# Ejercicio_cereales

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## Lectura Fichero de datos

```
datos <- read.csv("CEREALES.csv")  # import data
str(datos)
```

```
'data.frame':   173 obs. of  7 variables:
 $ VARIEDAD : chr  " AVENA" "TRIGO" "CEBADA" "TRIGO" ...
 $ MANGANESO: num  1.31 1.14 0.61 1.05 1.06 1.1 0.6 1.29 1.12 1.11 ...
 $ CALORIAS : num  151 193 126 197 193 ...
 $ FIBRA    : num  4.04 8.01 14.22 7.93 8.01 ...
 $ SELENIO  : num  19.1 24.8 36 24.9 25.8 ...
 $ FOSFORO  : num  178 120 224 120 113 ...
 $ N_MUESTRA: int  1 2 3 4 5 6 7 8 9 10 ...
```

```
summary(datos)
```

```
   VARIEDAD           MANGANESO       CALORIAS         FIBRA       
 Length:173         Min.   :0.58   Min.   :118.1   Min.   : 0.720  
 Class :character   1st Qu.:1.04   1st Qu.:148.1   1st Qu.: 4.180  
 Mode  :character   Median :1.11   Median :150.8   Median : 7.970  
                    Mean   :1.10   Mean   :163.6   Mean   : 7.931  
                    3rd Qu.:1.29   3rd Qu.:195.2   3rd Qu.: 8.190  
                    Max.   :3.84   Max.   :200.4   Max.   :15.210  
    SELENIO         FOSFORO        N_MUESTRA     
 Min.   :18.20   Min.   :105.9   Min.   :  1.0  
 1st Qu.:19.18   1st Qu.:121.9   1st Qu.: 43.0  
 Median :24.77   Median :164.5   Median : 85.0  
 Mean   :25.98   Mean   :162.3   Mean   : 85.3  
 3rd Qu.:26.78   3rd Qu.:177.4   3rd Qu.:128.0  
 Max.   :66.00   Max.   :255.2   Max.   :170.0  
```

```r
datos$VARIEDAD<-factor(datos$VARIEDAD)
str(datos)
```

```
'data.frame':   173 obs. of  7 variables:
 $ VARIEDAD : Factor w/ 3 levels " AVENA","CEBADA",..: 1 3 2 3 3 3 2 1 3 3 ...
 $ MANGANESO: num  1.31 1.14 0.61 1.05 1.06 1.1 0.6 1.29 1.12 1.11 ...
 $ CALORIAS : num  151 193 126 197 193 ...
 $ FIBRA    : num  4.04 8.01 14.22 7.93 8.01 ...
 $ SELENIO  : num  19.1 24.8 36 24.9 25.8 ...
 $ FOSFORO  : num  178 120 224 120 113 ...
 $ N_MUESTRA: int  1 2 3 4 5 6 7 8 9 10 ...
```

```r
table(datos$VARIEDAD)
```

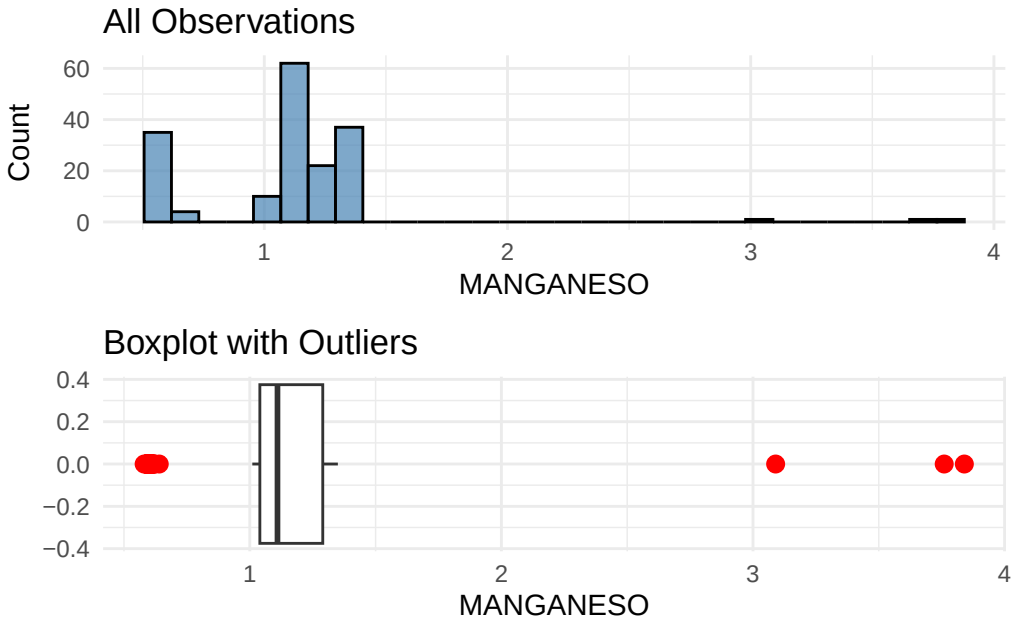
```
 AVENA CEBADA  TRIGO
    61     40     72
```

## Uso de la función outliers() y extreme()

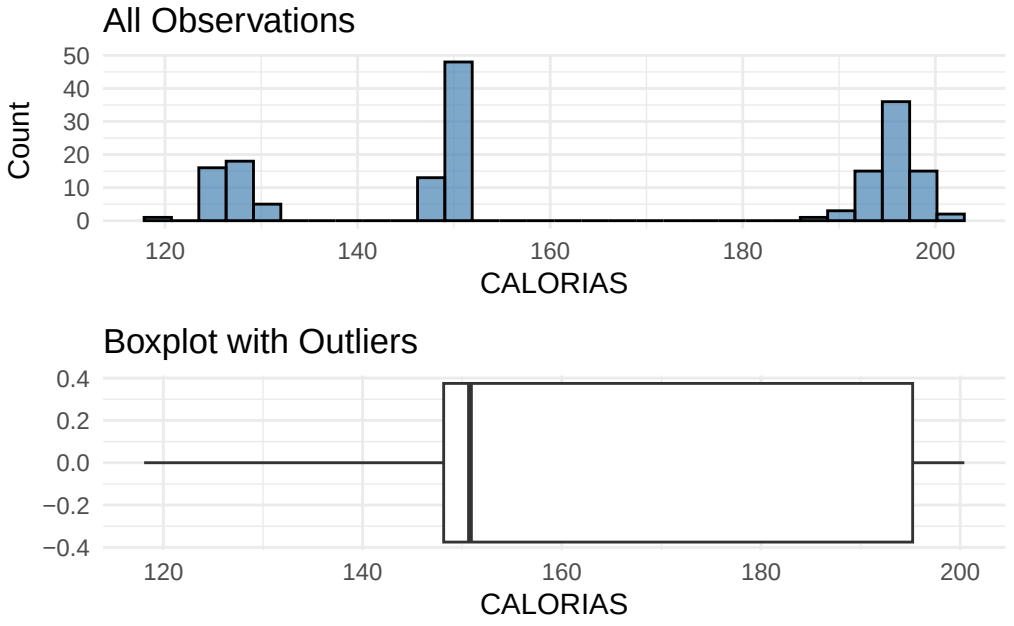
```r
source("outliers.R")
```

```
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
```

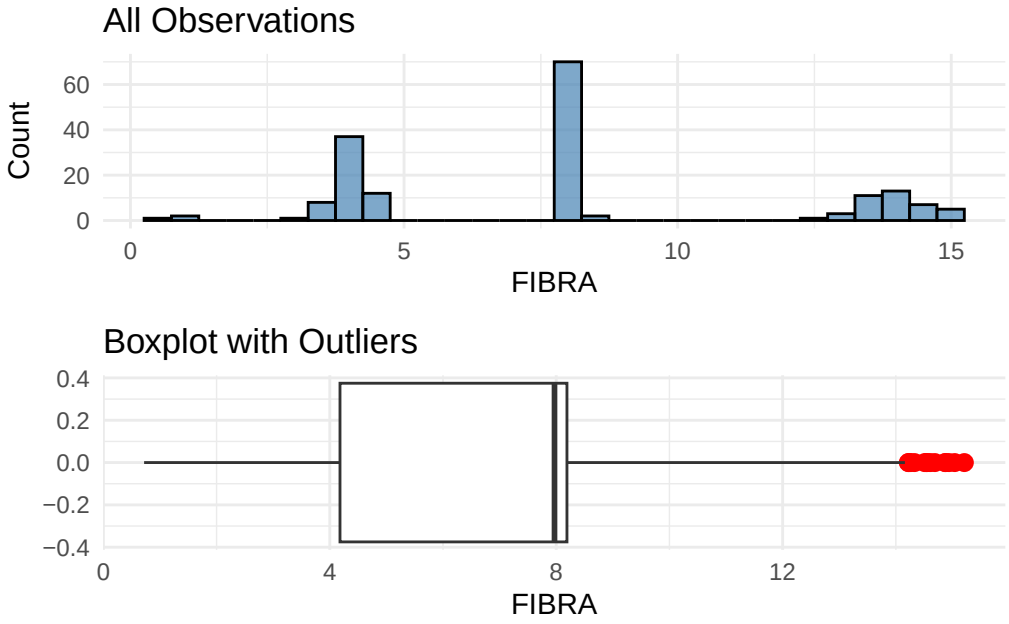
```r
# Aplicar la función a múltiples variables numéricas o enteras
numeric_integer_vars <- names(which(sapply(datos, is.numeric) | sapply(datos, is.integer)))
# Aplicar la función 'outliers' a cada una de las variables numéricas
outliers_results <- lapply(numeric_integer_vars, function(var) {
  outliers(datos, var)  # Llamar a la función pasando el nombre de la variable
})
```



