

Práctica 2: Limpieza y validación de los datos

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Carga de los datos

En esta actividad se usará el fichero winequality-red.csv del repositorio Github, el cual precisa tareas de preprocesado (limpieza, integración y validación) para posterior análisis. Los datos a tratar corresponden a variables fisicoquímicas correspondientes a variantes rojas del vino portugués “Vinho Verde”, las cuales se prestan a tareas de clasificación o análisis de regresión. Las clases están ordenadas y no son equilibradas (por ejemplo, hay muchos más vinos normales que vinos excelentes o pobres).

El archivo se denomina *C:/Users/Antonio/Desktop/UOC/Tipología y ciclo de vida de los datos/PRAC2/winequality-red.csv*, contiene 1599 registros y 12 variables. Estas variables son: fixed.acidity, volatile.acidity, citric.acid, residual.sugar, chlorides, free.sulfur.dioxide, total.sulfur.dioxide, density, pH, sulphates, alcohol, quality

```
# Cargo el archivo de datos "winequality-red.csv" y valido que los tipos
# de datos se interpretan correctamente
winequality.red <- read.csv("C:/Users/Antonio/Desktop/UOC/Tipología y
ciclo de vida de los datos/PRAC2/winequality-red.csv", stringsAsFactors =
FALSE, header = TRUE)
head(winequality.red[,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
```

Resolución

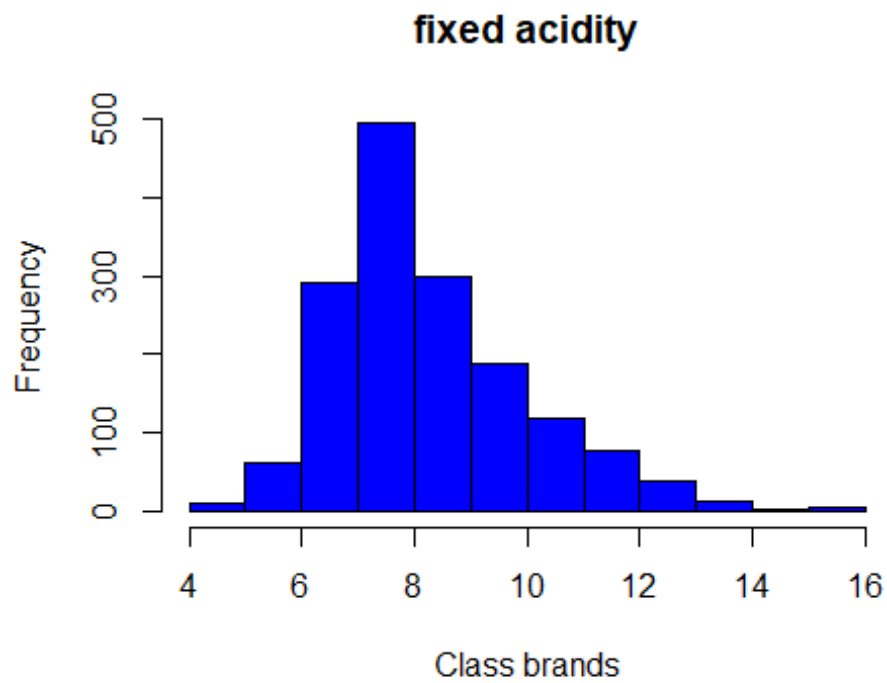
Examinamos el tipo de dato asociado a cada campo

```
# Tipo de dato asignado a cada campo
sapply(winequality.red, function(x) class(x))

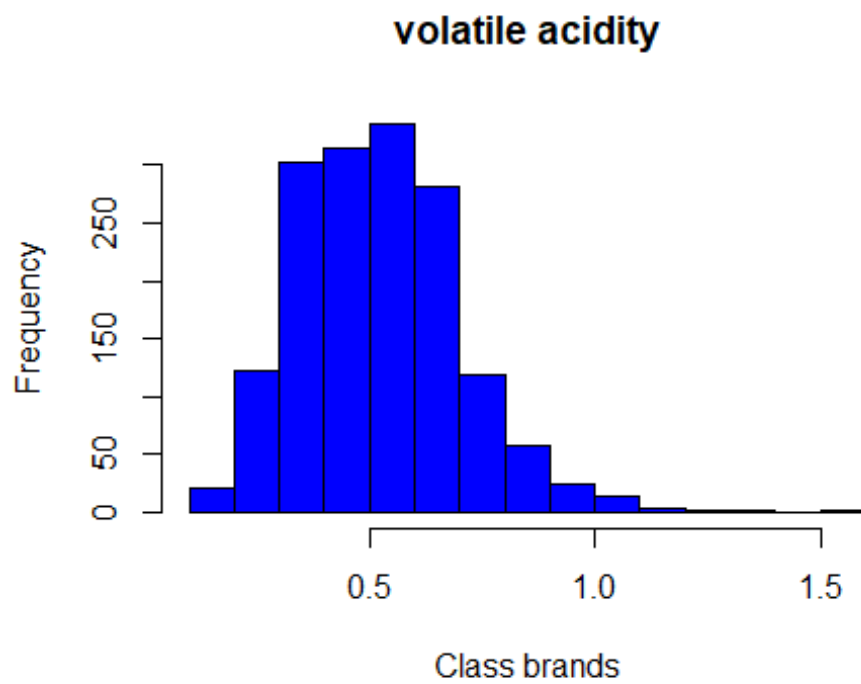
##      fixed.acidity      volatile.acidity      citric.acid
##      "numeric"      "numeric"      "numeric"
##      residual.sugar      chlorides      free.sulfur.dioxide
##      "numeric"      "numeric"      "numeric"
##      total.sulfur.dioxide      density      pH
##      "numeric"      "numeric"      "numeric"
##      sulphates      alcohol      quality
##      "numeric"      "numeric"      "integer"
```

Histograma de frecuencias absolutas para cada variable fisicoquímica

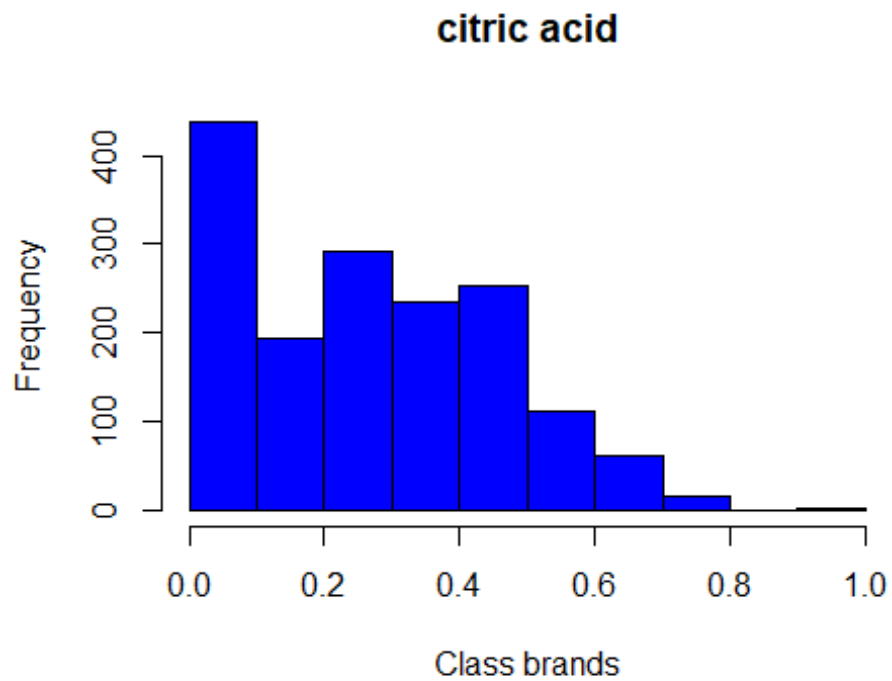
```
# Histograma de frecuencias absolutas de las variables fisicoquímicas
hist(winequality.red$fixed.acidity, main="fixed acidity", xlab="Class
brands", ylab="Frequency", col="blue")
```



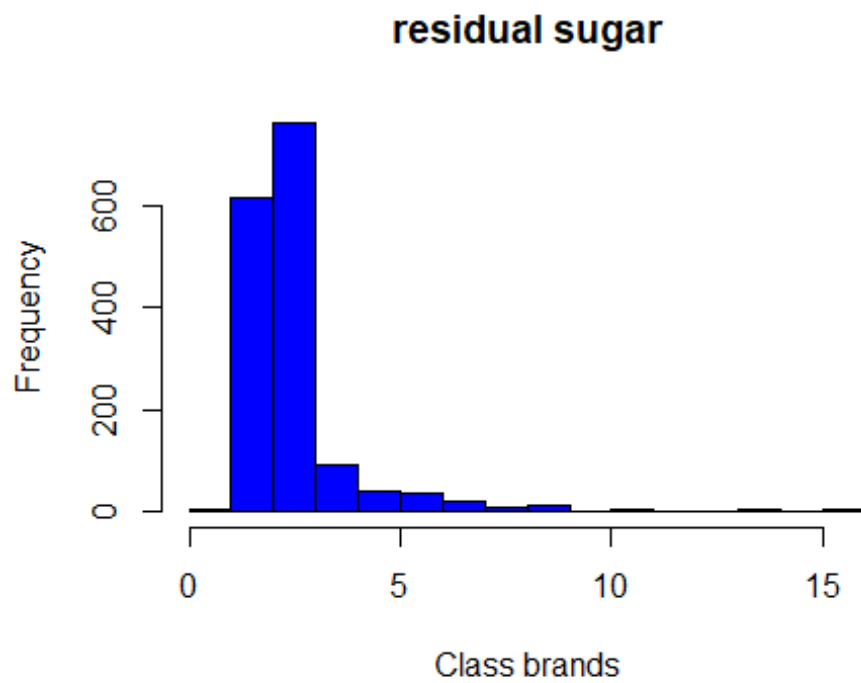
```
hist(winequality.red$volatile.acidity, main="volatile acidity",  
xlab="Class brands", ylab="Frequency", col="blue")
```



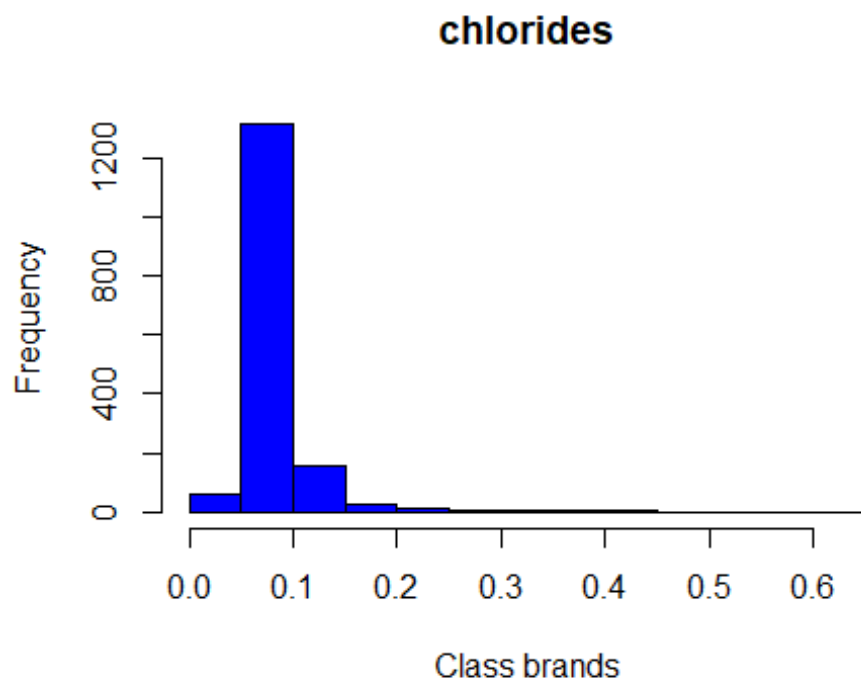
```
hist(winequality.red$citric.acid, main="citric acid", xlab="Class  
brands", ylab="Frequency", col="blue")
```



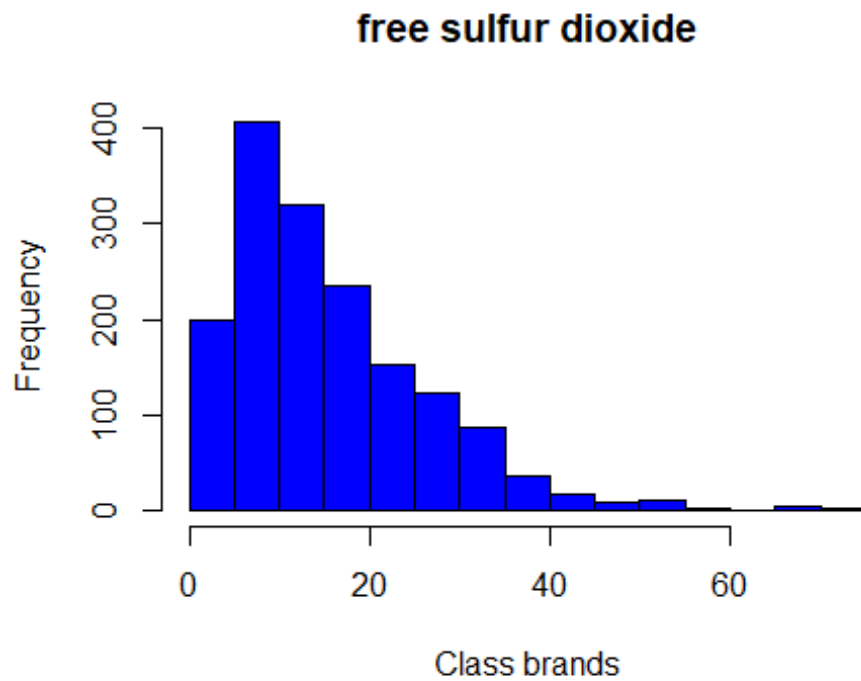
```
hist(winequality.red$residual.sugar, main="residual sugar", xlab="Class  
brands", ylab="Frequency", col="blue")
```



