2 13.2 15.9 13.3 12.9 12.6

[49] 12.6

> boxplot(vino$volatile.acidity)

> boxplot.stats(vino$volatile.acidity)$out

[1] 1.130 1.020 1.070 1.330 1.330 1.040 1.090 1.040 1.240 1.185 1.020 1.035 1.025

[14] 1.115 1.020 1.020 1.580 1.180 1.040

> boxplot(vino$citric.acid)

> boxplot.stats(vino$citric.acid)$out

[1] 1

> boxplot(vino$residual.sugar)

> boxplot.stats(vino$residual.sugar)$out

[1] 6.10 6.10 3.80 3.90 4.40 10.70 5.50 5.90 5.90 3.80 5.10 4.65 4.65

[14] 5.50 5.50 5.50 5.50 7.30 7.20 3.80 5.60 4.00 4.00 4.00 4.00 7.00

[27] 4.00 4.00 6.40 5.60 5.60 11.00 11.00 4.50 4.80 5.80 5.80 3.80 4.40

[40] 6.20 4.20 7.90 7.90 3.70 4.50 6.70 6.60 3.70 5.20 15.50 4.10 8.30

[53] 6.55 6.55 4.60 6.10 4.30 5.80 5.15 6.30 4.20 4.20 4.60 4.20 4.60

[66] 4.30 4.30 7.90 4.60 5.10 5.60 5.60 6.00 8.60 7.50 4.40 4.25 6.00

[79] 3.90 4.20 4.00 4.00 4.00 6.60 6.00 6.00 3.80 9.00 4.60 8.80 8.80

[92] 5.00 3.80 4.10 5.90 4.10 6.20 8.90 4.00 3.90 4.00 8.10 8.10 6.40

[105] 6.40 8.30 8.30 4.70 5.50 5.50 4.30 5.50 3.70 6.20 5.60 7.80 4.60

[118] 5.80 4.10 12.90 4.30 13.40 4.80 6.30 4.50 4.50 4.30 4.30 3.90 3.80

[131] 5.40 3.80 6.10 3.90 5.10 5.10 3.90 15.40 15.40 4.80 5.20 5.20 3.75

[144] 13.80 13.80 5.70 4.30 4.10 4.10 4.40 3.70 6.70 13.90 5.10 7.80

> boxplot(vino$chlorides)

> boxplot.stats(vino$chlorides)$out

[1] 0.176 0.170 0.368 0.341 0.172 0.332 0.464 0.401 0.467 0.122 0.178 0.146 0.236

[14] 0.610 0.360 0.270 0.039 0.337 0.263 0.611 0.358 0.343 0.186 0.213 0.214 0.121

[27] 0.122 0.122 0.128 0.120 0.159 0.124 0.122 0.122 0.174 0.121 0.127 0.413 0.152

[40] 0.152 0.125 0.122 0.200 0.171 0.226 0.226 0.250 0.148 0.122 0.124 0.124 0.143

[53] 0.222 0.039 0.157 0.422 0.034 0.387 0.415 0.157 0.157 0.243 0.241 0.190 0.132

[66] 0.126 0.038 0.165 0.145 0.147 0.012 0.012 0.039 0.194 0.132 0.161 0.120 0.120

[79] 0.123 0.123 0.414 0.216 0.171 0.178 0.369 0.166 0.166 0.136 0.132 0.132 0.123

[92] 0.123 0.123 0.403 0.137 0.414 0.166 0.168 0.415 0.153 0.415 0.267 0.123 0.214

[105] 0.214 0.169 0.205 0.205 0.039 0.235 0.230 0.038

> boxplot(vino$free.sulfur.dioxide)

> boxplot.stats(vino$free.sulfur.dioxide)$out

[1] 52 51 50 68 68 43 47 54 46 45 53 52 51 45 57 50 45 48 43 48 72 43 51 51 52 55

[27] 55 48 48 66

> boxplot(vino$ total.sulfur.dioxide)

> boxplot.stats(vino$total.sulfur.dioxide)$out

[1] 145 148 136 125 140 136 133 153 134 141 129 128 129 128 143 144 127 126 145 144

[21] 135 165 124 124 134 124 129 151 133 142 149 147 145 148 155 151 152 125 127 139

[41] 143 144 130 278 289 135 160 141 141 133 147 147 131 131 131

> boxplot(vino$density)

> boxplot.stats(vino$density)$out

[1] 0.99160 0.99160 1.00140 1.00150 1.00150 1.00180 0.99120 1.00220 1.00220 1.00140

[11] 1.00140 1.00140 1.00140 1.00320 1.00260 1.00140 1.00315 1.00315 1.00315 1.00210

[21] 1.00210 0.99170 0.99220 1.00260 0.99210 0.99154 0.99064 0.99064 1.00289 0.99162

[31] 0.99007 0.99007 0.99020 0.99220 0.99150 0.99157 0.99080 0.99084 0.99191 1.00369

[41] 1.00369 1.00242 0.99182 1.00242 0.99182

> boxplot(vino$pH)

