

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 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

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70 alcohólico

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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.acidity
> 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'

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

> 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