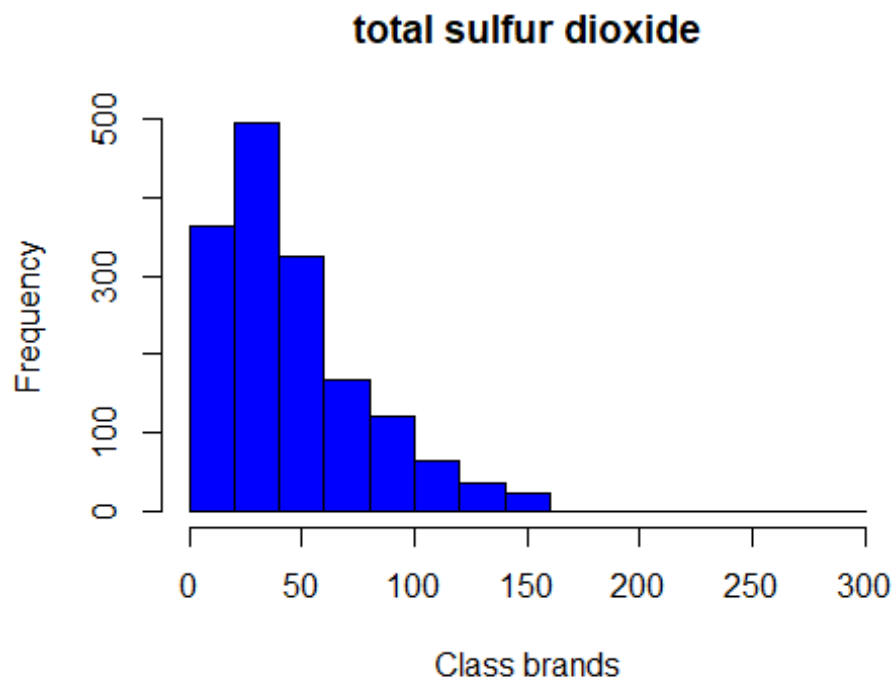
```
hist(winequality.red$chlorides, main="chlorides", xlab="Class brands",  
ylab="Frequency", col="blue")
```



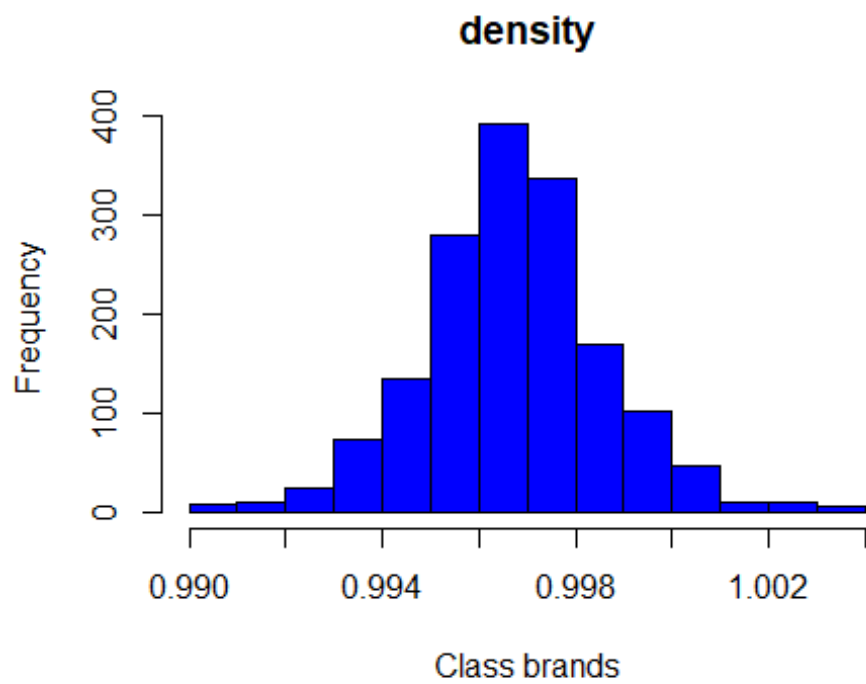
```
hist(winequality.red$free.sulfur.dioxide, main="free sulfur dioxide",  
xlab="Class brands", ylab="Frequency", col="blue")
```



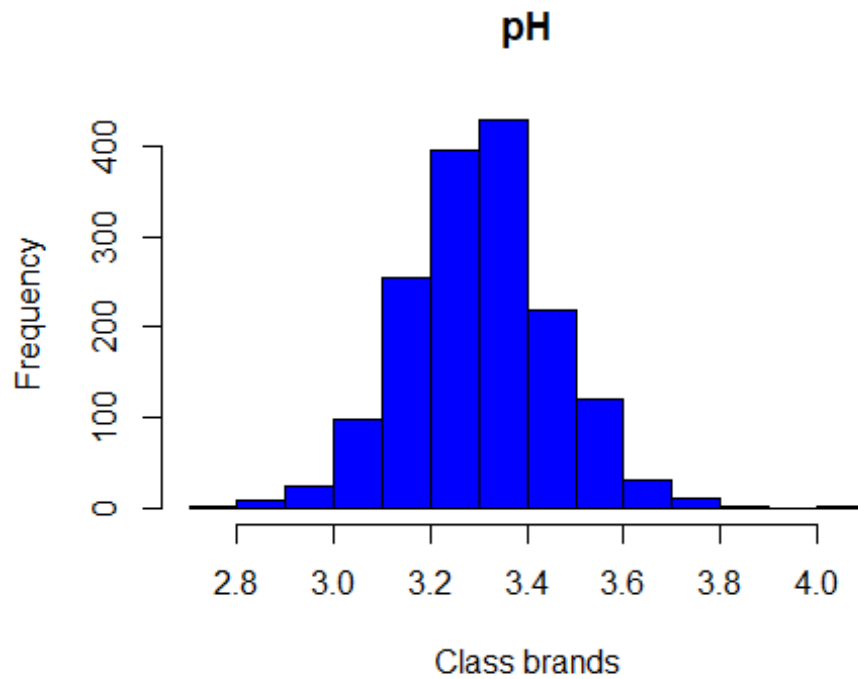
```
hist(winequality.red$total.sulfur.dioxide, main="total sulfur dioxide",  
xlab="Class brands", ylab="Frequency", col="blue")
```



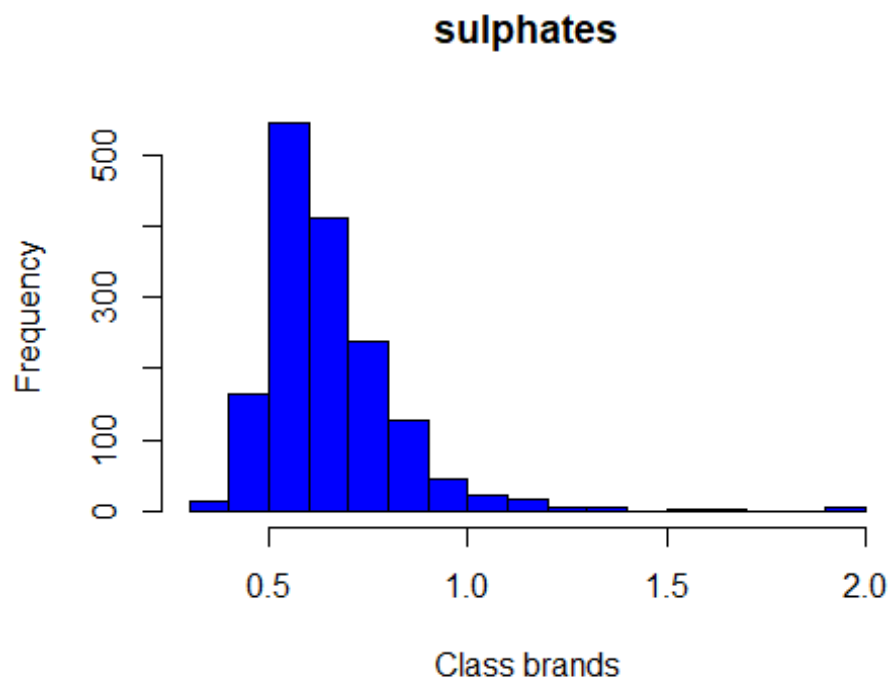
```
hist(winequality.red$density, main="density", xlab="Class brands",  
ylab="Frequency", col="blue")
```



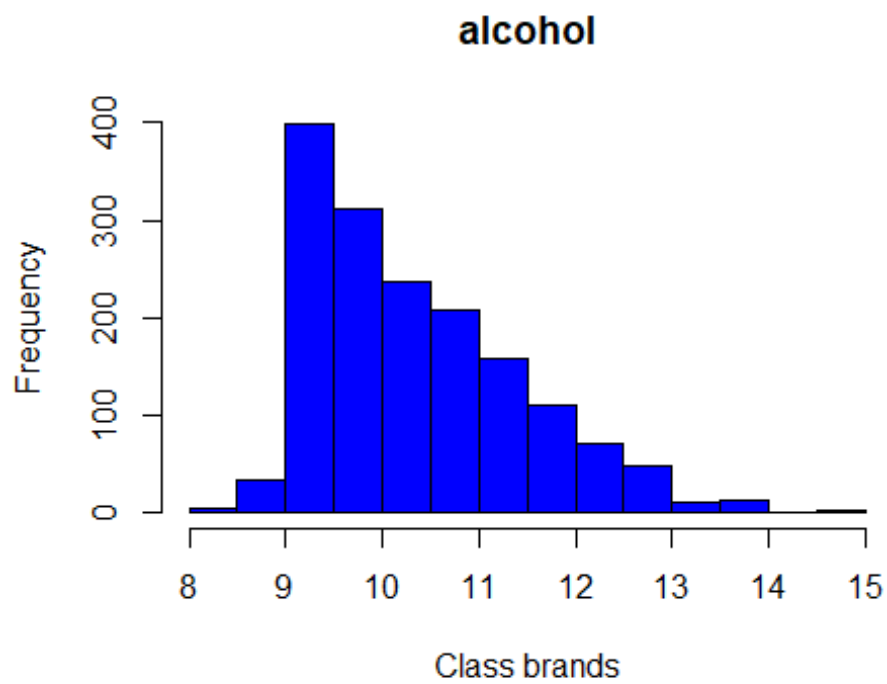
```
hist(winequality.red$pH, main="pH", xlab="Class brands",  
ylab="Frequency", col="blue")
```



```
hist(winequality.red$sulphates, main="sulphates", xlab="Class brands",  
ylab="Frequency", col="blue")
```

```
hist(winequality.red$alcohol, main="alcohol", xlab="Class brands",  
ylab="Frequency", col="blue")
```



```
hist(winequality.red$quality, main="quality", xlab="Class brands",
ylab="Frequency", col="blue", breaks = 5)
```



Integración y selección de los datos de interés

En esta sección, eliminamos columnas innecesarias o redundantes y fijamos el número de cifras decimales que deben contemplar. Se establece la columna “quality” de tipo numérico para facilitar cálculos y resultados posteriores.

```
# Eliminación de datos de columnas redundantes
winequality.red <- winequality.red[, -(6:6)]
# Unimos las dos columnas de acidez (fija y volátil) en una sola columna
winequality.red$fixed.acidity<-winequality.red$fixed.acidity +
winequality.red$volatile.acidity
winequality.red$fixed.acidity<-round(winequality.red$fixed.acidity,2)
colnames(winequality.red)[colnames(winequality.red)=="fixed.acidity"] <-
"acidity"
# Ahora que ya disponemos de la acidez total, eliminamos la columna
"volatile.acidity":
winequality.red <- winequality.red[, -(2:2)]
head(winequality.red)

##  acidity citric.acid residual.sugar chlorides total.sulfur.dioxide
## 1    8.10         0.00         1.9    0.076                34
```

```
## 2      8.68      0.00      2.6      0.098      67
## 3      8.56      0.04      2.3      0.092      54
## 4     11.48      0.56      1.9      0.075      60
## 5      8.10      0.00      1.9      0.076      34
## 6      8.06      0.00      1.8      0.075      40
## density pH sulphates alcohol quality
## 1 0.9978 3.51      0.56      9.4      5
## 2 0.9968 3.20      0.68      9.8      5
## 3 0.9970 3.26      0.65      9.8      5
## 4 0.9980 3.16      0.58      9.8      6
## 5 0.9978 3.51      0.56      9.4      5
## 6 0.9978 3.51      0.56      9.4      5

# Establecemos el número de cifras decimales en las columnas "acidity",
# "citric.acid" "chlorides" y "density"
winequality.red$acidity<-round(winequality.red$acidity, 2)
winequality.red$citric.acid<-round(winequality.red$citric.acid, 2)
winequality.red$chlorides<-round(winequality.red$chlorides, 3)
winequality.red$density<-round(winequality.red$density, 4)
# Convertimos la columna "quality" a tipo "numeric":
winequality.red$quality<-as.numeric(winequality.red$quality)
class(winequality.red$quality)

## [1] "numeric"
```