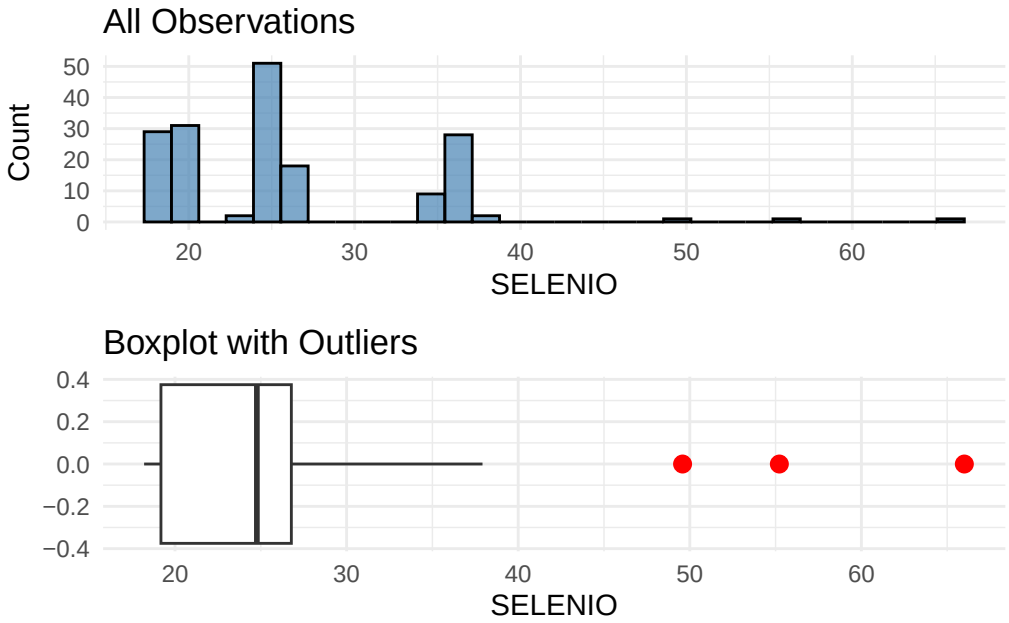

```
Outliers identified in MANGANESO :  42 outliers
Proportion (%) of outliers: 24.28 %
```



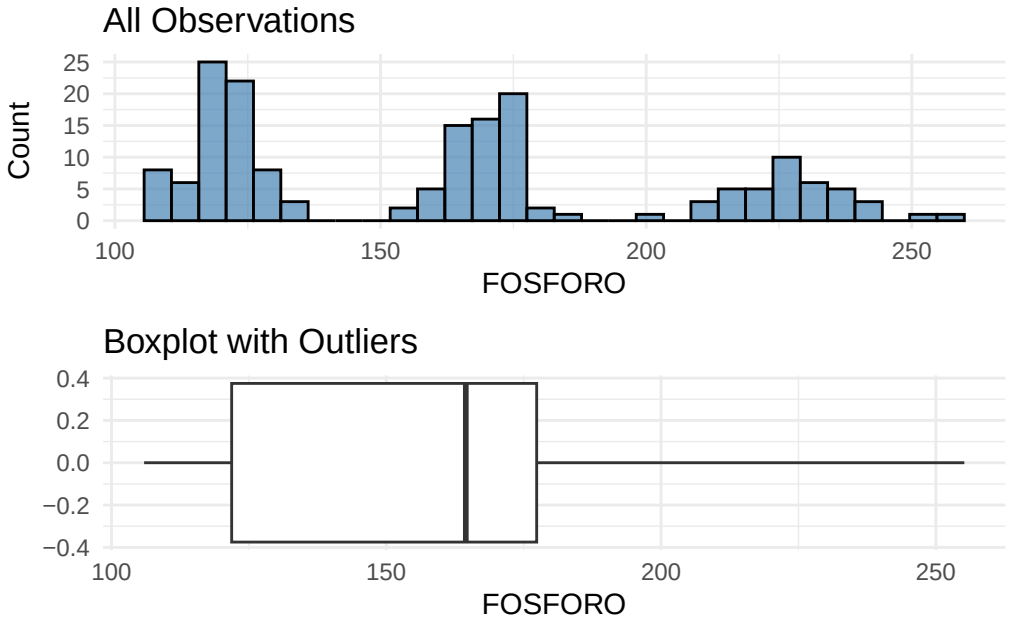
```
Outliers identified in CALORIAS :  0 outliers
Proportion (%) of outliers: 0 %
```



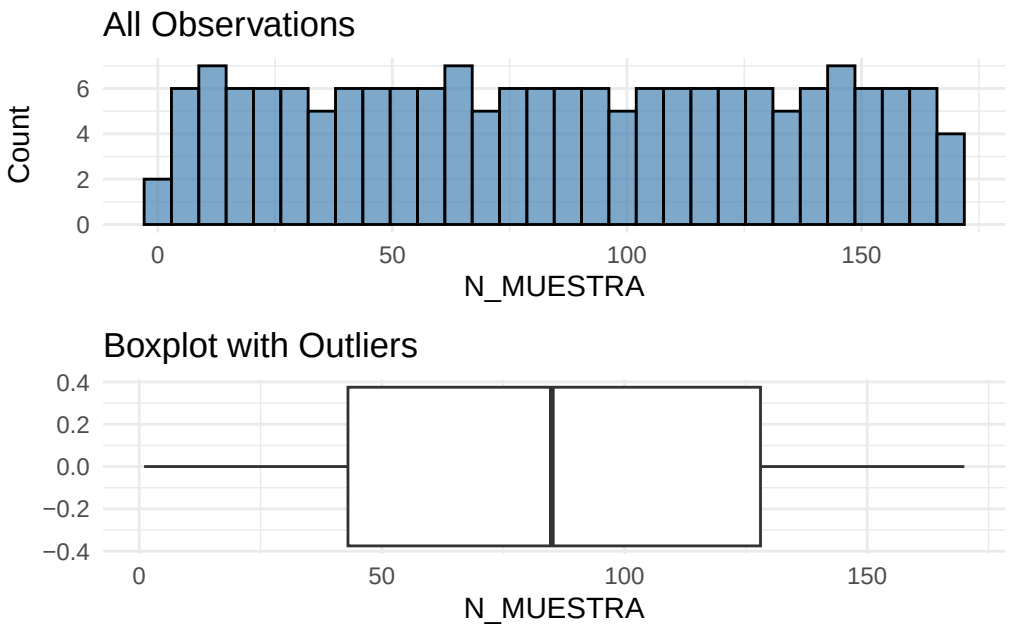

```
Outliers identified in FIBRA :  14 outliers
Proportion (%) of outliers: 8.09 %
```




```
Outliers identified in SELENIO :  3 outliers
Proportion (%) of outliers: 1.73 %
```