> boxplot.stats(vino$pH)$out

[1] 3.90 3.75 3.85 2.74 3.69 3.69 2.88 2.86 3.74 2.92 2.92 2.92 3.72 2.87 2.89 2.89

[17] 2.92 3.90 3.71 3.69 3.69 3.71 3.71 2.89 2.89 3.78 3.70 3.78 4.01 2.90 4.01 3.71

[33] 2.88 3.72 3.72

> boxplot(vino$sulphates)

> boxplot.stats(vino$sulphates)$out

[1] 1.56 1.28 1.08 1.20 1.12 1.28 1.14 1.95 1.22 1.95 1.98 1.31 2.00 1.08 1.59 1.02

[17] 1.03 1.61 1.09 1.26 1.08 1.00 1.36 1.18 1.13 1.04 1.11 1.13 1.07 1.06 1.06 1.05

[33] 1.06 1.04 1.05 1.02 1.14 1.02 1.36 1.36 1.05 1.17 1.62 1.06 1.18 1.07 1.34 1.16

[49] 1.10 1.15 1.17 1.17 1.33 1.18 1.17 1.03 1.17 1.10 1.01

> boxplot(vino$alcohol)

> boxplot.stats(vino$alcohol)$out

[1] 14.00000 14.00000 14.00000 14.00000 14.90000 14.00000 13.60000 13.60000

[9] 13.60000 14.00000 14.00000 13.56667 13.60000

> boxplot(vino$quality)

> boxplot.stats(vino$quality)$out

[1] 8 8 8 8 8 3 8 8 8 3 8 3 8 3 3 8 8 8 8 8 3 3 8 8 3 3 3 8

> library(nortest)

Error in library(nortest) : there is no package called ‘nortest’

> library(nortest)

Error in library(nortest) : there is no package called ‘nortest’

> alpha = 0.05

> col.names = colnames(vino)

> for (i in 1:ncol(vino)) {

+ if (i == 1) cat("Variables que no siguen una distribución normal:\n")

+ if (is.integer(vino[,i]) | is.numeric(vino[,i])) {

+ p\_val = ad.test(vino[,i])$p.value

+ if (p\_val < alpha) {

+ cat(col.names[i])

+ if (i < ncol(vino) - 1) cat(", ")

+ if (i %% 3 == 0) cat("\n")

+ }

+ }

+ }

Variables que no siguen una distribución normal:

Error in ad.test(vino[, i]) : no se pudo encontrar la función "ad.test"

> install.packages("nortest")

WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:

https://cran.rstudio.com/bin/windows/Rtools/

Installing package into ‘C:/Users/josej/Documents/R/win-library/3.6’

(as ‘lib’ is unspecified)

probando la URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/nortest\_1.0-4.zip'

Content type 'application/zip' length 39063 bytes (38 KB)

downloaded 38 KB

package ‘nortest’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\josej\AppData\Local\Temp\Rtmpqggy1L\downloaded\_packages

>

> library(nortest)

> alpha = 0.05

> col.names = colnames(vino)

> for (i in 1:ncol(vino)) {

+ if (i == 1) cat("Variables que no siguen una distribución normal:\n")

+ if (is.integer(vino[,i]) | is.numeric(vino[,i])) {

+ p\_val = ad.test(vino[,i])$p.value

+ if (p\_val < alpha) {

+ cat(col.names[i])

+ if (i < ncol(vino) - 1) cat(", ")

+ if (i %% 3 == 0) cat("\n")

+ }

+ }

+ }

Variables que no siguen una distribución normal:

fixed.acidity, volatile.acidity, citric.acid,

residual.sugar, chlorides, free.sulfur.dioxide,

total.sulfur.dioxide, density, pH,

sulphates, alcoholquality

> fligner.test(quality ~ fixed.acidity, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by fixed.acidity

Fligner-Killeen:med chi-squared = 68.457, df = 95, p-value = 0.9818

> fligner.test(quality ~ volatile.acidity, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by volatile.acidity

Fligner-Killeen:med chi-squared = 147.35, df = 142, p-value = 0.3621

> fligner.test(quality ~ citric.acid, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by citric.acid

Fligner-Killeen:med chi-squared = 87.67, df = 79, p-value = 0.2362

> fligner.test(quality ~ residual.sugar, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by residual.sugar

Fligner-Killeen:med chi-squared = 85.881, df = 90, p-value = 0.6033

> fligner.test(quality ~ chlorides, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by chlorides

Fligner-Killeen:med chi-squared = 148.54, df = 152, p-value = 0.5642

> fligner.test(quality ~ free.sulfur.dioxide, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by free.sulfur.dioxide

Fligner-Killeen:med chi-squared = 52.989, df = 59, p-value = 0.6955

> fligner.test(quality ~ total.sulfur.dioxide, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by total.sulfur.dioxide

Fligner-Killeen:med chi-squared = 180.55, df = 143, p-value = 0.01832

> fligner.test(quality ~ density, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by density

Fligner-Killeen:med chi-squared = 364.74, df = 435, p-value = 0.9938

> fligner.test(quality ~ pH, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by pH

Fligner-Killeen:med chi-squared = 86.558, df = 88, p-value = 0.5235

> fligner.test(quality ~ sulfates, data = vino)