Detección de ceros y elementos vacíos por campo

En esta sección, se lleva a cabo la detección de ceros y elementos vacíos por campo

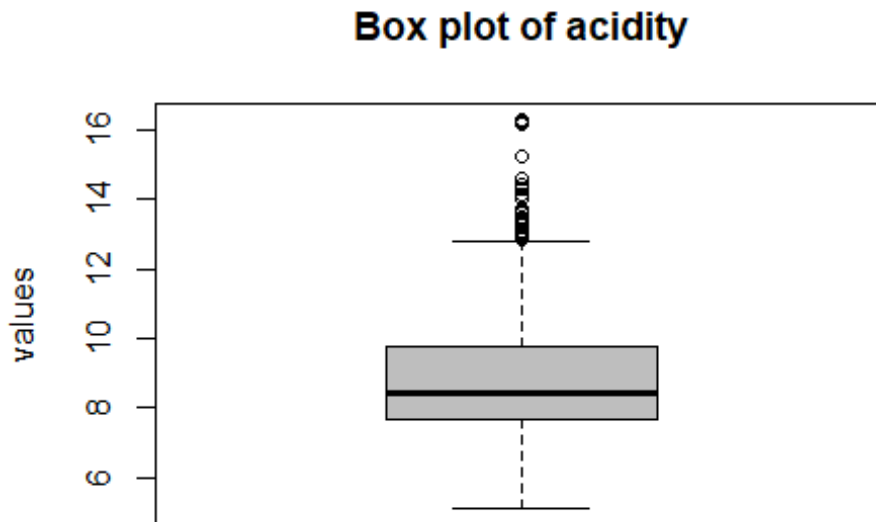
```
# Número de valores desconocidos por campo
sapply(winequality.red, function(x) sum(is.na(x)))

##          acidity          citric.acid      residual.sugar
##              0              0              0
## chlorides total.sulfur.dioxide          density
##              0              0              0
##          pH          sulphates          alcohol
##              0              0              0
##          quality
##              0
```

Valores extremos

Identificamos outliers de cada variable fisicoquímica mediante diagramas de caja y usando la función `boxplots.stats()` de R.

```
boxplot(winequality.red$acidity,main="Box plot of acidity",
col="gray",ylab="values")
```

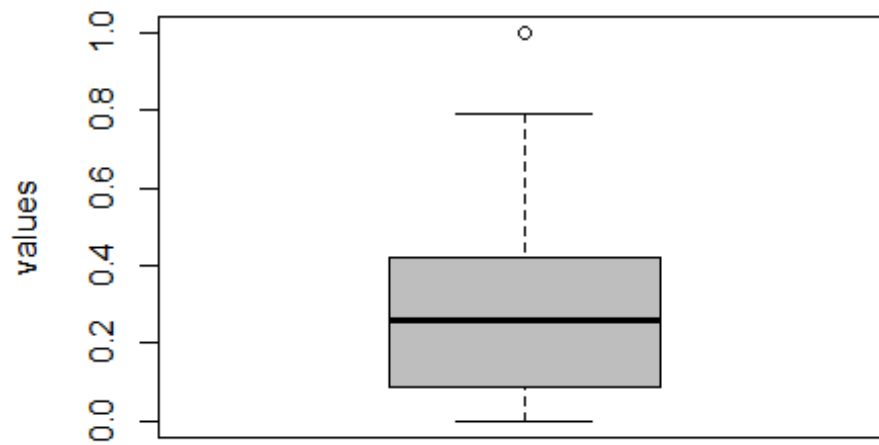


```
boxplot.stats(winequality.red$acidity)$out
```

```
## [1] 13.10 13.10 15.21 15.21 13.06 13.64 13.67 12.89 14.29 14.03 12.98
## [12] 12.96 13.42 13.42 14.41 14.11 14.11 13.30 12.96 13.64 12.91 16.29
## [23] 12.88 13.32 12.87 13.59 13.10 13.25 14.61 16.14 16.14 16.25 13.47
## [34] 13.30 13.47 13.30 13.29 13.66 13.66 13.58 16.26 13.73 13.40 13.01
## [45] 12.99
```

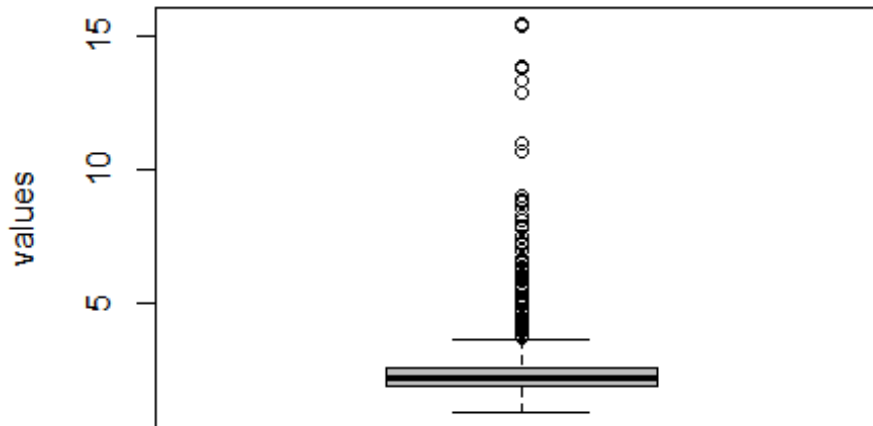
```
boxplot(winequality.red$citric.acid,main="Box plot of citric acid",
col="gray",ylab="values")
```

Box plot of citric acid



```
boxplot.stats(winequality.red$citric.acid)$out
## [1] 1
boxplot(winequality.red$residual.sugar,main="Box plot of residual sugar",
col="gray",ylab="values")
```

Box plot of residual sugar



```
boxplot.stats(winequality.red$residual.sugar)$out
```

```
## [1] 6.10 6.10 3.80 3.90 4.40 10.70 5.50 5.90 5.90 3.80
5.10
## [12] 4.65 4.65 5.50 5.50 5.50 5.50 7.30 7.20 3.80 5.60
4.00
## [23] 4.00 4.00 4.00 7.00 4.00 4.00 6.40 5.60 5.60 11.00
11.00
## [34] 4.50 4.80 5.80 5.80 3.80 4.40 6.20 4.20 7.90 7.90
3.70
## [45] 4.50 6.70 6.60 3.70 5.20 15.50 4.10 8.30 6.55 6.55
4.60
## [56] 6.10 4.30 5.80 5.15 6.30 4.20 4.20 4.60 4.20 4.60
4.30
## [67] 4.30 7.90 4.60 5.10 5.60 5.60 6.00 8.60 7.50 4.40
4.25
## [78] 6.00 3.90 4.20 4.00 4.00 4.00 6.60 6.00 6.00 3.80
9.00
## [89] 4.60 8.80 8.80 5.00 3.80 4.10 5.90 4.10 6.20 8.90
4.00
## [100] 3.90 4.00 8.10 8.10 6.40 6.40 8.30 8.30 4.70 5.50
5.50
## [111] 4.30 5.50 3.70 6.20 5.60 7.80 4.60 5.80 4.10 12.90
4.30
## [122] 13.40 4.80 6.30 4.50 4.50 4.30 4.30 3.90 3.80 5.40
3.80
## [133] 6.10 3.90 5.10 5.10 3.90 15.40 15.40 4.80 5.20 5.20
```

```

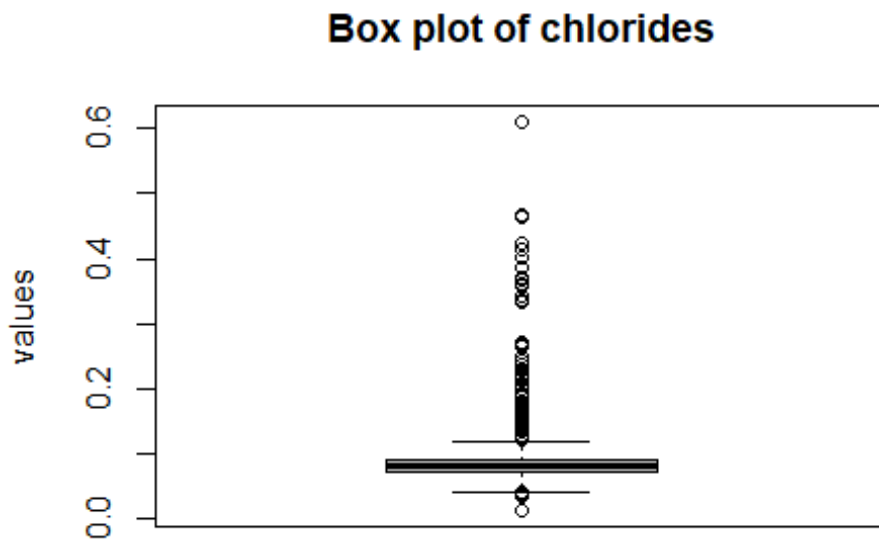
3.75
## [144] 13.80 13.80  5.70  4.30  4.10  4.10  4.40  3.70  6.70 13.90
5.10
## [155]  7.80

```

```

boxplot(winequality.red$chlorides,main="Box plot of chlorides",
col="gray",ylab="values")

```



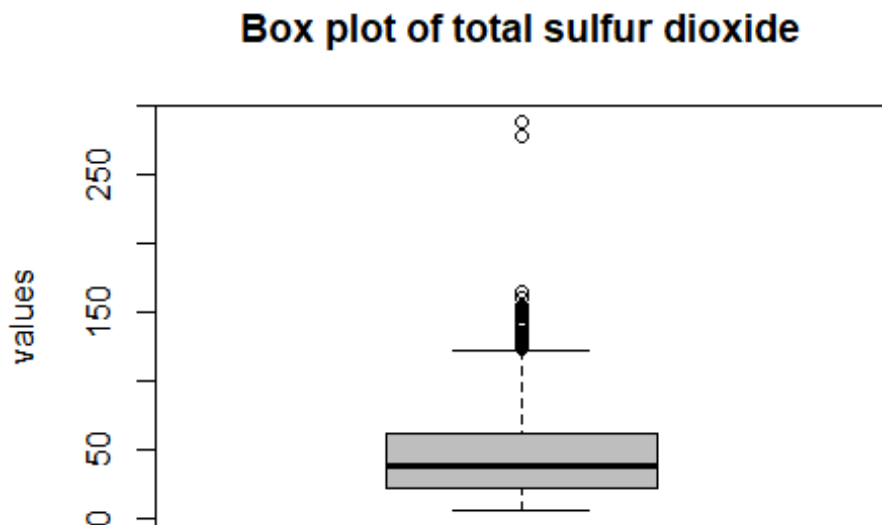
```

boxplot.stats(winequality.red$chlorides)$out
## [1] 0.176 0.170 0.368 0.341 0.172 0.332 0.464 0.401 0.467 0.122
0.178
## [12] 0.146 0.236 0.610 0.360 0.270 0.039 0.337 0.263 0.611 0.358
0.343
## [23] 0.186 0.213 0.214 0.121 0.122 0.122 0.128 0.120 0.159 0.124
0.122
## [34] 0.122 0.174 0.121 0.127 0.413 0.152 0.152 0.125 0.122 0.200
0.171
## [45] 0.226 0.226 0.250 0.148 0.122 0.124 0.124 0.143 0.222 0.039
0.157
## [56] 0.422 0.034 0.387 0.415 0.157 0.157 0.243 0.241 0.190 0.132
0.126
## [67] 0.038 0.165 0.145 0.147 0.012 0.012 0.039 0.194 0.132 0.161
0.120
## [78] 0.120 0.123 0.123 0.414 0.216 0.171 0.178 0.369 0.166 0.166
0.136
## [89] 0.132 0.132 0.123 0.123 0.123 0.403 0.137 0.414 0.166 0.168

```

```
0.415
## [100] 0.153 0.415 0.267 0.123 0.214 0.214 0.169 0.205 0.205 0.039
0.235
## [111] 0.230 0.038
```