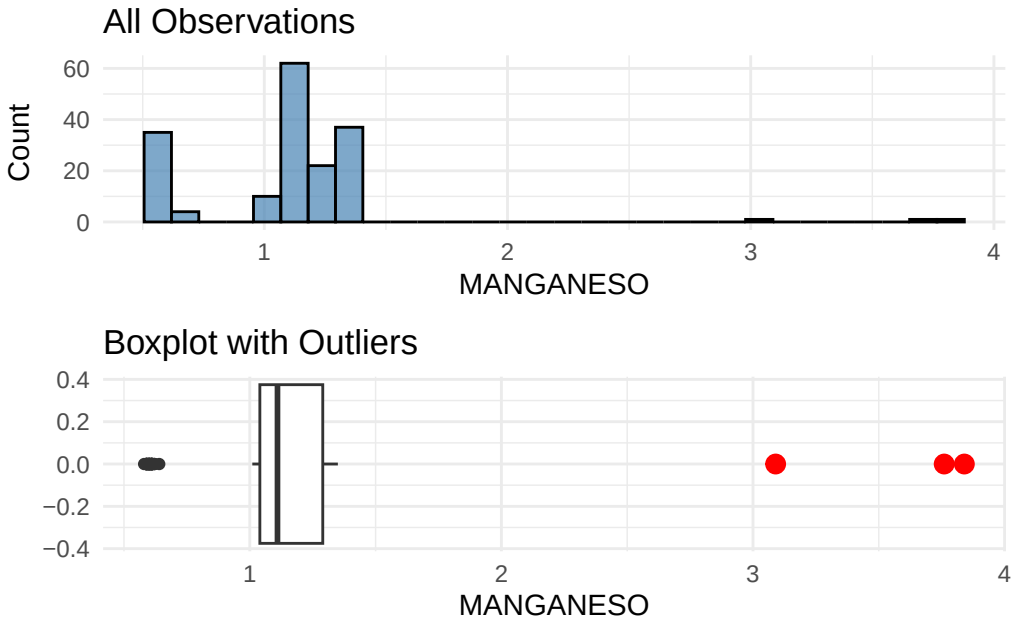


```
Outliers identified in FOSFORO :  0 outliers
Proportion (%) of outliers: 0 %
```

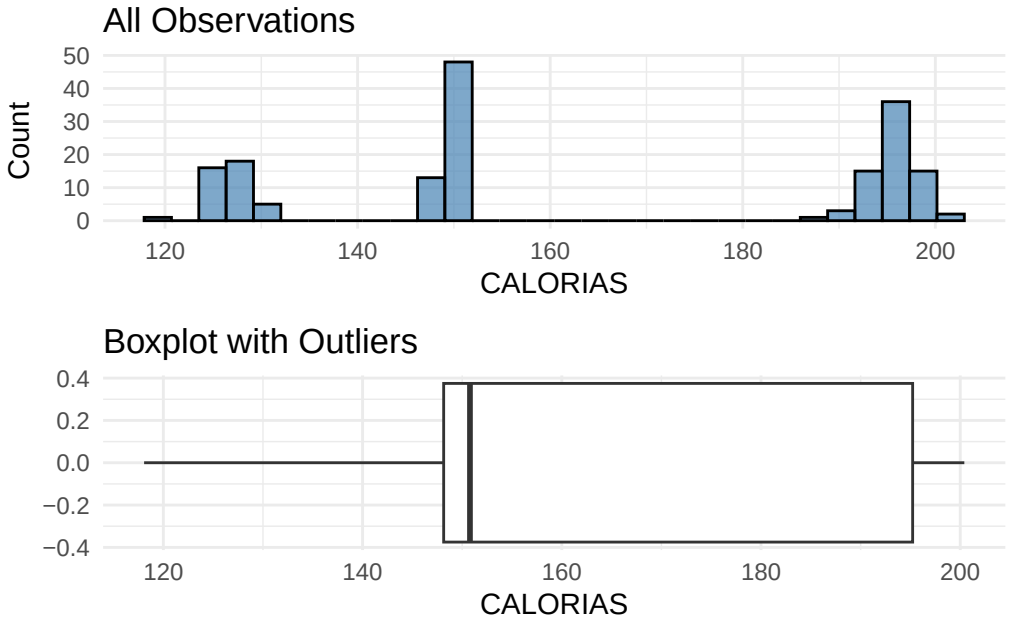



```
Outliers identified in N_MUESTRA :  0 outliers
Proportion (%) of outliers: 0 %
```

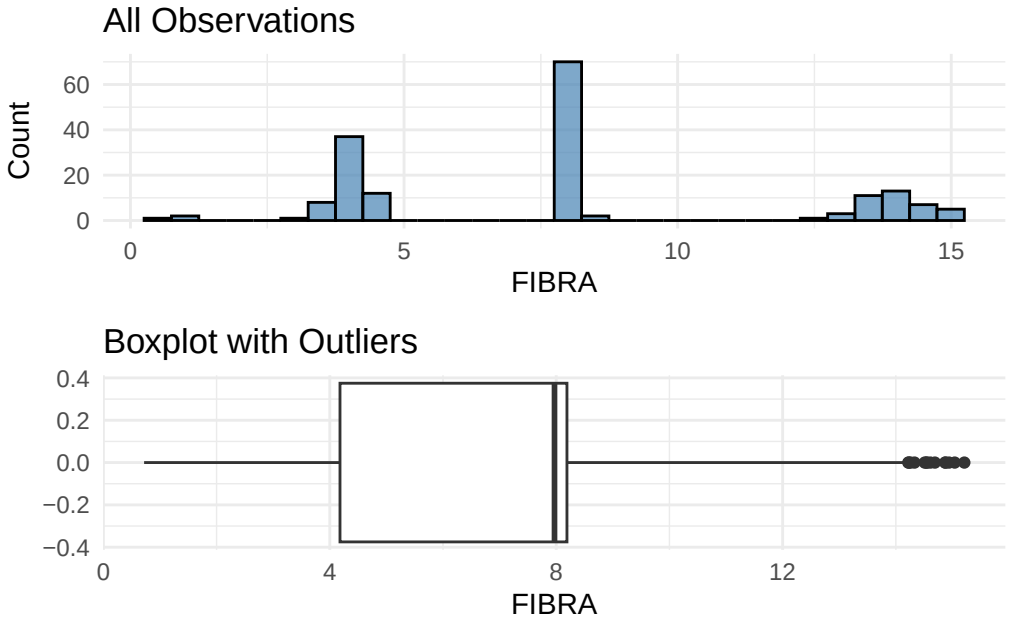
```
extreme_results <- lapply(numeric_integer_vars, function(var) {
  extreme(datos, var)  # Llamar a la función pasando el nombre de la variable
})
```



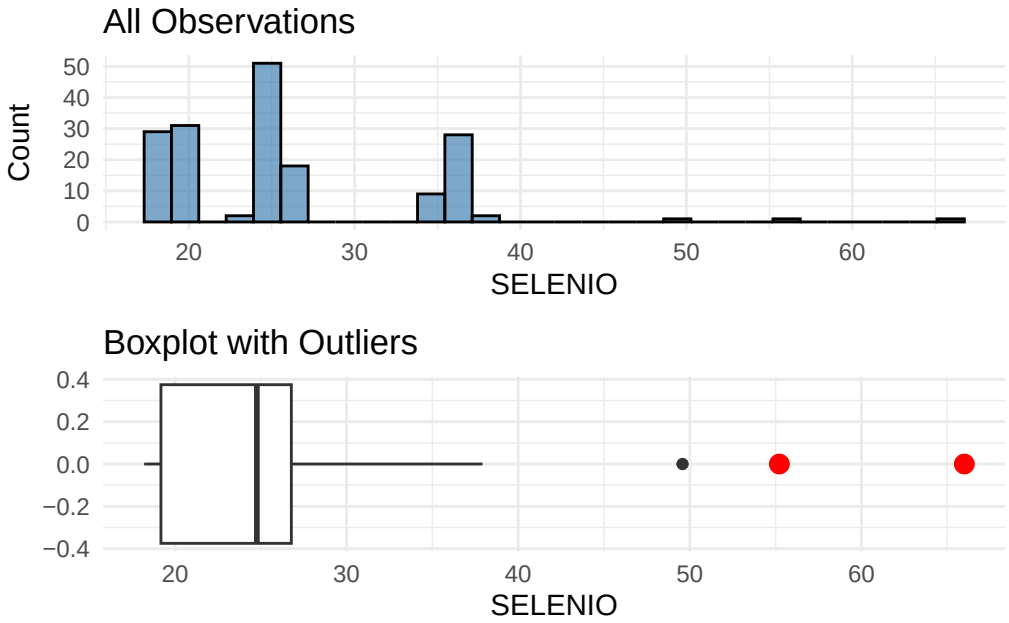

```
Outliers identified in MANGANESO :  3 outliers
Proportion (%) of outliers: 1.73 %
```