Error in eval(predvars, data, env) : objeto 'sulfates' no encontrado

> fligner.test(quality ~ sulphates, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by sulphates

Fligner-Killeen:med chi-squared = 120.2, df = 95, p-value = 0.04138

> fligner.test(quality ~ alcohol, data = vino)

Fligner-Killeen test of homogeneity of variances

data: quality by alcohol

Fligner-Killeen:med chi-squared = 135.98, df = 64, p-value = 4.157e-07

> corr\_matrix <- matrix(nc = 2, nr = 0)

> colnames(corr\_matrix) <- c("estimate", "p-value")

> for (i in 1:(ncol(vino) - 1)) {

+ if (is.integer(vino[,i]) | is.numeric(vino[,i])) {

+ spearman\_test = cor.test(vino[,i], vino[,length(vino)], method = "spearman")

+

+ corr\_coef = spearman\_test$estimate

+ p\_val = spearman\_test$p.value

+ pair = matrix(ncol = 2, nrow = 1)

+ pair[1][1] = corr\_coef

+ pair[2][1] = p\_val

+ corr\_matrix <- rbind(corr\_matrix, pair)

+ rownames(corr\_matrix)[nrow(corr\_matrix)] <- colnames(vino)[i]

+ }

+ }

There were 11 warnings (use warnings() to see them)

> warnings()

Warning messages:

1: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

2: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

3: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

4: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

5: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

6: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

7: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

8: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

9: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

10: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

11: In cor.test.default(vino[, i], vino[, length(vino)], method = "spearman") :

Cannot compute exact p-value with ties

> corr\_matrix <- matrix(nc = 2, nr = 0)

> colnames(corr\_matrix) <- c("estimate", "p-value")

> for (i in 1:(ncol(vino) - 1)) {

+ if (is.integer(vino[,i]) | is.numeric(vino[,i])) {

+ spearman\_test = cor.test(vino[,i], vino[,length(vino)], method = "spearman",exact=FALSE)

+ corr\_coef = spearman\_test$estimate

+ p\_val = spearman\_test$p.value

+ pair = matrix(ncol = 2, nrow = 1)

+ pair[1][1] = corr\_coef

+ pair[2][1] = p\_val

+ corr\_matrix <- rbind(corr\_matrix, pair)

+ rownames(corr\_matrix)[nrow(corr\_matrix)] <- colnames(vino)[i]

+ }

+ }

> print(corr\_matrix)

estimate p-value

fixed.acidity 0.11408367 4.801220e-06

volatile.acidity -0.38064651 2.734944e-56

citric.acid 0.21348091 6.158952e-18

residual.sugar 0.03204817 2.002454e-01

chlorides -0.18992234 1.882858e-14

free.sulfur.dioxide -0.05690065 2.288322e-02

total.sulfur.dioxide -0.19673508 2.046488e-15

density -0.17707407 9.918139e-13

pH -0.04367193 8.084594e-02

sulphates 0.37706020 3.477695e-55

alcohol 0.47853169 2.726838e-92

> vino2=vino

> vino2 %>%

+ mutate()

Error in vino2 %>% mutate() : no se pudo encontrar la función "%>%"

> vino2 %>%

+ mutate(alcohol2= case\_when(

+ alcohol>10.2~"alcohólico",

+ TRUE~"no alcohólico")

+ )

Error in vino2 %>% mutate(alcohol2 = case\_when(alcohol > 10.2 ~ "alcohólico", :

no se pudo encontrar la función "%>%"

> lybrary(dplyr)

Error in lybrary(dplyr) : no se pudo encontrar la función "lybrary"

> library(dplyr)

Attaching package: ‘dplyr’

The following objects are masked from ‘package:stats’:

filter, lag

The following objects are masked from ‘package:base’:

intersect, setdiff, setequal, union

> vino2 %>%

+ mutate(alcohol2= case\_when(

+ alcohol>10.2~"alcohólico",

+ TRUE~"no alcohólico")

+ )