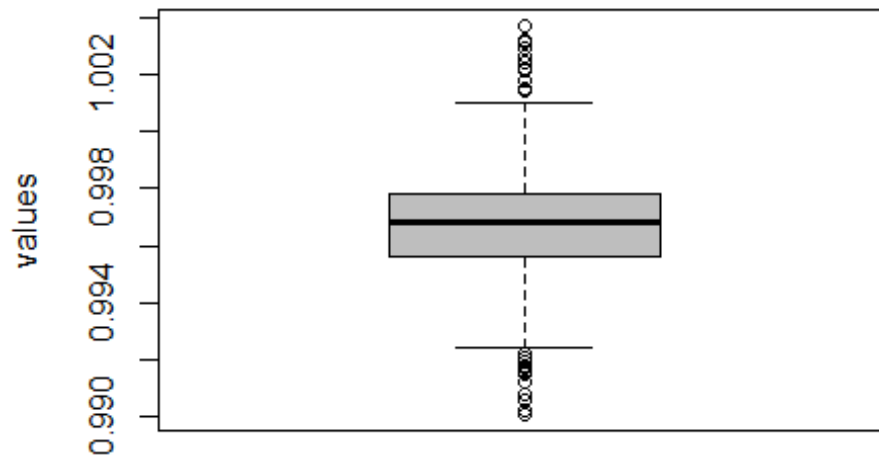
```
boxplot(winequality.red$total.sulfur.dioxide,main="Box plot of total
sulfur dioxide", col="gray",ylab="values")
```



```
boxplot.stats(winequality.red$total.sulfur.dioxide)$out
## [1] 145 148 136 125 140 136 133 153 134 141 129 128 129 128 143 144
127
## [18] 126 145 144 135 165 124 124 134 124 129 151 133 142 149 147 145
148
## [35] 155 151 152 125 127 139 143 144 130 278 289 135 160 141 141 133
147
## [52] 147 131 131 131
```

```
boxplot(winequality.red$density,main="Box plot of density",
col="gray",ylab="values")
```


Box plot of density

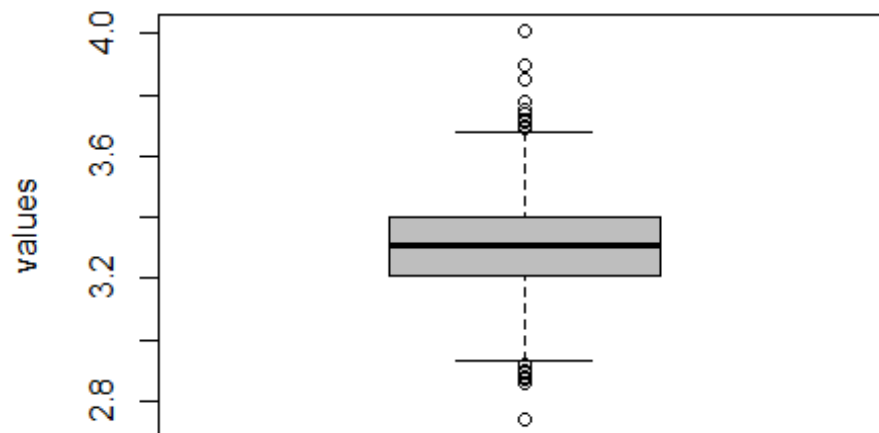


```
boxplot.stats(winequality.red$density)$out
```

```
## [1] 0.9916 0.9916 1.0014 1.0015 1.0015 1.0018 0.9912 1.0022 1.0022  
1.0014  
## [11] 1.0014 1.0014 1.0014 1.0032 1.0026 1.0014 1.0031 1.0031 1.0031  
1.0021  
## [21] 1.0021 0.9917 0.9922 1.0026 0.9921 0.9915 0.9906 0.9906 1.0029  
0.9916  
## [31] 0.9901 0.9901 0.9902 0.9922 0.9915 0.9916 0.9908 0.9908 0.9919  
1.0037  
## [41] 1.0037 1.0024 0.9918 1.0024 0.9918
```

```
boxplot(winequality.red$pH,main="Box plot of pH",  
col="gray",ylab="values")
```

Box plot of pH



```
boxplot.stats(winequality.red$pH)$out
```

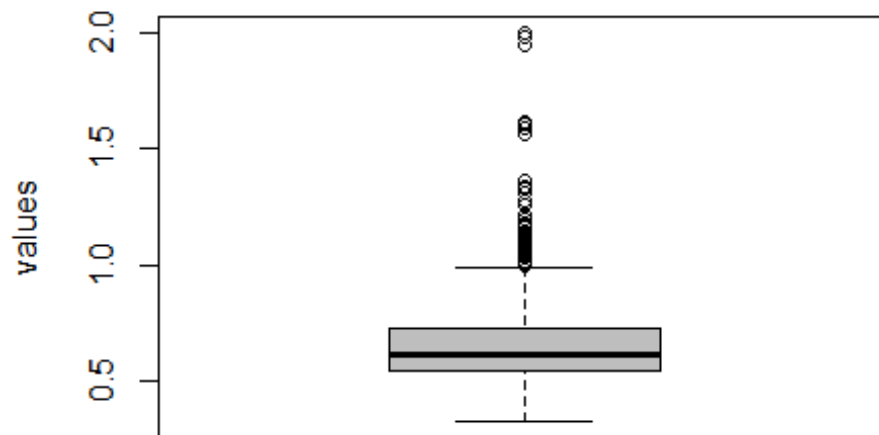
```
## [1] 3.90 3.75 3.85 2.74 3.69 3.69 2.88 2.86 3.74 2.92 2.92 2.92 3.72  
2.87
```

```
## [15] 2.89 2.89 2.92 3.90 3.71 3.69 3.69 3.71 3.71 2.89 2.89 3.78 3.70  
3.78
```

```
## [29] 4.01 2.90 4.01 3.71 2.88 3.72 3.72
```

```
boxplot(winequality.red$sulphates,main="Box plot of sulphates",  
col="gray",ylab="values")
```

Box plot of sulphates

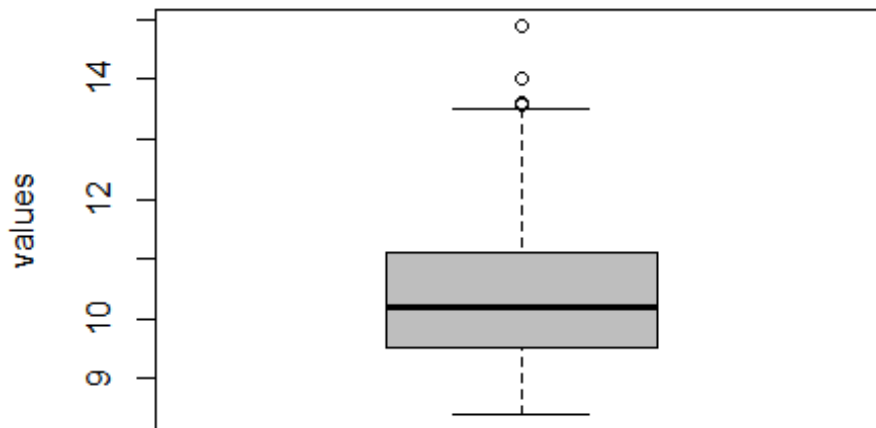


```
boxplot.stats(winequality.red$sulphates)$out
```

```
## [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  
## [15] 1.59 1.02 1.03 1.61 1.09 1.26 1.08 1.00 1.36 1.18 1.13 1.04 1.11  
1.13  
## [29] 1.07 1.06 1.06 1.05 1.06 1.04 1.05 1.02 1.14 1.02 1.36 1.36 1.05  
1.17  
## [43] 1.62 1.06 1.18 1.07 1.34 1.16 1.10 1.15 1.17 1.17 1.33 1.18 1.17  
1.03  
## [57] 1.17 1.10 1.01
```

```
boxplot(winequality.red$alcohol,main="Box plot of alcohol",  
col="gray",ylab="values")
```

Box plot of alcohol



```
boxplot.stats(winequality.red$alcohol)$out

## [1] 14.00000 14.00000 14.00000 14.00000 14.90000 14.00000 13.60000
## [8] 13.60000 13.60000 14.00000 14.00000 13.56667 13.60000

# Eliminamos valores outliers de cada una de las variables
fisicoquímicas.

outliers.acidity <- boxplot(winequality.red$acidity, plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$acidity %in%
outliers.acidity),]

outliers.citric.acid <- boxplot(winequality.red$citric.acid,
plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$citric.acid
%in% outliers.citric.acid),]

outliers.residual.sugar <- boxplot(winequality.red$residual.sugar,
plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$residual.sugar
%in% outliers.residual.sugar),]

outliers.chlorides <- boxplot(winequality.red$chlorides, plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$chlorides %in%
outliers.chlorides),]

outliers.total.sulfur.dioxide <-
```

```

boxplot(winequality.red$total.sulfur.dioxide, plot=FALSE)$out
winequality.red <- winequality.red[-
which(winequality.red$total.sulfur.dioxide %in%
outliers.total.sulfur.dioxide),]

outliers.density <- boxplot(winequality.red$density, plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$density %in%
outliers.density),]

outliers.pH <- boxplot(winequality.red$pH, plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$pH %in%
outliers.pH),]

outliers.sulphates <- boxplot(winequality.red$sulphates, plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$sulphates %in%
outliers.sulphates),]

outliers.alcohol <- boxplot(winequality.red$alcohol, plot=FALSE)$out
winequality.red <- winequality.red[-which(winequality.red$alcohol %in%
outliers.alcohol),]

# Número de columnas y registros o filas del nuevo dataset
ncol(winequality.red)

## [1] 10

nrow(winequality.red)

## [1] 1182

```

Exportación de los datos preprocesados

Una vez limpiados los datos, los guardamos en un fichero llamado winequality-red_data_clean.csv

```

write.csv(winequality.red, "C:/Users/Antonio/Desktop/UOC/Tipología y
ciclo de vida de los datos/PRAC2/winequality-red_data_clean.csv")

```

Análisis de resultados

Selección de los grupos de datos que se quieren comparar

Establecemos grupos dentro del conjunto de datos para posteriores análisis y comparaciones.

```
# Agrupación por valores de densidad
low.density <- winequality.red[winequality.red$density <=
mean(winequality.red$density),]
high.density <- winequality.red[winequality.red$density >
mean(winequality.red$density),]

# Agrupación por porcentaje de alcohol en vino
low.alcohol.percentage<- winequality.red[winequality.red$alcohol <=
11.5,]
high.alcohol.percentage <- winequality.red[winequality.red$alcohol >
11.5,]

# Agrupación por cantidad de sal presente en el vino
low.clhorides <- winequality.red[winequality.red$chlorides <=
mean(winequality.red$chlorides),]
high.clhorides <- winequality.red[winequality.red$chlorides >
mean(winequality.red$chlorides),]
```

Pruebas de normalidad y homogeneidad de la varianza

Pruebas de normalidad de Anderson-Darling

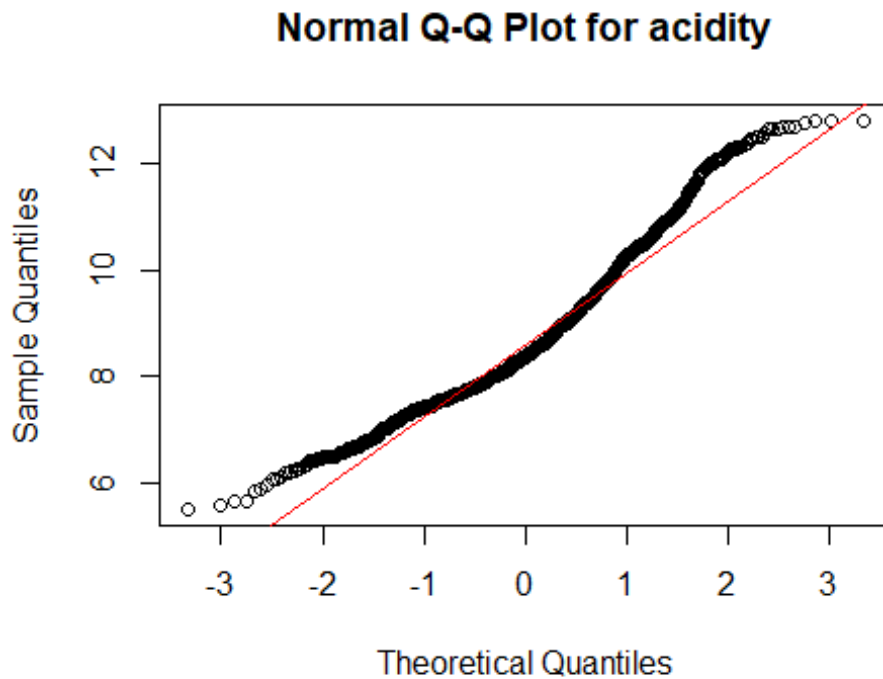
```
library(nortest)
alpha = 0.05
col.names = colnames(winequality.red)
for (i in 1:ncol(winequality.red)) {
  if (i == 1) cat("Listado de variables fisicoquímicas que no siguen una
distribución normal:\n")
  if (is.integer(winequality.red[,i]) | is.numeric(winequality.red[,i])) {
    p_val = ad.test(winequality.red[,i])$p.value
    if (p_val < alpha) {
      cat(col.names[i])
    }
  }
  # Format output
  if (i < ncol(winequality.red) - 1) cat(", ")
  if (i %% 3 == 0) cat("\n")
}
}
}

## Listado de variables fisicoquímicas que no siguen una distribución
normal:
```

```
## acidity, citric.acid, residual.sugar,  
## chlorides, total.sulfur.dioxide, density,  
## pH, sulphates, alcohol  
## quality
```