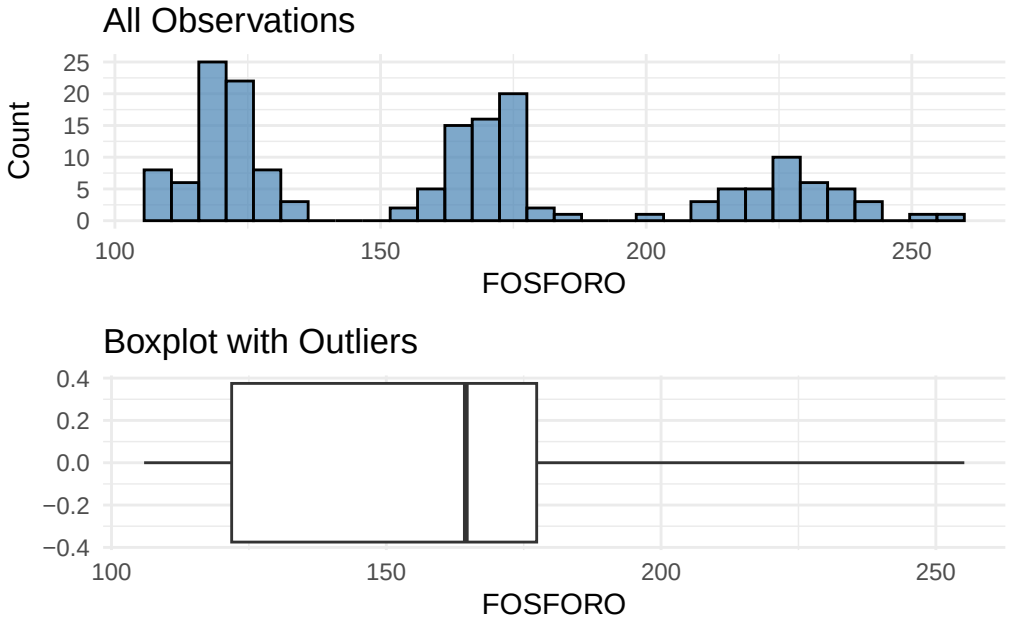
```
Outliers identified in CALORIAS :  0 outliers
Proportion (%) of outliers: 0 %
```



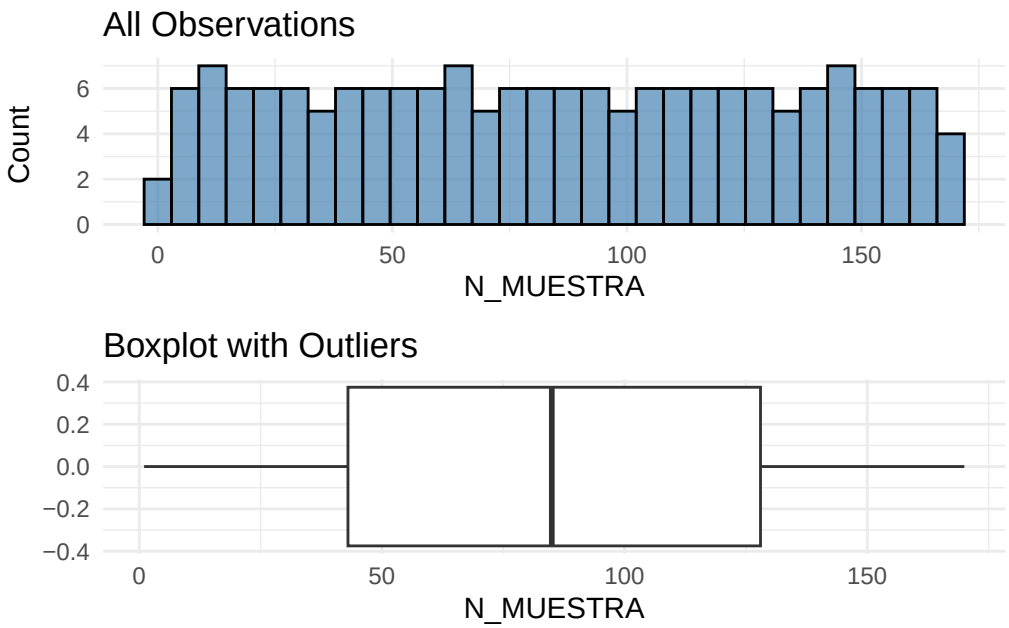

```
Outliers identified in FIBRA :  0 outliers
Proportion (%) of outliers: 0 %
```




```
Outliers identified in SELENIO :  2 outliers
Proportion (%) of outliers: 1.16 %
```



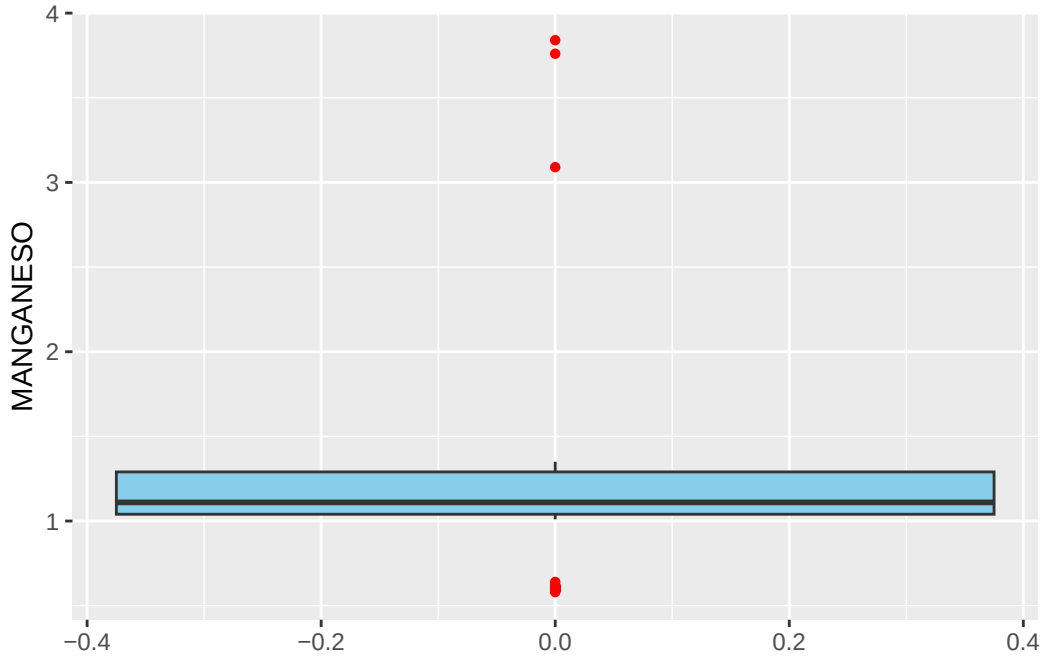
```
Outliers identified in FOSFORO :  0 outliers
Proportion (%) of outliers: 0 %
```




```
Outliers identified in N_MUESTRA :  0 outliers
Proportion (%) of outliers: 0 %
```

## Estudio de la variable MANGANESO

```
##### MANGANESO #####
ggplot(datos, aes(y = MANGANESO)) +
  geom_boxplot(fill = "skyblue", outlier.color = "red", outlier.shape = 16)
```




```
###Los valores atípicos son:
outlier_values <- boxplot.stats(datos$MANGANESO)$out  # outlier values.
out_ind <- which(datos$MANGANESO %in% c(outlier_values))
datos[out_ind,]
```

| | VARIEDAD | MANGANESO | CALORIAS | FIBRA | SELENIO | FOSFORO | N_MUESTRA |
|---|---|---|---|---|---|---|---|
| 3 | CEBADA | 0.61 | 125.51 | 14.22 | 36.02 | 223.60 | 3 |
| 7 | CEBADA | 0.60 | 125.79 | 14.55 | 35.62 | 241.42 | 7 |
| 14 | CEBADA | 0.61 | 128.85 | 15.21 | 37.24 | 224.16 | 14 |
| 16 | CEBADA | 0.61 | 125.91 | 14.10 | 35.93 | 223.52 | 16 |
| 18 | CEBADA | 0.62 | 125.96 | 13.71 | 36.01 | 224.21 | 18 |
| 22 | CEBADA | 0.61 | 128.38 | 13.60 | 36.12 | 198.93 | 22 |
| 29 | CEBADA | 0.59 | 128.49 | 14.33 | 37.08 | 239.49 | 29 |
| 31 | CEBADA | 0.60 | 124.93 | 13.72 | 36.64 | 217.40 | 31 |
| 40 | CEBADA | 0.59 | 128.05 | 14.05 | 36.03 | 231.20 | 39 |
| 41 | CEBADA | 0.61 | 129.63 | 13.76 | 34.84 | 223.49 | 40 |
| 48 | CEBADA | 0.59 | 129.72 | 14.51 | 35.59 | 211.20 | 47 |
| 50 | CEBADA | 0.61 | 126.18 | 14.88 | 37.92 | 227.01 | 49 |
| 52 | CEBADA | 0.61 | 127.05 | 13.38 | 35.92 | 223.63 | 51 |
| 54 | CEBADA | 0.59 | 118.07 | 14.69 | 36.86 | 227.43 | 53 |
| 61 | CEBADA | 3.09 | 130.02 | 15.04 | 36.14 | 232.83 | 60 |
| 68 | CEBADA | 0.61 | 128.52 | 14.26 | 36.91 | 234.63 | 67 |