fixed.acidity volatile.acidity citric.acid residual.sugar chlorides

1 7.4 0.700 0.00 1.90 0.076

2 7.8 0.880 0.00 2.60 0.098

3 7.8 0.760 0.04 2.30 0.092

4 11.2 0.280 0.56 1.90 0.075

5 7.4 0.700 0.00 1.90 0.076

6 7.4 0.660 0.00 1.80 0.075

7 7.9 0.600 0.06 1.60 0.069

8 7.3 0.650 0.00 1.20 0.065

9 7.8 0.580 0.02 2.00 0.073

10 7.5 0.500 0.36 6.10 0.071

11 6.7 0.580 0.08 1.80 0.097

12 7.5 0.500 0.36 6.10 0.071

13 5.6 0.615 0.00 1.60 0.089

14 7.8 0.610 0.29 1.60 0.114

15 8.9 0.620 0.18 3.80 0.176

16 8.9 0.620 0.19 3.90 0.170

17 8.5 0.280 0.56 1.80 0.092

18 8.1 0.560 0.28 1.70 0.368

19 7.4 0.590 0.08 4.40 0.086

20 7.9 0.320 0.51 1.80 0.341

21 8.9 0.220 0.48 1.80 0.077

22 7.6 0.390 0.31 2.30 0.082

23 7.9 0.430 0.21 1.60 0.106

24 8.5 0.490 0.11 2.30 0.084

25 6.9 0.400 0.14 2.40 0.085

26 6.3 0.390 0.16 1.40 0.080

27 7.6 0.410 0.24 1.80 0.080

28 7.9 0.430 0.21 1.60 0.106

29 7.1 0.710 0.00 1.90 0.080

30 7.8 0.645 0.00 2.00 0.082

31 6.7 0.675 0.07 2.40 0.089

32 6.9 0.685 0.00 2.50 0.105

33 8.3 0.655 0.12 2.30 0.083

34 6.9 0.605 0.12 10.70 0.073

35 5.2 0.320 0.25 1.80 0.103

36 7.8 0.645 0.00 5.50 0.086

37 7.8 0.600 0.14 2.40 0.086

38 8.1 0.380 0.28 2.10 0.066

39 5.7 1.130 0.09 1.50 0.172

40 7.3 0.450 0.36 5.90 0.074

41 7.3 0.450 0.36 5.90 0.074

42 8.8 0.610 0.30 2.80 0.088

43 7.5 0.490 0.20 2.60 0.332

44 8.1 0.660 0.22 2.20 0.069

45 6.8 0.670 0.02 1.80 0.050

46 4.6 0.520 0.15 2.10 0.054

47 7.7 0.935 0.43 2.20 0.114

48 8.7 0.290 0.52 1.60 0.113

49 6.4 0.400 0.23 1.60 0.066

50 5.6 0.310 0.37 1.40 0.074

51 8.8 0.660 0.26 1.70 0.074

52 6.6 0.520 0.04 2.20 0.069

53 6.6 0.500 0.04 2.10 0.068

54 8.6 0.380 0.36 3.00 0.081

55 7.6 0.510 0.15 2.80 0.110

56 7.7 0.620 0.04 3.80 0.084

57 10.2 0.420 0.57 3.40 0.070

58 7.5 0.630 0.12 5.10 0.111

59 7.8 0.590 0.18 2.30 0.076

60 7.3 0.390 0.31 2.40 0.074

61 8.8 0.400 0.40 2.20 0.079

62 7.7 0.690 0.49 1.80 0.115

63 7.5 0.520 0.16 1.90 0.085

64 7.0 0.735 0.05 2.00 0.081

65 7.2 0.725 0.05 4.65 0.086

66 7.2 0.725 0.05 4.65 0.086

67 7.5 0.520 0.11 1.50 0.079

68 6.6 0.705 0.07 1.60 0.076

69 9.3 0.320 0.57 2.00 0.074

70 8.0 0.705 0.05 1.90 0.074

71 7.7 0.630 0.08 1.90 0.076

72 7.7 0.670 0.23 2.10 0.088

73 7.7 0.690 0.22 1.90 0.084

74 8.3 0.675 0.26 2.10 0.084

75 9.7 0.320 0.54 2.50 0.094

76 8.8 0.410 0.64 2.20 0.093

free.sulfur.dioxide total.sulfur.dioxide density pH sulphates alcohol quality

1 11 34 0.9978 3.51 0.56 9.4 5

2 25 67 0.9968 3.20 0.68 9.8 5

3 15 54 0.9970 3.26 0.65 9.8 5

4 17 60 0.9980 3.16 0.58 9.8 6

5 11 34 0.9978 3.51 0.56 9.4 5

6 13 40 0.9978 3.51 0.56 9.4 5

7 15 59 0.9964 3.30 0.46 9.4 5

8 15 21 0.9946 3.39 0.47 10.0 7

9 9 18 0.9968 3.36 0.57 9.5 7

10 17 102 0.9978 3.35 0.80 10.5 5

11 15 65 0.9959 3.28 0.54 9.2 5

12 17 102 0.9978 3.35 0.80 10.5 5

13 16 59 0.9943 3.58 0.52 9.9 5

14 9 29 0.9974 3.26 1.56 9.1 5

15 52 145 0.9986 3.16 0.88 9.2 5

16 51 148 0.9986 3.17 0.93 9.2 5

17 35 103 0.9969 3.30 0.75 10.5 7

18 16 56 0.9968 3.11 1.28 9.3 5

19 6 29 0.9974 3.38 0.50 9.0 4

20 17 56 0.9969 3.04 1.08 9.2 6

21 29 60 0.9968 3.39 0.53 9.4 6

22 23 71 0.9982 3.52 0.65 9.7 5

23 10 37 0.9966 3.17 0.91 9.5 5

24 9 67 0.9968 3.17 0.53 9.4 5

25 21 40 0.9968 3.43 0.63 9.7 6

26 11 23 0.9955 3.34 0.56 9.3 5