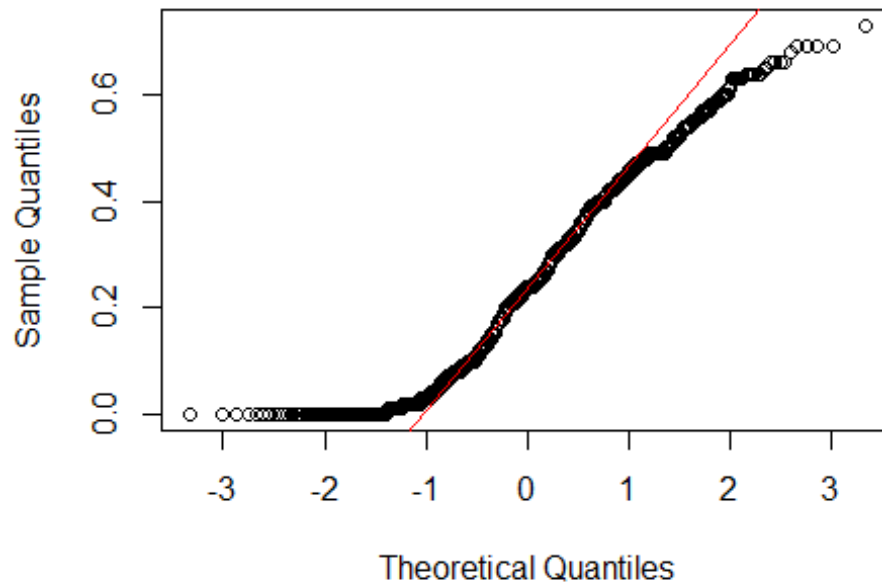
Test de normalidad Shapiro-Wilk y gráficos Q-Q

```
qqnorm(winequality.red$acidity, main = "Normal Q-Q Plot for acidity")  
qqline(winequality.red$acidity, col = "red")
```



```
shapiro.test(winequality.red$acidity)  
  
##  
##  Shapiro-Wilk normality test  
##  
## data:  winequality.red$acidity  
## W = 0.95654, p-value < 2.2e-16  
  
qqnorm(winequality.red$citric.acid, main = "Normal Q-Q Plot for citric  
acid")  
qqline(winequality.red$citric.acid, col = "red")
```

Normal Q-Q Plot for citric acid



```
shapiro.test(winequality.red$citric.acid)
```

```
##
```

```
##  Shapiro-Wilk normality test
```

```
##
```

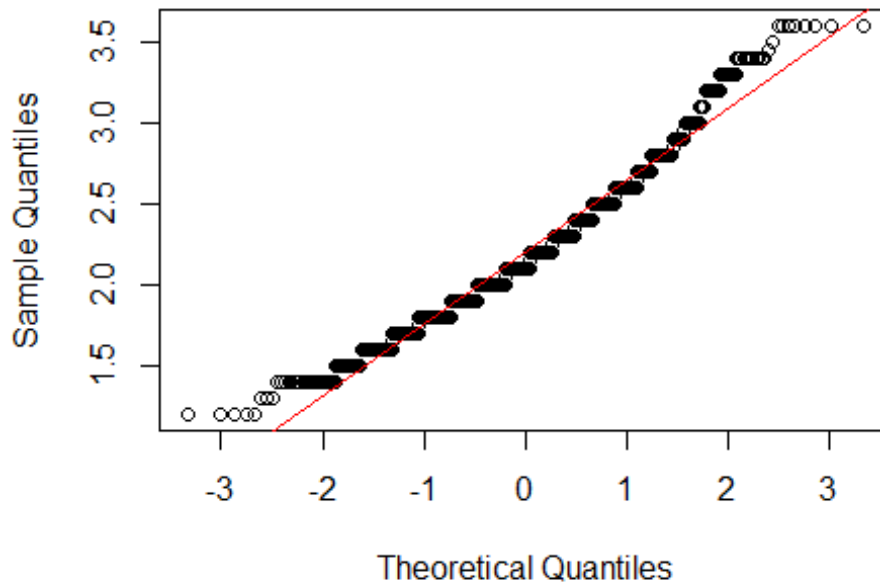
```
## data:  winequality.red$citric.acid
```

```
## W = 0.94951, p-value < 2.2e-16
```

```
qqnorm(winequality.red$residual.sugar, main = "Normal Q-Q Plot for  
redidual sugar")
```

```
qqline(winequality.red$residual.sugar, col = "red")
```


Normal Q-Q Plot for residual sugar

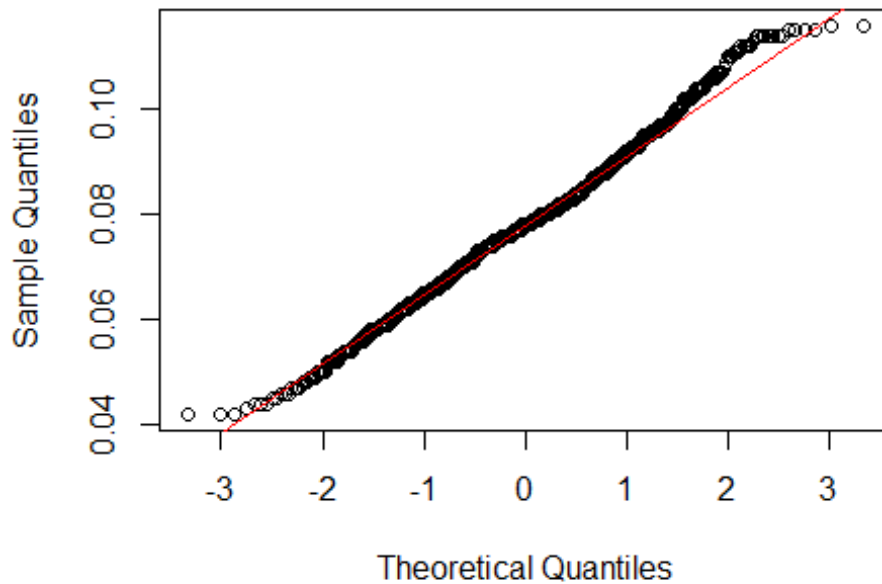


```
shapiro.test(winequality.red$residual.sugar)

##
##  Shapiro-Wilk normality test
##
## data:  winequality.red$residual.sugar
## W = 0.97058, p-value = 9.184e-15

qqnorm(winequality.red$chlorides, main = "Normal Q-Q Plot for chlorides")
qqline(winequality.red$chlorides, col = "red")
```

Normal Q-Q Plot for chlorides

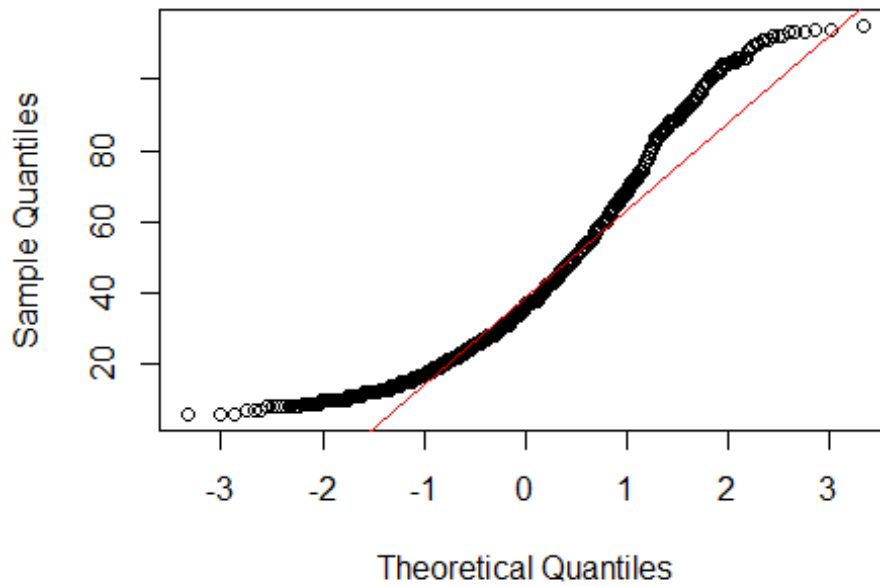


```
shapiro.test(winequality.red$chlorides)

##
##  Shapiro-Wilk normality test
##
## data:  winequality.red$chlorides
## W = 0.99382, p-value = 8.049e-05

qqnorm(winequality.red$total.sulfur.dioxide, main = "Normal Q-Q Plot for
total sulfur dioxide")
qqline(winequality.red$total.sulfur.dioxide, col = "red")
```

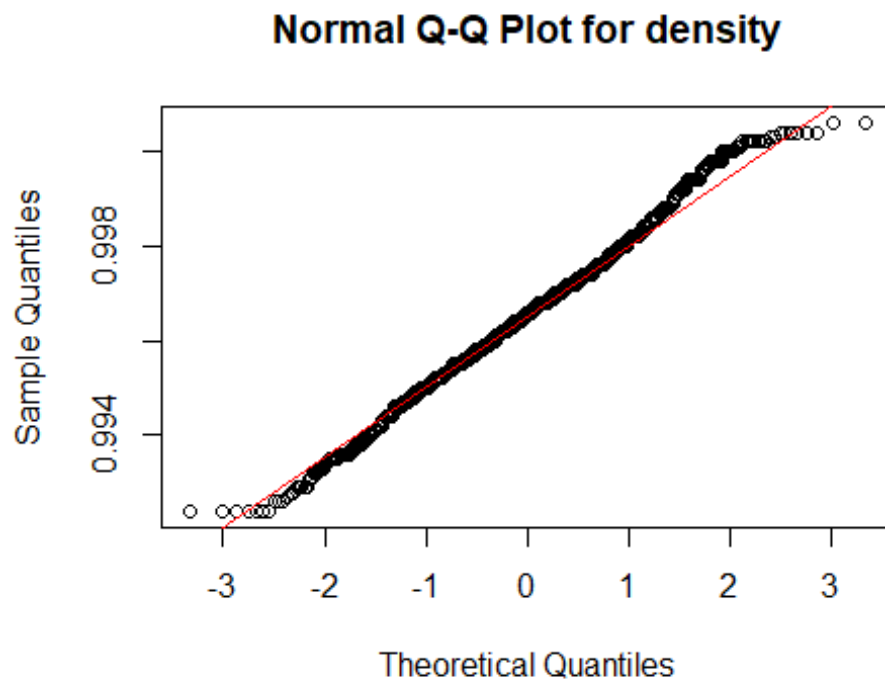
Normal Q-Q Plot for total sulfur dioxide



```
shapiro.test(winequality.red$total.sulfur.dioxide)

##
##  Shapiro-Wilk normality test
##
## data:  winequality.red$total.sulfur.dioxide
## W = 0.92227, p-value < 2.2e-16

qqnorm(winequality.red$density, main = "Normal Q-Q Plot for density")
qqline(winequality.red$density, col = "red")
```

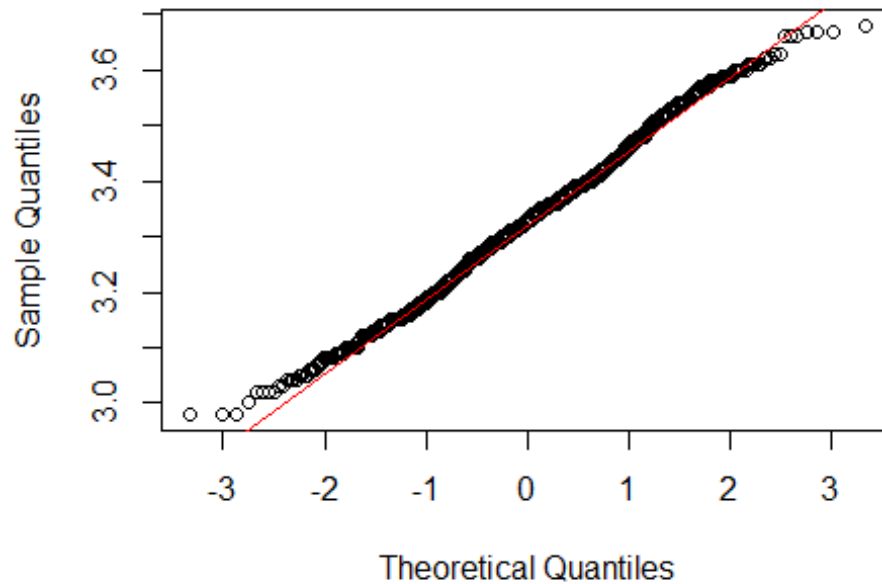


```
shapiro.test(winequality.red$density)

##
##  Shapiro-Wilk normality test
##
## data:  winequality.red$density
## W = 0.99502, p-value = 0.0006067

qqnorm(winequality.red$pH, main = "Normal Q-Q Plot for pH")
qqline(winequality.red$pH, col = "red")
```

Normal Q-Q Plot for pH



```
shapiro.test(winequality.red$pH)
```

```
##
```

```
##  Shapiro-Wilk normality test
```

```
##
```