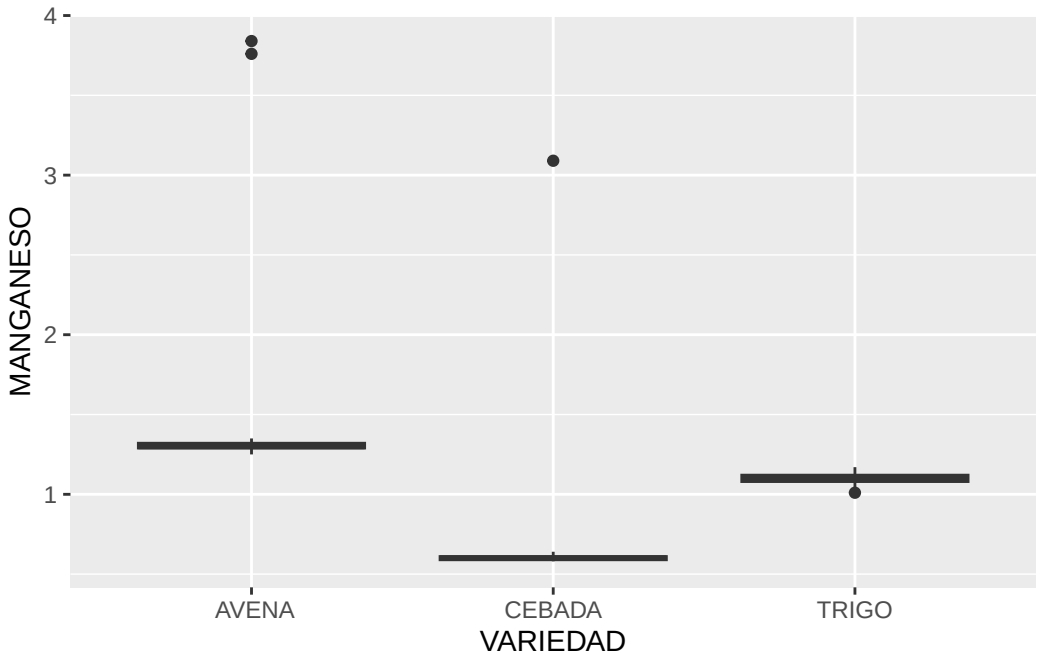
| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 69 | CEBADA | 0.60 | 130.14 | 13.19 | 66.00 | 228.88 | 68 |
| 77 | CEBADA | 0.59 | 125.04 | 14.61 | 35.78 | 217.11 | 76 |
| 85 | CEBADA | 0.61 | 129.19 | 12.91 | 36.27 | 224.26 | 84 |
| 87 | CEBADA | 0.61 | 124.95 | 13.44 | 34.82 | 209.90 | 86 |
| 88 | CEBADA | 0.60 | 126.85 | 13.75 | 35.55 | 212.31 | 87 |
| 97 | CEBADA | 0.59 | 124.56 | 13.76 | 34.63 | 237.14 | 96 |
| 98 | CEBADA | 0.60 | 127.36 | 13.41 | 35.64 | 227.27 | 97 |
| 99 | CEBADA | 0.58 | 124.43 | 14.87 | 34.87 | 250.89 | 98 |
| 105 | CEBADA | 0.60 | 124.60 | 13.63 | 35.12 | 224.93 | 104 |
| 108 | CEBADA | 0.59 | 126.64 | 12.63 | 36.02 | 232.20 | 106 |
| 110 | CEBADA | 0.60 | 126.32 | 13.99 | 36.51 | 226.30 | 108 |
| 112 | AVENA | 3.76 | 150.18 | 0.83 | 18.99 | 162.01 | 110 |
| 113 | CEBADA | 0.59 | 126.65 | 13.31 | 36.03 | 255.18 | 111 |
| 117 | CEBADA | 0.60 | 125.66 | 14.04 | 35.40 | 241.55 | 115 |
| 122 | CEBADA | 0.61 | 126.38 | 14.23 | 35.90 | 238.78 | 120 |
| 127 | AVENA | 3.84 | 150.51 | 0.72 | 18.67 | 167.37 | 125 |
| 131 | CEBADA | 0.62 | 126.83 | 13.37 | 34.74 | 216.66 | 129 |
| 137 | CEBADA | 0.60 | 128.03 | 13.16 | 35.17 | 218.92 | 135 |
| 138 | CEBADA | 0.59 | 127.53 | 14.54 | 36.33 | 234.38 | 136 |
| 139 | CEBADA | 0.60 | 124.55 | 13.82 | 36.08 | 218.57 | 137 |
| 145 | CEBADA | 0.61 | 126.32 | 13.74 | 35.38 | 217.58 | 143 |
| 154 | CEBADA | 0.64 | 128.94 | 14.94 | 35.86 | 231.59 | 152 |
| 155 | CEBADA | 0.60 | 127.24 | 13.57 | 36.53 | 229.52 | 153 |
| 161 | CEBADA | 0.59 | 128.60 | 14.16 | 36.86 | 238.80 | 159 |
| 170 | CEBADA | 0.60 | 125.52 | 14.02 | 36.46 | 231.55 | 167 |
| 172 | CEBADA | 0.62 | 127.74 | 13.95 | 35.94 | 226.46 | 169 |

```
###Los valores extremos son:
extreme_values <- boxplot.stats(datos$MANGANESO,coef=3)$out  # extreme values.
ext_ind <- which(datos$MANGANESO %in% c(extreme_values))
datos[ext_ind,]
```

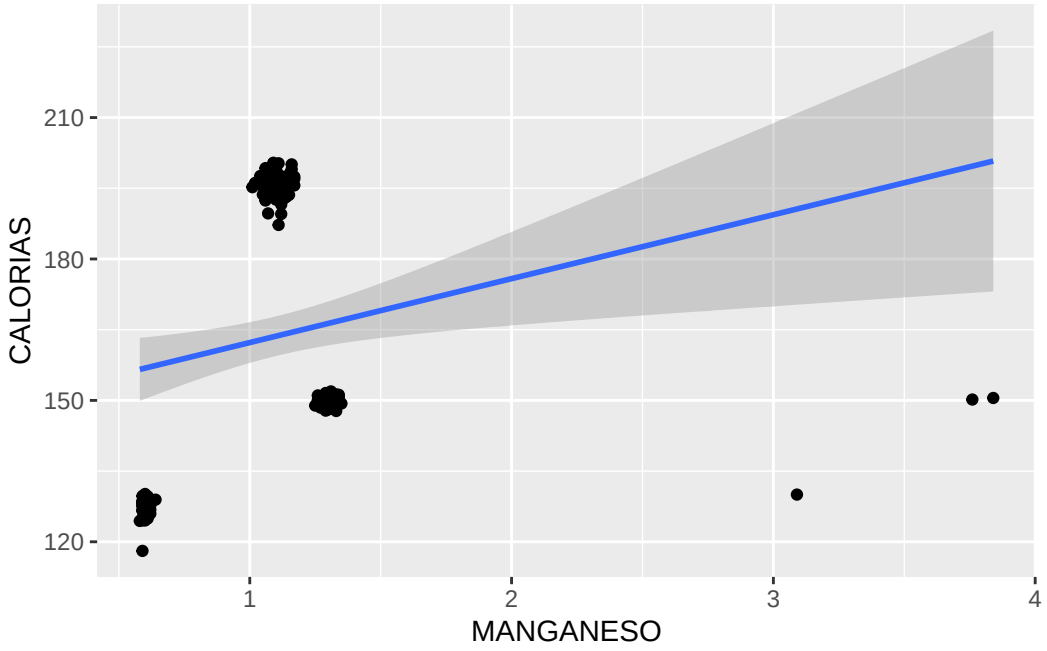
| | VARIEDAD | MANGANESO | CALORIAS | FIBRA | SELENIO | FOSFORO | N_MUESTRA |
|---|---|---|---|---|---|---|---|
| 61 | CEBADA | 3.09 | 130.02 | 15.04 | 36.14 | 232.83 | 60 |
| 112 | AVENA | 3.76 | 150.18 | 0.83 | 18.99 | 162.01 | 110 |
| 127 | AVENA | 3.84 | 150.51 | 0.72 | 18.67 | 167.37 | 125 |

```
library(patchwork)  # Para combinar gráficos fácilmente

# Gráfico 1: Manganeso por variedad
p1 <- ggplot(datos, aes(x = VARIEDAD, y = MANGANESO)) +
  geom_boxplot(fill = "lightblue")
```