27 4 11 0.9962 3.28 0.59 9.5 5

28 10 37 0.9966 3.17 0.91 9.5 5

29 14 35 0.9972 3.47 0.55 9.4 5

30 8 16 0.9964 3.38 0.59 9.8 6

31 17 82 0.9958 3.35 0.54 10.1 5

32 22 37 0.9966 3.46 0.57 10.6 6

33 15 113 0.9966 3.17 0.66 9.8 5

34 40 83 0.9993 3.45 0.52 9.4 6

35 13 50 0.9957 3.38 0.55 9.2 5

36 5 18 0.9986 3.40 0.55 9.6 6

37 3 15 0.9975 3.42 0.60 10.8 6

38 13 30 0.9968 3.23 0.73 9.7 7

39 7 19 0.9940 3.50 0.48 9.8 4

40 12 87 0.9978 3.33 0.83 10.5 5

41 12 87 0.9978 3.33 0.83 10.5 5

42 17 46 0.9976 3.26 0.51 9.3 4

43 8 14 0.9968 3.21 0.90 10.5 6

44 9 23 0.9968 3.30 1.20 10.3 5

45 5 11 0.9962 3.48 0.52 9.5 5

46 8 65 0.9934 3.90 0.56 13.1 4

47 22 114 0.9970 3.25 0.73 9.2 5

48 12 37 0.9969 3.25 0.58 9.5 5

49 5 12 0.9958 3.34 0.56 9.2 5

50 12 96 0.9954 3.32 0.58 9.2 5

51 4 23 0.9971 3.15 0.74 9.2 5

52 8 15 0.9956 3.40 0.63 9.4 6

53 6 14 0.9955 3.39 0.64 9.4 6

54 30 119 0.9970 3.20 0.56 9.4 5

55 33 73 0.9955 3.17 0.63 10.2 6

56 25 45 0.9978 3.34 0.53 9.5 5

57 4 10 0.9971 3.04 0.63 9.6 5

58 50 110 0.9983 3.26 0.77 9.4 5

59 17 54 0.9975 3.43 0.59 10.0 5

60 9 46 0.9962 3.41 0.54 9.4 6

61 19 52 0.9980 3.44 0.64 9.2 5

62 20 112 0.9968 3.21 0.71 9.3 5

63 12 35 0.9968 3.38 0.62 9.5 7

64 13 54 0.9966 3.39 0.57 9.8 5

65 4 11 0.9962 3.41 0.39 10.9 5

66 4 11 0.9962 3.41 0.39 10.9 5

67 11 39 0.9968 3.42 0.58 9.6 5

68 6 15 0.9962 3.44 0.58 10.7 5

69 27 65 0.9969 3.28 0.79 10.7 5

70 8 19 0.9962 3.34 0.95 10.5 6

71 15 27 0.9967 3.32 0.54 9.5 6

72 17 96 0.9962 3.32 0.48 9.5 5

73 18 94 0.9961 3.31 0.48 9.5 5

74 11 43 0.9976 3.31 0.53 9.2 4

75 28 83 0.9984 3.28 0.82 9.6 5

76 9 42 0.9986 3.54 0.66 10.5 5

alcohol2

1 no alcohólico

2 no alcohólico

3 no alcohólico

4 no alcohólico

5 no alcohólico

6 no alcohólico

7 no alcohólico

8 no alcohólico

9 no alcohólico

10 alcohólico

11 no alcohólico

12 alcohólico

13 no alcohólico

14 no alcohólico

15 no alcohólico

16 no alcohólico

17 alcohólico

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62 no alcohólico

63 no alcohólico

64 no alcohólico

65 alcohólico

66 alcohólico

67 no alcohólico

68 alcohólico

69 alcohólico

70 alcohólico

71 no alcohólico

72 no alcohólico

73 no alcohólico

74 no alcohólico

75 no alcohólico

76 alcohólico

[ reached 'max' / getOption("max.print") -- omitted 1523 rows ]

> View(vino2)

> vino2<-vino2 %>%

+ mutate(alcohol2= case\_when(

+ alcohol>10.2~"alcohólico",

+ TRUE~"no alcohólico")

+ )

> vino2.alcoholico.calidad <- vino2[vino2$alcohol2 == "alcoholico",]$quality

> vino2.noalcoholico.calidad <- vino2[vino2$alcohol2 == "no alcoholico",]$quality

> t.test(vino2.alcoholico.calidad, vino2.noalcoholico.calidad, alternative = "less")

Error in t.test.default(vino2.alcoholico.calidad, vino2.noalcoholico.calidad, :

not enough 'x' observations

> vino2.alcoholico.calidad <- vino2[vino2$alcohol2 == "alcohólico",]$quality

> vino2.noalcoholico.calidad <- vino2[vino2$alcohol2 == "no alcohólico",]$quality

> t.test(vino2.alcoholico.calidad, vino2.noalcoholico.calidad, alternative = "less")

Welch Two Sample t-test

data: vino2.alcoholico.calidad and vino2.noalcoholico.calidad

t = 17.584, df = 1417.3, p-value = 1

alternative hypothesis: true difference in means is less than 0

95 percent confidence interval:

-Inf 0.7202451

sample estimates:

mean of x mean of y

5.982827 5.324228

> afija = vino$fixed.acidity

> avolatil = vino$volatile.acidty

> acitrica = vino$citric.acid

> azucar = vino$residual.sugar

> avolatil = vino$volatile.acidity

> cloruro = vino$chlorides

> fazufre = vino$free.sulfur.dioxide

> tazufre = vino$total.sulfur.dioxide

> densidad = vino$density

> ph = vino$pH

> sulfato = vino$sulphates

> alcohol = vino$alcohol

> modelo1 <- lm(quality ~ afija – avolatil + acitrica + azucar - cloruro – fazufre – tazufre – densidad – ph + sulfato + alcohol, data = vino)

Error: unexpected input in "modelo1 <- lm(quality ~ afija –"

> modelo1 <- lm(calidad ~ afija – avolatil + acitrica + azucar - cloruro – fazufre – tazufre – densidad – ph + sulfato + alcohol, data = vino)

Error: unexpected input in "modelo1 <- lm(calidad ~ afija –"

> modelo1 <- lm(calidad ~ afija –avolatil + acitrica + azucar - cloruro – fazufre – tazufre – densidad – ph + sulfato + alcohol, data = vino)

Error: unexpected input in "modelo1 <- lm(calidad ~ afija –"

> calidad=vino$quality

> modelo1 <- lm(calidad ~ afija – avolatil + acitrica + azucar - cloruro – fazufre – tazufre – densidad – ph + sulfato + alcohol, data = vino)

Error: unexpected input in "modelo1 <- lm(calidad ~ afija –"

> modelo1 <- lm(calidad ~ afija – avolatil + acitrica + azucar - cloruro – fazufre – tazufre – densidad – ph + sulfato + alcohol, data = vino)

Error: unexpected input in "modelo1 <- lm(calidad ~ afija –"

> modelo1<-lm(calidad~afija-avolatil+acitrica+azucar-cloruro-fazufre-tazufre-denisdad-ph+sulfato+alcohol, data=vino)

Error in eval(predvars, data, env) : objeto 'denisdad' no encontrado

> modelo1<-lm(calidad~afija-avolatil+acitrica+azucar-cloruro-fazufre-tazufre-densidad-ph+sulfato+alcohol, data=vino)

> modelo2<-lm(calidad~afija-avolatil+acitrica-cloruro-tazufre-densidad+sulfato+alcohol, data=vino))

Error: inesperado ')' in "modelo2<-lm(calidad~afija-avolatil+acitrica-cloruro-tazufre-densidad+sulfato+alcohol, data=vino))"

> modelo2<-lm(calidad~afija-avolatil+acitrica-cloruro-tazufre-densidad+sulfato+alcohol, data=vino)

> modelo3<-lm(calidad~afija-avolatil+azucar-cloruro-fazufre-tazufre+sulfato+alcohol, data=vino)

> modelo4<-lm(calidad~avolatil-fazufre-tazufre-densidad-ph+sulfato+alcohol, data=vino)

> tabla.coeficientes <- matrix(c(1, summary(modelo1)$r.squared, 2, summary(modelo2)$r.squared, 3, summary(modelo3)$r.squared, 4, summary(modelo4)$r.squared), ncol = 2, byrow = TRUE)

>

> colnames(tabla.coeficientes) <- c("Modelo", "R^2")

> tabla.coeficientes

Modelo R^2

[1,] 1 0.2868853

[2,] 2 0.2862314

[3,] 3 0.2838601

[4,] 4 0.3358973

> modelo5<-lm(calidad~avolatil-fazufre-ph+sulfato+alcohol, data=vino)

> tabla.coeficientes <- matrix(c(1, summary(modelo1)$r.squared, 2, summary(modelo2)$r.squared, 3, summary(modelo3)$r.squared, 4, summary(modelo4)$r.squared, 5, summary(modelo5)$r.squared), ncol = 2, byrow = TRUE)

> colnames(tabla.coeficientes) <- c("Modelo", "R^2")

> tabla.coeficientes

Modelo R^2

[1,] 1 0.2868853

[2,] 2 0.2862314

[3,] 3 0.2838601

[4,] 4 0.3358973

[5,] 5 0.3358973

> save.image("~/PRA2\_Datos/Pra2\_Datos/Pra2.RData")

> modelo6<-lm(calidad~alcohol, data=vino)

> tabla.coeficientes <- matrix(c(1, summary(modelo1)$r.squared, 2, summary(modelo2)$r.squared, 3, summary(modelo3)$r.squared, 4, summary(modelo4)$r.squared, 5, summary(modelo5)$r.squared, 6, summary(modelo6)$r.squared), ncol = 2, byrow = TRUE)

> colnames(tabla.coeficientes) <- c("Modelo", "R^2")

> tabla.coeficientes

Modelo R^2

[1,] 1 0.2868853

[2,] 2 0.2862314

[3,] 3 0.2838601

[4,] 4 0.3358973

[5,] 5 0.3358973

[6,] 6 0.2267344

> library(psych)

Error in library(psych) : there is no package called ‘psych’

> install.packages("psych")

WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:

https://cran.rstudio.com/bin/windows/Rtools/

Installing package into ‘C:/Users/josej/Documents/R/win-library/3.6’

(as ‘lib’ is unspecified)

also installing the dependencies ‘tmvnsim’, ‘mnormt’

probando la URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/tmvnsim\_1.0-2.zip'