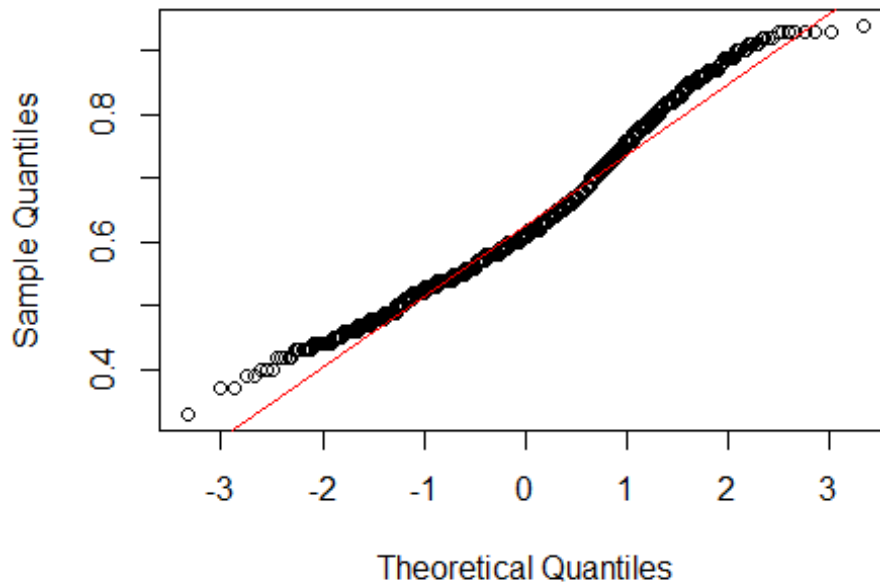
```
## data:  winequality.red$pH
```

```
## W = 0.99516, p-value = 0.0007893
```

```
qqnorm(winequality.red$sulphates, main = "Normal Q-Q Plot for sulphates")
```

```
qqline(winequality.red$sulphates, col = "red")
```

Normal Q-Q Plot for sulphates



```
shapiro.test(winequality.red$sulphates)
```

```
##
```

```
##  Shapiro-Wilk normality test
```

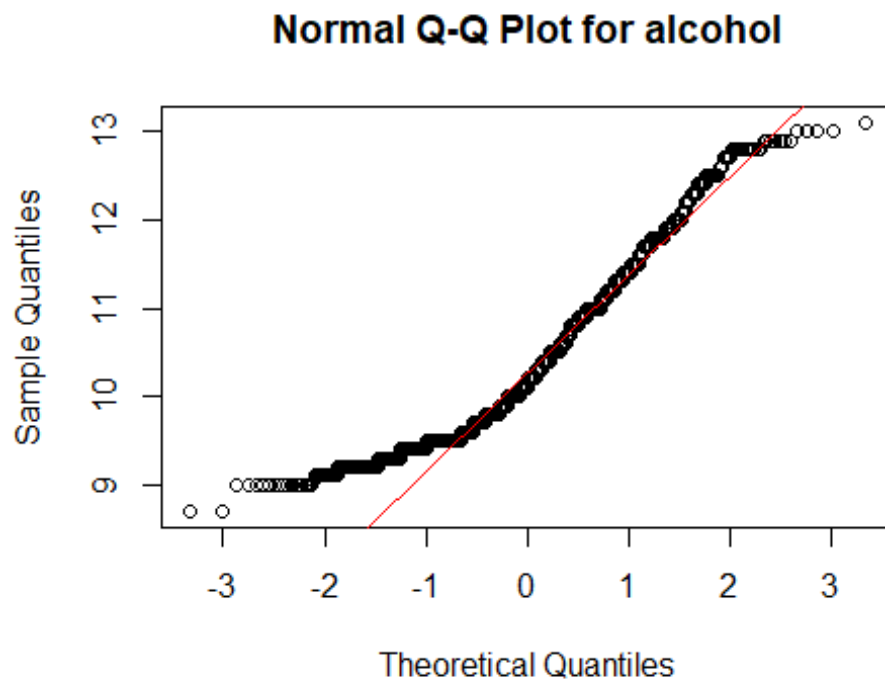
```
##
```

```
## data:  winequality.red$sulphates
```

```
## W = 0.9721, p-value = 2.543e-14
```

```
qqnorm(winequality.red$alcohol, main = "Normal Q-Q Plot for alcohol")
```

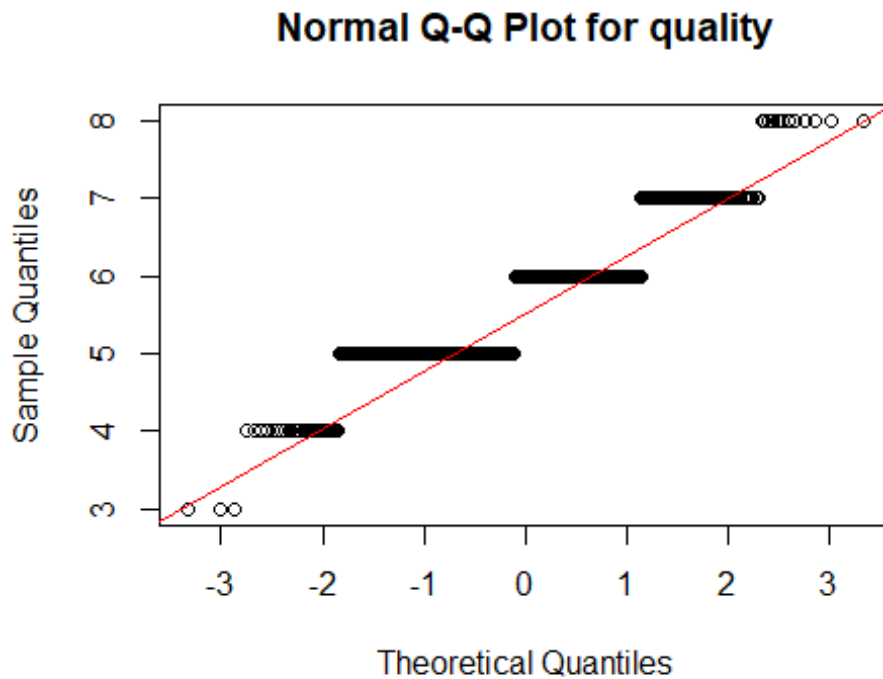
```
qqline(winequality.red$alcohol, col = "red")
```



```
shapiro.test(winequality.red$alcohol)

##
##  Shapiro-Wilk normality test
##
## data:  winequality.red$alcohol
## W = 0.93279, p-value < 2.2e-16

qqnorm(winequality.red$quality, main = "Normal Q-Q Plot for quality")
qqline(winequality.red$quality, col = "red")
```



```
shapiro.test(winequality.red$quality)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  winequality.red$quality
## W = 0.84742, p-value < 2.2e-16
```

Estudio de la homogeneidad de las varianzas. Test de Fligner-Kileen

```
fligner.test(quality ~ density, data = winequality.red)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  quality by density
## Fligner-Killeen:med chi-squared = 84.586, df = 77, p-value =
## 0.2593
```

```
fligner.test(quality ~ alcohol, data = winequality.red)
```

```
##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  quality by alcohol
## Fligner-Killeen:med chi-squared = 72.047, df = 50, p-value =
## 0.02225
```



```

fligner.test(quality ~ chlorides, data = winequality.red)

##
##  Fligner-Killeen test of homogeneity of variances
##
## data:  quality by chlorides
## Fligner-Killeen:med chi-squared = 82.893, df = 73, p-value =
## 0.2007

```

Pruebas estadísticas

Influencia de las variables fisicoquímicas en la calidad de los vinos

```

corr_matrix <- matrix(nc = 2, nr = 0)
colnames(corr_matrix) <- c("estimate", "p-value")
# Calcular el coeficiente de correlación para cada variable fisicoquimica
# con respecto al campo "quality"
for (i in 1:(ncol(winequality.red) - 1)) {
  if (is.integer(winequality.red[,i]) | is.numeric(winequality.red[,i])) {
    spearman_test = cor.test(winequality.red[,i],
                             winequality.red[,length(winequality.red)],
                             method = "spearman")
    corr_coef = spearman_test$estimate
    p_val = spearman_test$p.value
    # Add row to matrix
    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(winequality.red)[i]
  }
}

## Warning in cor.test.default(winequality.red[, i], winequality.red[,
## length(winequality.red)], : Cannot compute exact p-value with ties

## Warning in cor.test.default(winequality.red[, i], winequality.red[,
## length(winequality.red)], : Cannot compute exact p-value with ties

## Warning in cor.test.default(winequality.red[, i], winequality.red[,
## length(winequality.red)], : Cannot compute exact p-value with ties

## Warning in cor.test.default(winequality.red[, i], winequality.red[,

```

```
## length(winequality.red)], : Cannot compute exact p-value with ties

## Warning in cor.test.default(winequality.red[, i], winequality.red[,
## length(winequality.red)], : Cannot compute exact p-value with ties

## Warning in cor.test.default(winequality.red[, i], winequality.red[,
## length(winequality.red)], : Cannot compute exact p-value with ties

## Warning in cor.test.default(winequality.red[, i], winequality.red[,
## length(winequality.red)], : Cannot compute exact p-value with ties

## Warning in cor.test.default(winequality.red[, i], winequality.red[,
## length(winequality.red)], : Cannot compute exact p-value with ties

print(corr_matrix)

##              estimate      p-value
## acidity          0.06334928 2.941751e-02
## citric.acid       0.22587602 3.864772e-15
## residual.sugar    0.02399919 4.097446e-01
## chlorides        -0.20202975 2.367987e-12
## total.sulfur.dioxide -0.14232988 8.960679e-07
## density          -0.21470668 8.584723e-14
## pH               -0.06304193 3.021513e-02
## sulphates         0.43853552 9.900814e-57
## alcohol          0.48457880 1.261876e-70
```

Matriz de correlación entre variables

```
library(PerformanceAnalytics)

## Loading required package: xts

## Loading required package: zoo

##
## Attaching package: 'zoo'

## The following objects are masked from 'package:base':
##
##      as.Date, as.Date.numeric

##
## Attaching package: 'xts'

## The following objects are masked from 'package:dplyr':
##
##      first, last
```

```

## The following objects are masked from 'package:data.table':
##
##      first, last
##
## Attaching package: 'PerformanceAnalytics'
##
## The following object is masked from 'package:gplots':
##
##      textplot
##
## The following object is masked from 'package:graphics':
##
##      legend

# Guardamos datos en un data.frame
acidity<-winequality.red$acidity
citric.acid<-winequality.red$citric.acid
residual.sugar<-winequality.red$residual.sugar
chlorides<-winequality.red$chlorides
total.sulfur.dioxide<-winequality.red$total.sulfur.dioxide
density<-winequality.red$density
pH<-winequality.red$pH
sulphates<-winequality.red$sulphates
alcohol<-winequality.red$alcohol
quality<-winequality.red$quality
data <- data.frame(acidity, citric.acid, residual.sugar, chlorides,
total.sulfur.dioxide, density, pH, sulphates, alcohol, quality)
colnames(data) <- c("acidity", "citric acid", "residual
sugar", "chlorides", "total sulfur dioxide", "density", "pH", "sulphates",
"alcohol", "quality")
cor(data)

##              acidity  citric acid residual sugar
chlorides
## acidity              1.00000000  0.603353709      0.24484897
0.19254182
## citric acid          0.60335371  1.000000000      0.15025882
0.06902013
## residual sugar      0.24484897  0.150258817      1.00000000
0.24054793
## chlorides           0.19254182  0.069020125      0.24054793
1.00000000
## total sulfur dioxide -0.07812217  0.002177295      0.17088644
0.16974256
## density             0.62718180  0.300976996      0.39804848
0.40341417
## pH                  -0.67289768 -0.482954798     -0.05565157 -
0.15070000
## sulphates           0.12300305  0.275666484      0.04069258 -
0.09583778

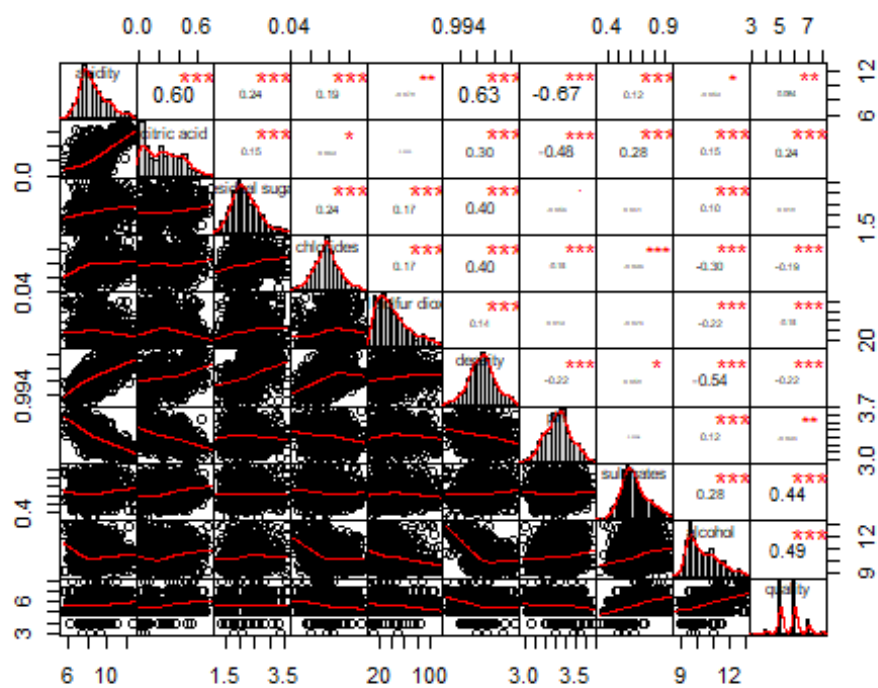
```

```

## alcohol          -0.05935530  0.146719282    0.10393533  -
0.29691699
## quality          0.08447757  0.244631954    0.01784264  -
0.18985018
##                  total sulfur dioxide    density    pH
## acidity          -0.078122174  0.62718180 -0.672897678
## citric acid       0.002177295  0.30097700 -0.482954798
## residual sugar    0.170886444  0.39804848 -0.055651570
## chlorides         0.169742556  0.40341417 -0.150699998
## total sulfur dioxide 1.000000000  0.14109698  0.019098399
## density           0.141096985  1.000000000 -0.223299857
## pH                0.019098399 -0.22329986  1.000000000
## sulphates         -0.024142466  0.05816787  0.003591845
## alcohol           -0.223753777 -0.54100848  0.117723679
## quality           -0.151868436 -0.21581441 -0.093901964
##                  sulphates    alcohol    quality
## acidity           0.123003050 -0.0593553  0.08447757
## citric acid       0.275666484  0.1467193  0.24463195
## residual sugar    0.040692585  0.1039353  0.01784264
## chlorides         -0.095837782 -0.2969170 -0.18985018
## total sulfur dioxide -0.024142466 -0.2237538 -0.15186844
## density           0.058167875 -0.5410085 -0.21581441
## pH                0.003591845  0.1177237 -0.09390196
## sulphates         1.000000000  0.2787311  0.43968490
## alcohol           0.278731106  1.0000000  0.49172395
## quality           0.439684896  0.4917240  1.000000000