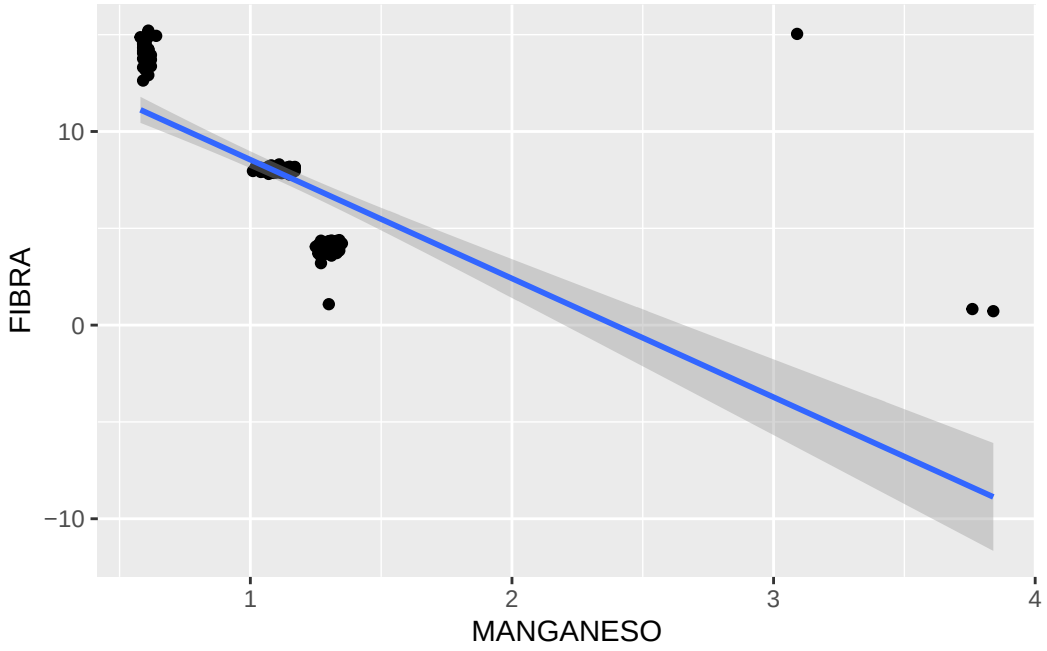
```
p1
```



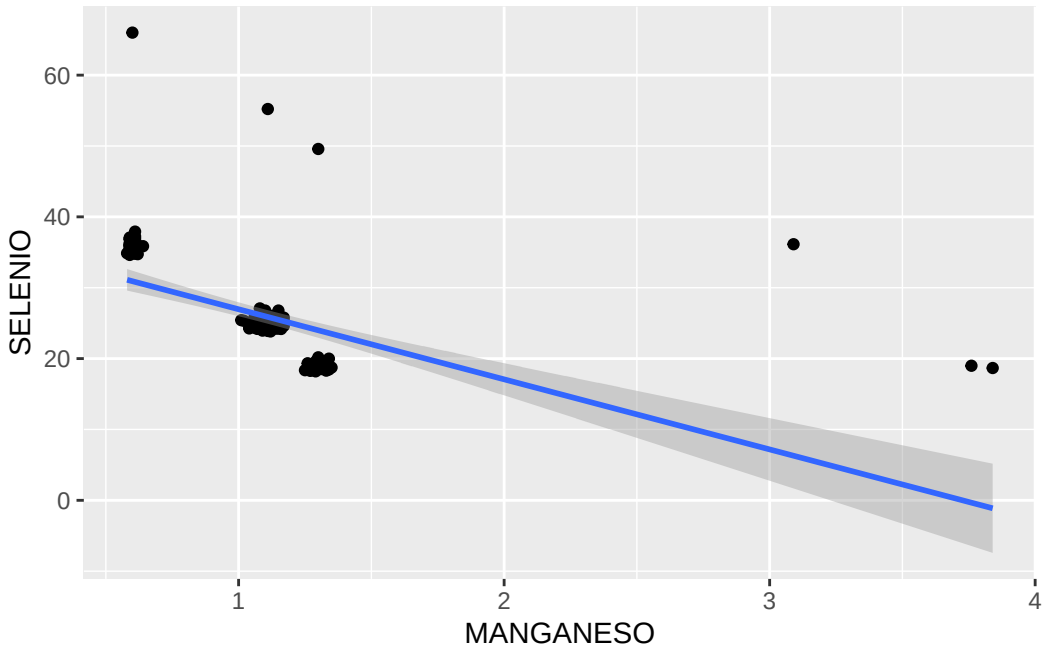

```
ggp <- ggplot(datos,aes(MANGANESO, CALORIAS)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```



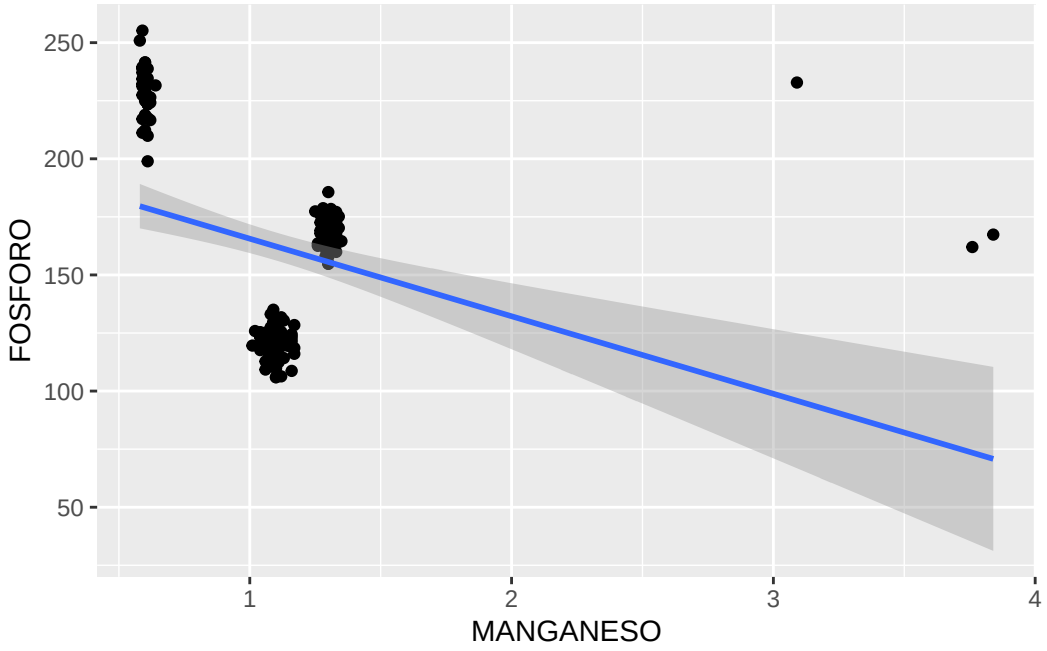

```
ggp <- ggplot(datos,aes(MANGANESO, FIBRA)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```




```
ggp <- ggplot(datos,aes(MANGANESO, SELENIO)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```



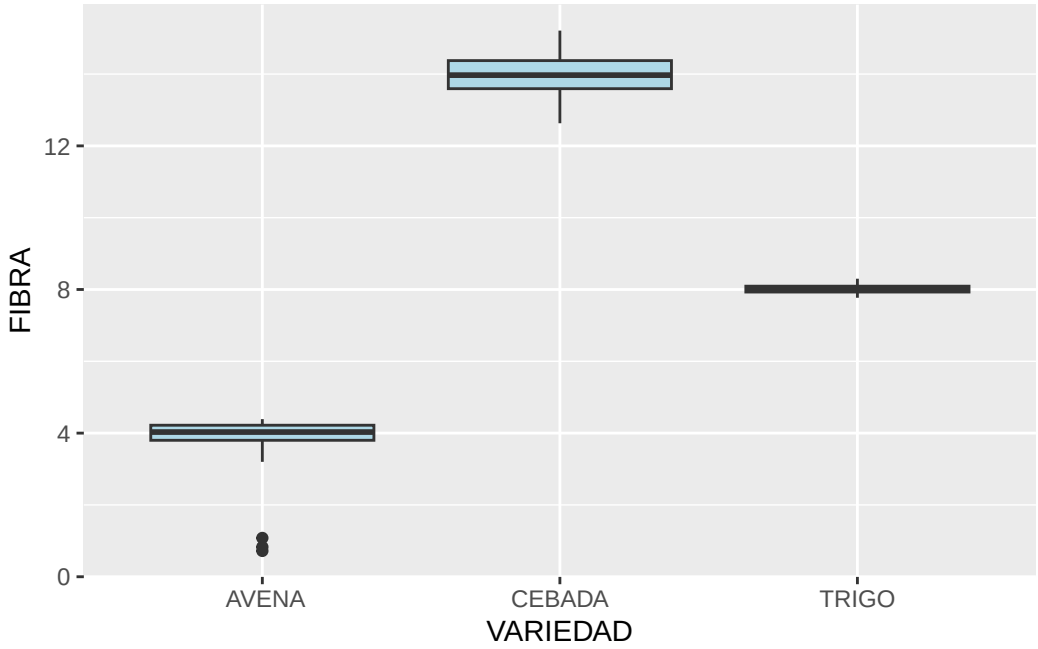

```
ggp <- ggplot(datos,aes(MANGANESO, FOSFORO)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```




Los outliers son un porcentaje muy elevado, pero los extremos corresponden a un 1.73%, y además en la inspección gráfico vemos claramente que son outliers. Los borraremos.