Content type 'application/zip' length 37318 bytes (36 KB)

downloaded 36 KB

probando la URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/mnormt\_2.0.2.zip'

Content type 'application/zip' length 201329 bytes (196 KB)

downloaded 196 KB

probando la URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/psych\_2.0.12.zip'

Content type 'application/zip' length 4807124 bytes (4.6 MB)

downloaded 4.6 MB

package ‘tmvnsim’ successfully unpacked and MD5 sums checked

package ‘mnormt’ successfully unpacked and MD5 sums checked

package ‘psych’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\josej\AppData\Local\Temp\Rtmpqggy1L\downloaded\_packages

> library(psych)

Warning message:

package ‘psych’ was built under R version 3.6.3

> corPlot(data=vino, cex = 1.2, main = "Matriz de correlación")

Error in corPlot(data = vino, cex = 1.2, main = "Matriz de correlación") :

el argumento "r" está ausente, sin valor por omisión

> plot(fixed.acidity, quality, pch = 19, col = "lightblue")

Error in plot(fixed.acidity, quality, pch = 19, col = "lightblue") :

objeto 'fixed.acidity' no encontrado

> plot(vino$fixed.acidity, vino$quality, pch = 19, col = "lightblue")

> abline(lm(vino$quality ~ vino$fixed.acidity), col = "red", lwd = 3)

> text(paste("Correlación:", round(cor(vino$fixed.acidity, vino$quality), 2)), vino$fixed.acidity = 25, vino$quality = 95)

Error: inesperado '=' in "text(paste("Correlación:", round(cor(vino$fixed.acidity, vino$quality), 2)), vino$fixed.acidity ="

> text(paste("Correlación:", round(cor(x, y), 2)), x = 25, y = 95)

Error in is.data.frame(y) : objeto 'y' no encontrado

> text(paste("Correlación:", round(cor(x, y), 2)), x = 25, y = 95)

Error in is.data.frame(y) : objeto 'y' no encontrado

> vino.cor<-cor(vino, method="pearson")

> round(vino.cor, digits=2)

fixed.acidity volatile.acidity citric.acid residual.sugar

fixed.acidity 1.00 -0.26 0.67 0.11

volatile.acidity -0.26 1.00 -0.55 0.00

citric.acid 0.67 -0.55 1.00 0.14

residual.sugar 0.11 0.00 0.14 1.00

chlorides 0.09 0.06 0.20 0.06

free.sulfur.dioxide -0.15 -0.01 -0.06 0.19

total.sulfur.dioxide -0.11 0.08 0.04 0.20

density 0.67 0.02 0.36 0.36

pH -0.68 0.23 -0.54 -0.09

sulphates 0.18 -0.26 0.31 0.01

alcohol -0.06 -0.20 0.11 0.04

quality 0.12 -0.39 0.23 0.01

chlorides free.sulfur.dioxide total.sulfur.dioxide density

fixed.acidity 0.09 -0.15 -0.11 0.67

volatile.acidity 0.06 -0.01 0.08 0.02

citric.acid 0.20 -0.06 0.04 0.36

residual.sugar 0.06 0.19 0.20 0.36

chlorides 1.00 0.01 0.05 0.20

free.sulfur.dioxide 0.01 1.00 0.67 -0.02

total.sulfur.dioxide 0.05 0.67 1.00 0.07

density 0.20 -0.02 0.07 1.00

pH -0.27 0.07 -0.07 -0.34

sulphates 0.37 0.05 0.04 0.15

alcohol -0.22 -0.07 -0.21 -0.50

quality -0.13 -0.05 -0.19 -0.17

pH sulphates alcohol quality

fixed.acidity -0.68 0.18 -0.06 0.12

volatile.acidity 0.23 -0.26 -0.20 -0.39

citric.acid -0.54 0.31 0.11 0.23

residual.sugar -0.09 0.01 0.04 0.01

chlorides -0.27 0.37 -0.22 -0.13

free.sulfur.dioxide 0.07 0.05 -0.07 -0.05

total.sulfur.dioxide -0.07 0.04 -0.21 -0.19

density -0.34 0.15 -0.50 -0.17

pH 1.00 -0.20 0.21 -0.06

sulphates -0.20 1.00 0.09 0.25

alcohol 0.21 0.09 1.00 0.48

quality -0.06 0.25 0.48 1.00

> corrplot(vino.cor)

Error in corrplot(vino.cor) : no se pudo encontrar la función "corrplot"

> install.packages("corrplot")

WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:

https://cran.rstudio.com/bin/windows/Rtools/

Installing package into ‘C:/Users/josej/Documents/R/win-library/3.6’

(as ‘lib’ is unspecified)

probando la URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/corrplot\_0.84.zip'

Content type 'application/zip' length 5450649 bytes (5.2 MB)

downloaded 5.2 MB

package ‘corrplot’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\josej\AppData\Local\Temp\Rtmpqggy1L\downloaded\_packages

> corrplot(vino.cor)

Error in corrplot(vino.cor) : no se pudo encontrar la función "corrplot"