```

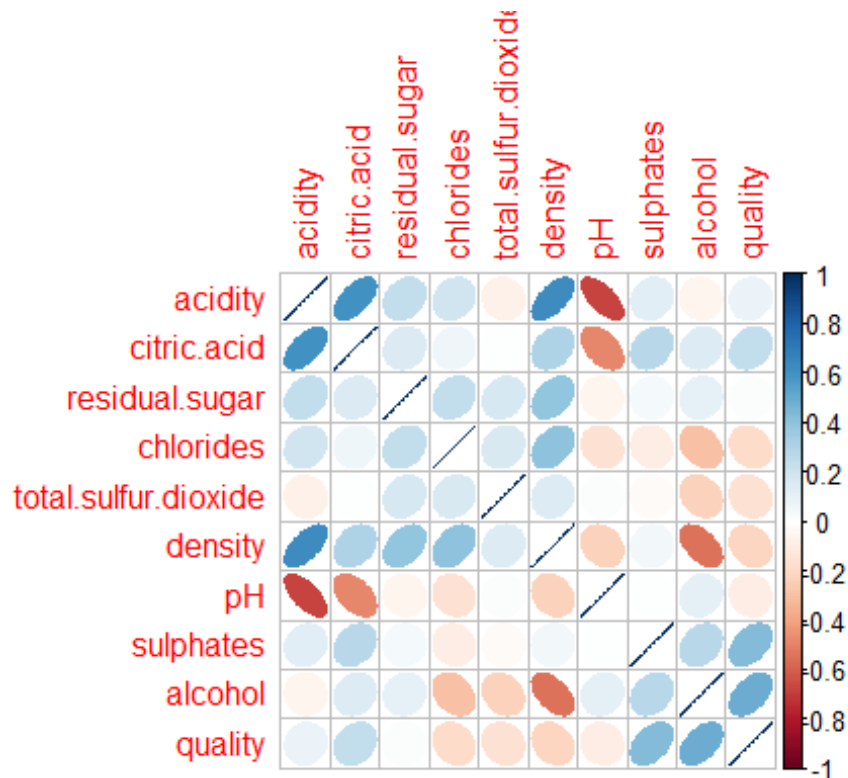
chart.Correlation(data)



```
library(corrplot)

## corrplot 0.84 loaded

M<-cor(winequality.red)
corrplot(M, method = "ellipse")
```



Contrastes de hipótesis

¿La calidad de los vinos con densidad inferior a la media supera la de los vinos con densidad por encima de la media?

```
low.density.quality <- winequality.red[winequality.red$density <=
mean(winequality.red$density),]$quality
high.density.quality <- winequality.red[winequality.red$density >
mean(winequality.red$density),]$quality

t.test(low.density.quality, high.density.quality, alternative = "less",
conf.level = 0.95)

##
##  Welch Two Sample t-test
##
## data: low.density.quality and high.density.quality
## t = 5.4571, df = 1155.5, p-value = 1
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##      -Inf 0.3162226
## sample estimates:
## mean of x mean of y
##  5.764605  5.521667
```

¿La calidad de los vinos con menos sal es igual o diferente a la de los vinos más salados?

```

low.chlorides.quality <- winequality.red[winequality.red$chlorides <=
mean(winequality.red$chlorides),]$quality
high.chlorides.quality <- winequality.red[winequality.red$chlorides >
mean(winequality.red$chlorides),]$quality

t.test(low.chlorides.quality, high.chlorides.quality, alternative =
"two.sided", conf.level = 0.95)

##
## Welch Two Sample t-test
##
## data: low.chlorides.quality and high.chlorides.quality
## t = 5.5282, df = 1178.3, p-value = 3.981e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1576308 0.3310735
## sample estimates:
## mean of x mean of y
##  5.757674  5.513321

```

Modelo de regresión lineal

Modelo de regresión multilíneal para predecir la calidad

```

# Regresores cuantitativos más influyentes en la calidad de los vinos
alcohol<-winequality.red$alcohol
sulphates<-winequality.red$sulphates
citric.acid<-winequality.red$citric.acid
density<-winequality.red$density
chlorides<-winequality.red$chlorides
total.sulfur.dioxide<-winequality.red$total.sulfur.dioxide
# Variable que se quiere predecir
quality<-winequality.red$quality
# Modelos de regresión lineal
modelo1 <- lm(quality ~ alcohol + sulphates + citric.acid, data =
winequality.red)
modelo2 <- lm(quality ~ alcohol + sulphates + citric.acid + chlorides,
data = winequality.red)
modelo3 <- lm(quality ~ alcohol + sulphates + citric.acid + chlorides +
density, data = winequality.red)
modelo4 <- lm(quality ~ alcohol + sulphates + citric.acid + density +
total.sulfur.dioxide, data = winequality.red)

# Tabla con los coeficientes de determinación de cada modelo
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 0.3510071
## [2,]      2 0.3539755
## [3,]      3 0.3572902
## [4,]      4 0.3594511

summary(modelo4)

##
## Call:
## lm(formula = quality ~ alcohol + sulphates + citric.acid + density +
##      total.sulfur.dioxide, data = winequality.red)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.4797 -0.3792 -0.0628  0.4683  1.9680
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   4.805e+01  1.545e+01   3.109  0.00192 **
## alcohol       2.543e-01  2.564e-02   9.919 < 2e-16 ***
## sulphates     2.154e+00  1.731e-01  12.443 < 2e-16 ***
## citric.acid   5.990e-01  1.150e-01   5.207 2.26e-07 ***
## density      -4.664e+01  1.537e+01  -3.034  0.00247 **
## total.sulfur.dioxide -1.831e-03  7.327e-04  -2.499  0.01258 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6201 on 1176 degrees of freedom
## Multiple R-squared:  0.3595, Adjusted R-squared:  0.3567
## F-statistic: 132 on 5 and 1176 DF, p-value: < 2.2e-16
```

Predicción de la calidad con el modelo de regresión lineal

```
newdata <- data.frame(
  alcohol = mean(winequality.red$alcohol),
  sulphates = mean(winequality.red$sulphates),
  citric.acid = mean(winequality.red$citric.acid),
  density = mean(winequality.red$density),
  total.sulfur.dioxide = mean(winequality.red$total.sulfur.dioxide)
)
# Predecir el precio
predict(modelo4, newdata)

##      1
## 5.641286
```

Modelo de regresión multilíneal para predecir la acidez

```
# Regresores cuantitativos más influyentes en la calidad de los vinos
citric.acid <- winequality.red$citric.acid
density <- winequality.red$density
```



```

pH<-winequality.red$pH
# Variable que se quiere predecir
acidity<-winequality.red$acidity
# Modelo de regresión lineal
modelo <- lm(acidity ~ citric.acid + density + pH)
summary(modelo)

##
## Call:
## lm(formula = acidity ~ citric.acid + density + pH)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.58139 -0.47482 -0.02323  0.49081  2.39549
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -376.8421    14.0437  -26.83  <2e-16 ***
## citric.acid     1.9641     0.1379   14.25  <2e-16 ***
## density       402.5965    14.0285   28.70  <2e-16 ***
## pH            -4.8608     0.1843  -26.38  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7289 on 1178 degrees of freedom
## Multiple R-squared:  0.7374, Adjusted R-squared:  0.7368
## F-statistic: 1103 on 3 and 1178 DF, p-value: < 2.2e-16

```

Predecimos la acidez para unos valores de ácido cítrico, densidad y pH

```

data <- data.frame(citric.acid = 0.489, density = 0.998, pH = 3.8)
# Predicción de La acidez
predict(modelo, data)

##      1
## 7.438701

```

Modelo de regresión logístico

```

# Creación de La variable binaria "high.density"
winequality.red$density[winequality.red$density >= 1]<1

## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [12] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [23] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE

winequality.red$density[winequality.red$density < 1]<-0
high.density<-winequality.red$density
high.density<-factor(high.density)
# Variables explicativas de La densidad
acidity<-winequality.red$acidity
alcohol<-winequality.red$alcohol

```

```

residual.sugar<-winequality.red$residual.sugar
chlorides<-winequality.red$chlorides
# Estimación del modelo de regresión Logística
reglog <- glm(high.density ~ acidity+alcohol+residual.sugar+chlorides,
data = winequality.red, family = binomial, control = list(maxit = 1000))
summary(reglog)

##
## Call:
## glm(formula = high.density ~ acidity + alcohol + residual.sugar +
##      chlorides, family = binomial, data = winequality.red, control =
##      list(maxit = 1000))
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7816  -0.0736  -0.0213  -0.0073   3.4087
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -19.2219     4.4742  -4.296 1.74e-05 ***
## acidity         1.6387     0.2325   7.048 1.82e-12 ***
## alcohol        -1.3362     0.3947  -3.385 0.000711 ***
## residual.sugar  2.4316     0.5298   4.590 4.44e-06 ***
## chlorides      72.4817    21.9921   3.296 0.000981 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 294.12  on 1181  degrees of freedom
## Residual deviance: 135.26  on 1177  degrees of freedom
## AIC: 145.26
##
## Number of Fisher Scoring iterations: 9

# Creación del dataset con Los datos necesarios para La predicción
newdata = data.frame(acidity = 6.36,alcohol = 8.496, residual.sugar =
2.226, chlorides=0.198)
# Usamos la función predict() para calcular La probabilidad predicha.
Para obtener la predicción, se incluye el argumento type = "response"
predict(reglog, newdata, type="response")

##           1
## 0.4041297

```

Tabla resumen de los datos preprocesados y representación en forma de boxplots

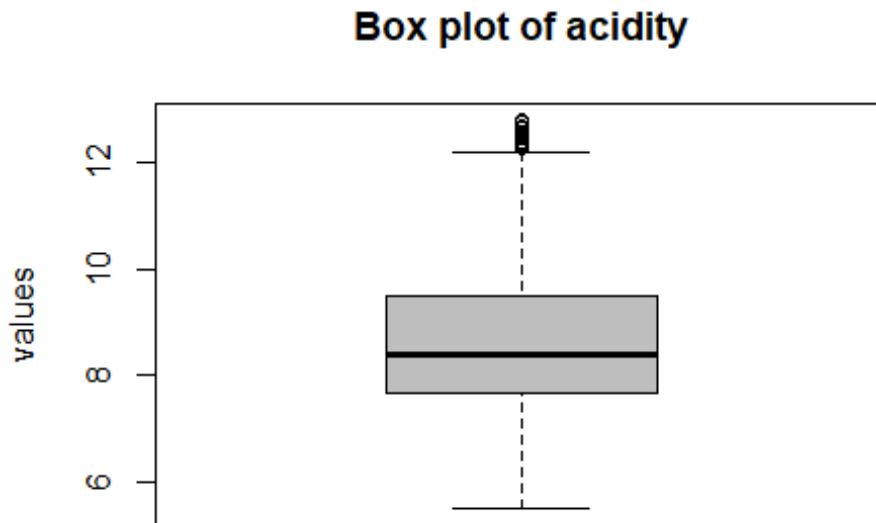
```

# Tabla resumen de Las principales variables fisicoquímicas del conjunto
de datos
summary(winequality.red)