## Estudio de la variable FIBRA

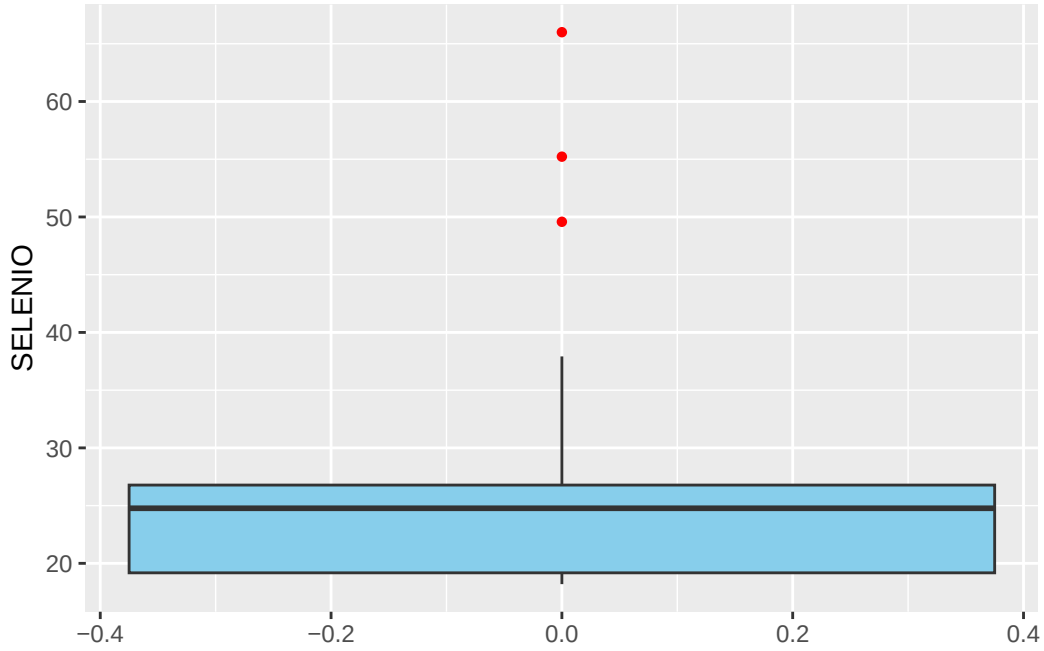
```
# Gráfico 1: Manganeso por variedad
p1 <- ggplot(datos, aes(x = VARIEDAD, y = FIBRA)) +
  geom_boxplot(fill = "lightblue")

p1
```




El porcentaje de ouliers es de un 8% y además se ve claramente que es debido a una distribución asimétrica, por tanto, no vamos a borrarlos, no son outliers

## Estudio de la variable SELENIO

```
##### SELENIO #####
ggplot(datos, aes(y = SELENIO)) +
  geom_boxplot(fill = "skyblue", outlier.color = "red", outlier.shape = 16)
```




```
###Los valores atípicos son:
outlier_values <- boxplot.stats(datos$SELENIO)$out  # outlier values.
out_ind <- which(datos$SELENIO %in% c(outlier_values))
datos[out_ind,]
```

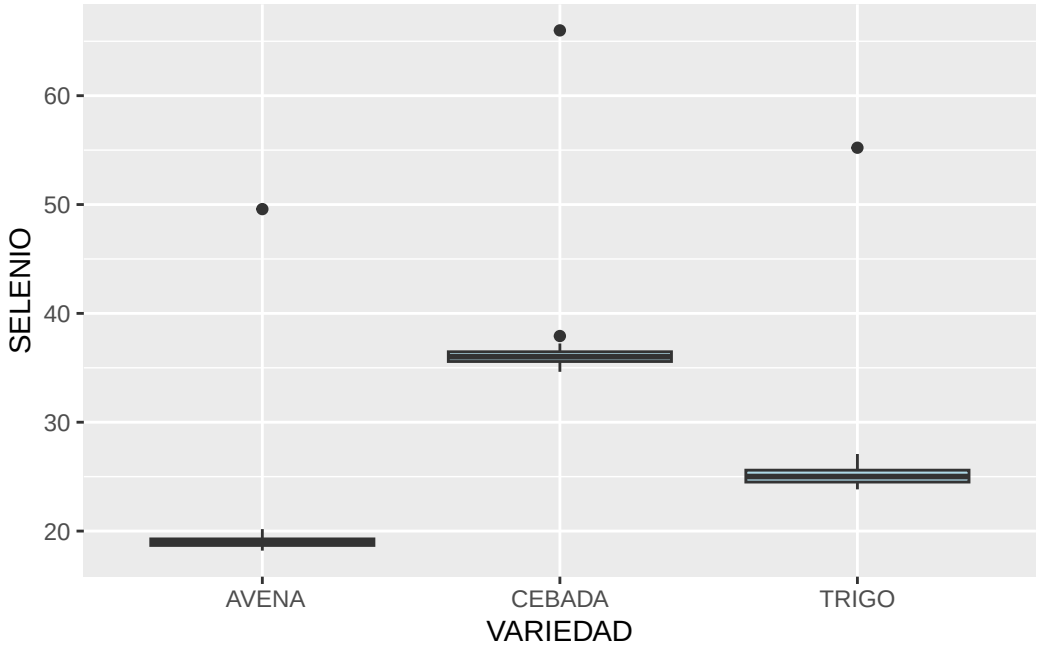
```
    VARIEDAD MANGANESO CALORIAS FIBRA SELENIO FOSFORO N_MUESTRA
23     TRIGO      1.11   187.22  7.95   55.22  126.64        23
69    CEBADA      0.60   130.14 13.19   66.00  228.88        68
142    AVENA      1.30   150.18  1.08   49.58  168.59       140
```

```
###Los valores extremos son:
extreme_values <- boxplot.stats(datos$SELENIO,coef=3)$out  # extreme values.
ext_ind <- which(datos$SELENIO %in% c(extreme_values))
datos[ext_ind,]
```

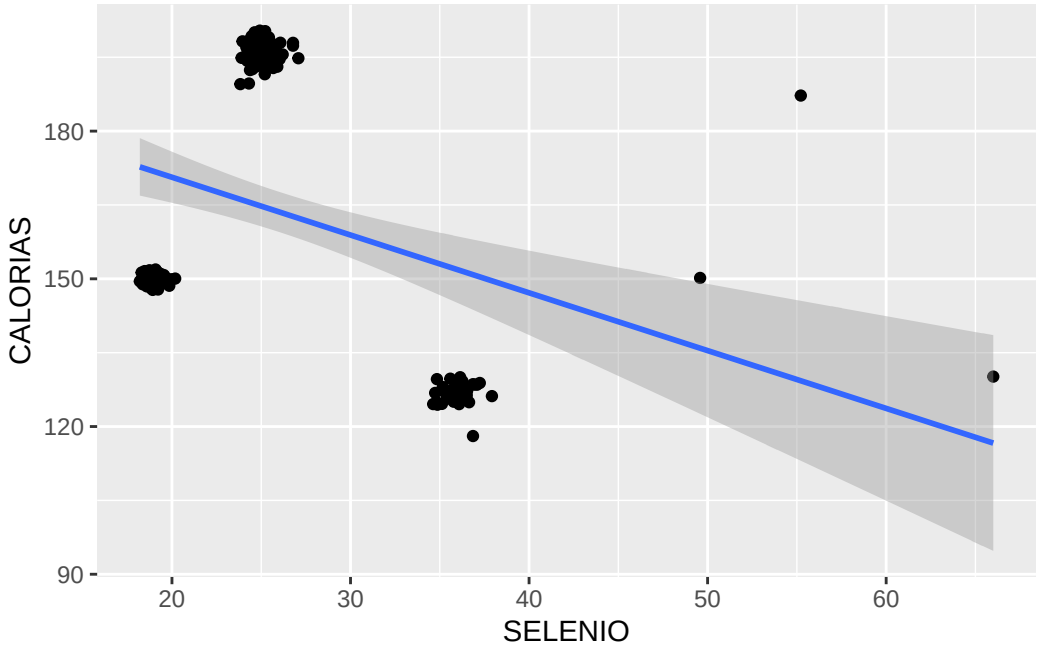
```
   VARIEDAD MANGANESO CALORIAS FIBRA SELENIO FOSFORO N_MUESTRA
23    TRIGO      1.11   187.22  7.95   55.22  126.64        23
69   CEBADA      0.60   130.14 13.19   66.00  228.88        68
```

```
# Gráfico 1: Pressure Height por mes
p1 <- ggplot(datos, aes(x = VARIEDAD, y = SELENIO)) +
```