> par(mfrow=c(1, 2))

> plot(x=vino$fixed.acidity, y=vino$quality)

> plot(x=vino$fixed.acidity, y=vino$quality, pch='.',

+ xlab='Fixed Acidity',

+ ylab='Calidad del vino')

> save.image("~/PRA2\_Datos/Pra2\_Datos/Pra2.RData")

> correlation\_matrix = vino.corr()

Error in vino.corr() : no se pudo encontrar la función "vino.corr"

> corrplot(cor(vino), method = "circle")

Error in corrplot(cor(vino), method = "circle") :

no se pudo encontrar la función "corrplot"

> install.packages("corrplot")

WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:

https://cran.rstudio.com/bin/windows/Rtools/

Installing package into ‘C:/Users/josej/Documents/R/win-library/3.6’

(as ‘lib’ is unspecified)

probando la URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/corrplot\_0.84.zip'

Content type 'application/zip' length 5450649 bytes (5.2 MB)

downloaded 5.2 MB

package ‘corrplot’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\josej\AppData\Local\Temp\Rtmpqggy1L\downloaded\_packages

> library("corrplot")

corrplot 0.84 loaded

Warning message:

package ‘corrplot’ was built under R version 3.6.3

> corrplot(cor(vino), method = "circle")

> install.packages("ggcorrplot")

WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:

https://cran.rstudio.com/bin/windows/Rtools/

Installing package into ‘C:/Users/josej/Documents/R/win-library/3.6’

(as ‘lib’ is unspecified)

probando la URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/ggcorrplot\_0.1.3.zip'

Content type 'application/zip' length 28911 bytes (28 KB)

downloaded 28 KB

package ‘ggcorrplot’ successfully unpacked and MD5 sums checked

The downloaded binary packages are in

C:\Users\josej\AppData\Local\Temp\Rtmpqggy1L\downloaded\_packages

> library("ggcorrplot")

Loading required package: ggplot2

Attaching package: ‘ggplot2’

The following objects are masked from ‘package:psych’:

%+%, alpha

Warning message:

package ‘ggcorrplot’ was built under R version 3.6.3

> ggcorrplot(cor(vino))

> save.image("~/PRA2\_Datos/Pra2\_Datos/Pra2.RData")

> pairs(vino)

> boxplot(vino2$quality ~ vino2$alcohol2, col = "blue", main = "Calidad del vino según alcohol")

> step(object = modelo1, direction = "both", trace = 1)

Start: AIC=-1213.14

calidad ~ afija - avolatil + acitrica + azucar - cloruro - fazufre -

tazufre - densidad - ph + sulfato + alcohol

Df Sum of Sq RSS AIC

- azucar 1 0.681 743.86 -1213.67

<none> 743.18 -1213.14

- afija 1 2.789 745.97 -1209.15

- acitrica 1 3.153 746.34 -1208.37

- sulfato 1 27.373 770.56 -1157.30

- alcohol 1 206.821 950.00 -822.55

Step: AIC=-1213.67

calidad ~ afija + acitrica + sulfato + alcohol

Df Sum of Sq RSS AIC

<none> 743.86 -1213.67

+ azucar 1 0.681 743.18 -1213.14

- afija 1 2.712 746.58 -1209.86

- acitrica 1 2.918 746.78 -1209.41

- sulfato 1 27.795 771.66 -1157.01

- alcohol 1 206.250 950.11 -824.36

Call:

lm(formula = calidad ~ afija + acitrica + sulfato + alcohol,

data = vino)

Coefficients:

(Intercept) afija acitrica sulfato alcohol

1.1382 0.0325 0.3121 0.8211 0.3456

> modelo7<-lm(calidad~afija + acitrica + sulfato + alcohol, data=vino)

> library(ggplot2)

> library(gridExtra)

Attaching package: ‘gridExtra’

The following object is masked from ‘package:dplyr’:

combine

> library(dplyr)

> plot1 <- ggplot(data = vino, aes(acidezfija, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> plot2 <- ggplot(data = vino, aes(acidocitrico, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> plot3 <- ggplot(data = vino, aes(sulfato, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> plot4 <- ggplot(data = vino, aes(alcohol, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> grid.arrange(plot1, plot2, plot3, plot4)

Error in FUN(X[[i]], ...) : objeto 'acidezfija' no encontrado

> plot1 <- ggplot(data = vino, aes(afija, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> plot2 <- ggplot(data = vino, aes(acitrica, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> plot3 <- ggplot(data = vino, aes(sulfato, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> plot4 <- ggplot(data = vino, aes(alcohol, modelo7$residuals)) + geom\_point() + geom\_smooth(color = "firebrick") + geom\_hline(yintercept = 0) + theme\_bw()

> grid.arrange(plot1, plot2, plot3, plot4)

`geom\_smooth()` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'

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> qqnorm(modelo7$residuals)

> qqline(modelo7$residuals)

> qqnorm(modelo7$residuals)

> qqline(modelo7$residuals)

> shapiro.test(modelo7$residuals)

Shapiro-Wilk normality test

data: modelo7$residuals

W = 0.9819, p-value = 2.58e-13