```

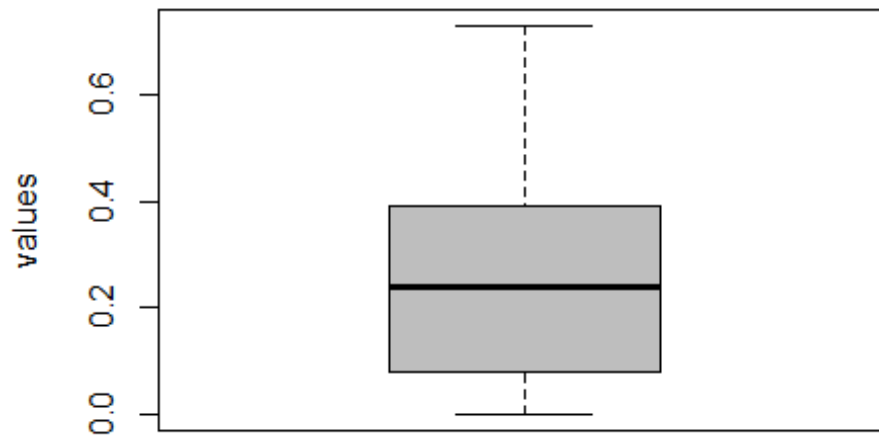
```
##      acidity      citric.acid      residual.sugar      chlorides
## Min.   : 5.520    Min.    :0.0000    Min.    :1.200    Min.    :0.04200
## 1st Qu.: 7.680    1st Qu.:0.0800    1st Qu.:1.900    1st Qu.:0.06900
## Median : 8.380    Median :0.2400    Median :2.100    Median :0.07800
## Mean   : 8.681    Mean    :0.2459    Mean    :2.183    Mean    :0.07817
## 3rd Qu.: 9.498    3rd Qu.:0.3900    3rd Qu.:2.500    3rd Qu.:0.08675
## Max.   :12.800    Max.    :0.7300    Max.    :3.600    Max.    :0.11600
## total.sulfur.dioxide density      pH      sulphates
## Min.   : 6.00     Min.    :0.00000    Min.    :2.980    Min.    :0.3300
## 1st Qu.: 22.00     1st Qu.:0.00000    1st Qu.:3.230    1st Qu.:0.5500
## Median : 36.00     Median :0.00000    Median :3.330    Median :0.6100
## Mean   : 41.79     Mean    :0.02708    Mean    :3.326    Mean    :0.6294
## 3rd Qu.: 55.00     3rd Qu.:0.00000    3rd Qu.:3.410    3rd Qu.:0.7000
## Max.   :115.00     Max.    :1.00060    Max.    :3.680    Max.    :0.9400
##      alcohol      quality
## Min.   : 8.70     Min.    :3.000
## 1st Qu.: 9.50     1st Qu.:5.000
## Median :10.10     Median :6.000
## Mean   :10.37     Mean    :5.641
## 3rd Qu.:11.00     3rd Qu.:6.000
## Max.   :13.10     Max.    :8.000
```

```
boxplot(winequality.red$acidity,main="Box plot of acidity",
col="gray",ylab="values")
```



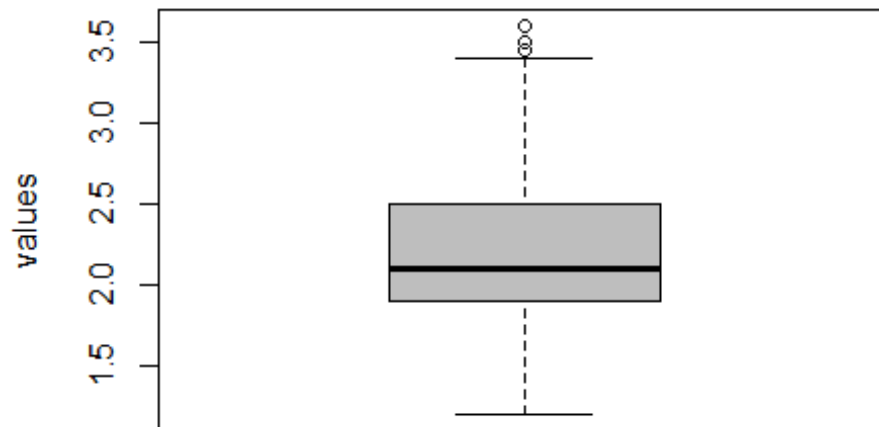
```
boxplot(winequality.red$citric.acid,main="Box plot of citric acid",
col="gray",ylab="values")
```

Box plot of citric acid

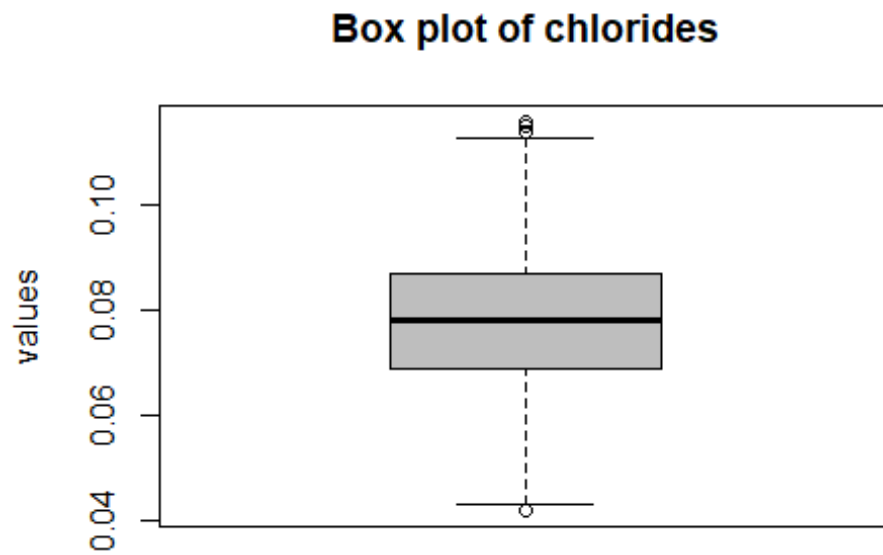


```
boxplot(winequality.red$residual.sugar,main="Box plot of residual sugar",  
col="gray",ylab="values")
```

Box plot of residual sugar

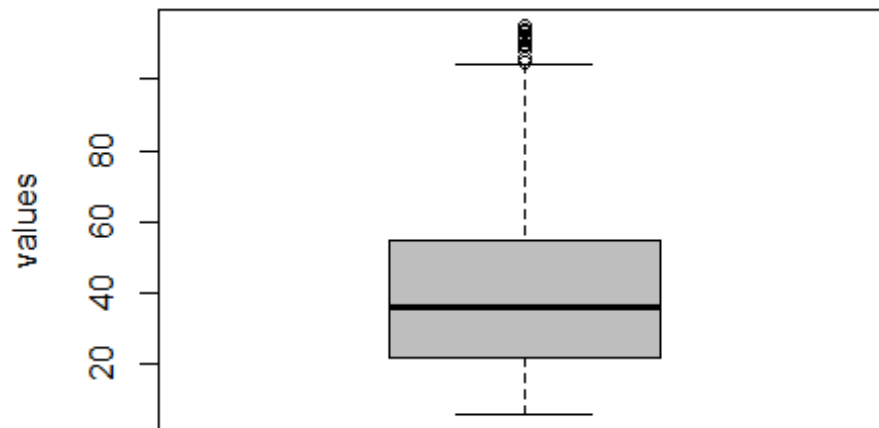


```
boxplot(winequality.red$chlorides,main="Box plot of chlorides",  
col="gray",ylab="values")
```



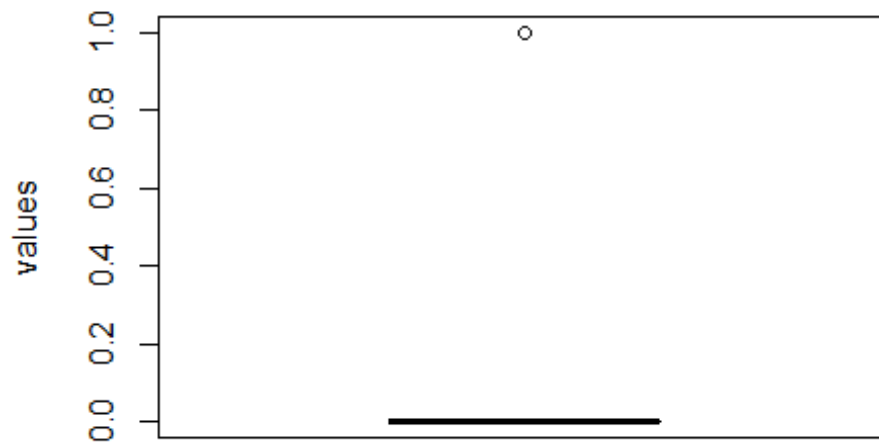
```
boxplot(winequality.red$total.sulfur.dioxide,main="Box plot of total  
sulfur dioxide", col="gray",ylab="values")
```

Box plot of total sulfur dioxide

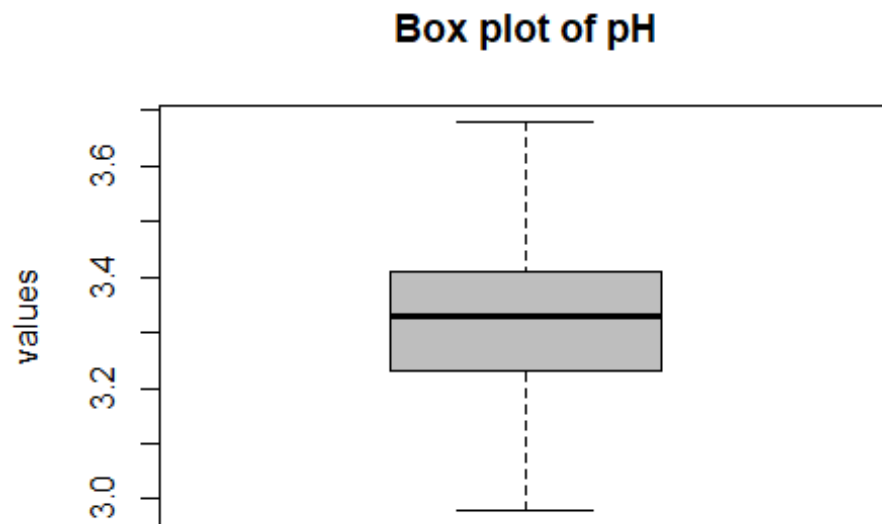


```
boxplot(winequality.red$density,main="Box plot of density",  
col="gray",ylab="values")
```

Box plot of density

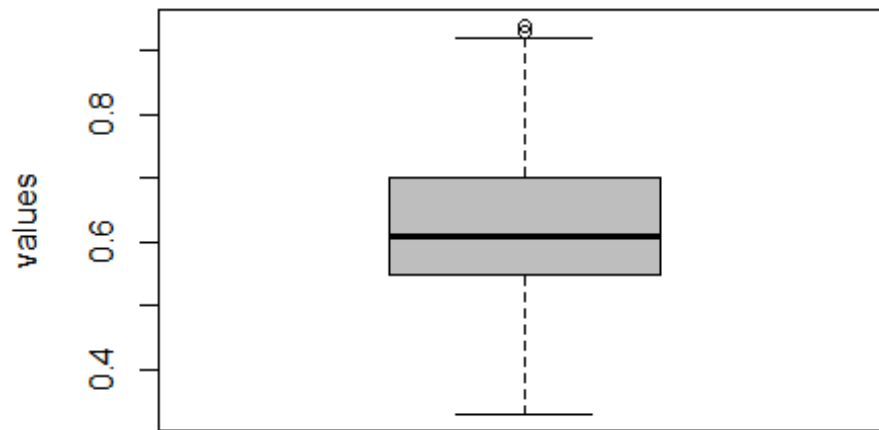


```
boxplot(winequality.red$pH,main="Box plot of pH",  
col="gray",ylab="values")
```



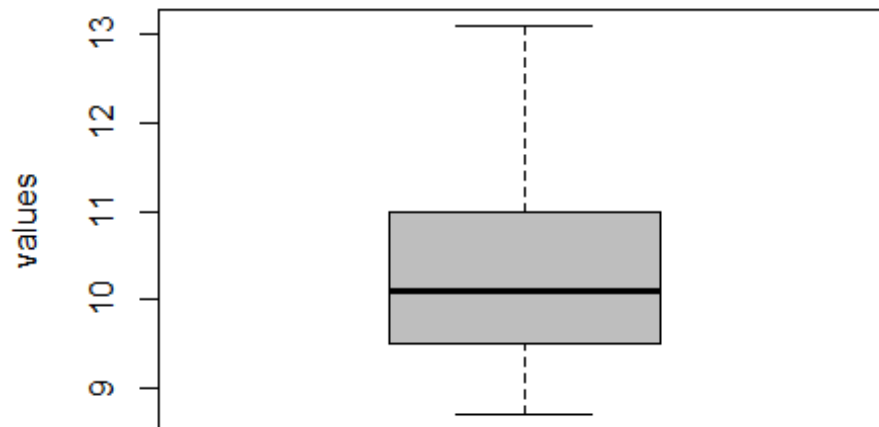
```
boxplot(winequality.red$sulphates,main="Box plot of sulphates",  
col="gray",ylab="values")
```

Box plot of sulphates



```
boxplot(winequality.red$alcohol,main="Box plot of alcohol",  
col="gray",ylab="values")
```

Box plot of alcohol



Referencias

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Tutorial de Github (<https://guides.github.com/activities/hello-world/>)