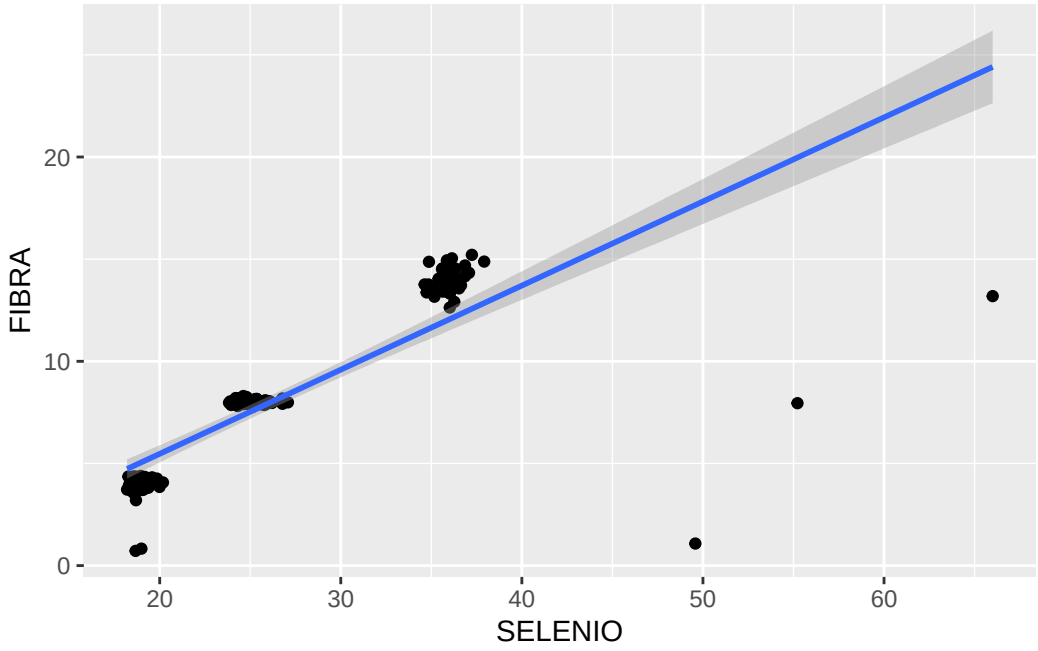
```
  geom_boxplot(fill = "lightblue")

p1
```



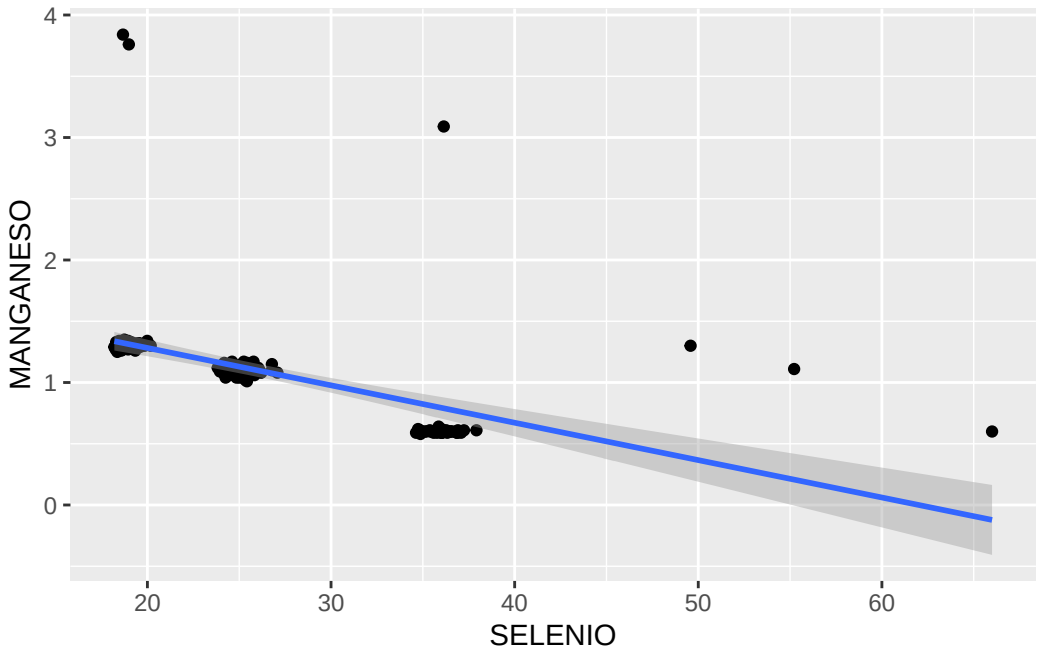

```
ggp <- ggplot(datos,aes(SELENIO, CALORIAS)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```



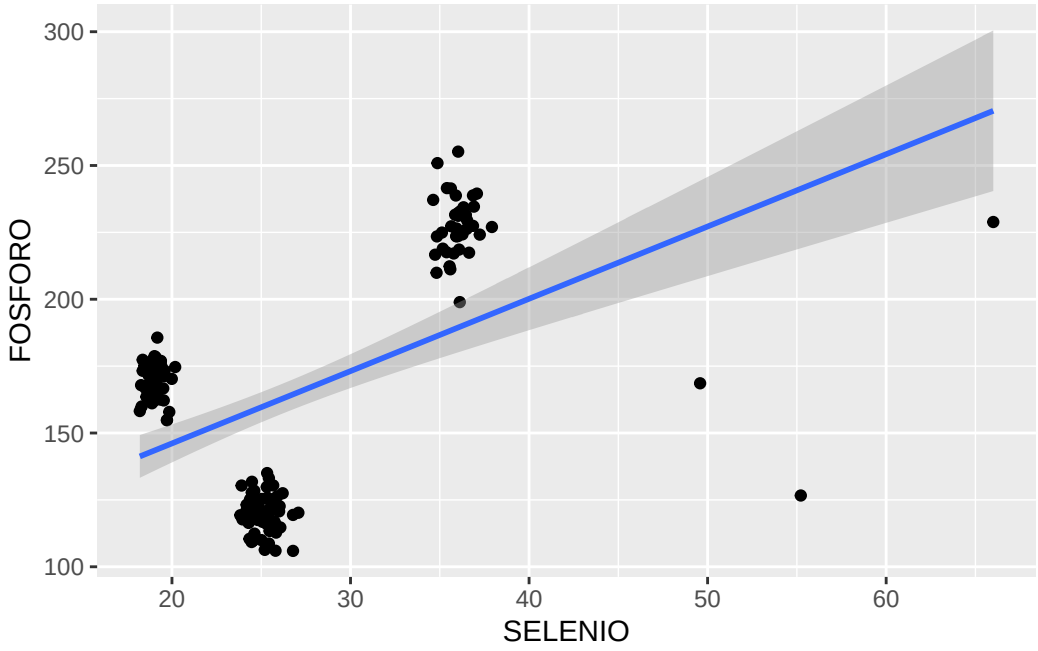

```
ggp <- ggplot(datos,aes(SELENIO, FIBRA)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```




```
ggp <- ggplot(datos,aes(SELENIO, MANGANESO)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```




```
ggp <- ggplot(datos,aes(SELENIO, FOSFORO)) + geom_point()
ggp + stat_smooth(method = "lm",
                  formula = y ~ x,
                  geom = "smooth")
```




Vamos a borrar los outliers de SELENIO y los extremos de manganeso

```
extreme_values <- boxplot.stats(datos$MANGANESO,coef=3)$out  # extreme values.
ext_ind <- which(datos$MANGANESO %in% c(extreme_values))
datos[ext_ind,]
```

```
    VARIEDAD MANGANESO CALORIAS FIBRA SELENIO FOSFORO N_MUESTRA
61    CEBADA      3.09   130.02 15.04   36.14  232.83        60
112    AVENA      3.76   150.18  0.83   18.99  162.01       110
127    AVENA      3.84   150.51  0.72   18.67  167.37       125
```

```
datos$MANGANESO[ext_ind]<-NA


outlier_values <- boxplot.stats(datos$SELENIO)$out  # outlier values.
out_ind <- which(datos$SELENIO %in% c(outlier_values))
datos[out_ind,]
```

```
    VARIEDAD MANGANESO CALORIAS FIBRA SELENIO FOSFORO N_MUESTRA
23     TRIGO      1.11   187.22  7.95   55.22  126.64        23
69    CEBADA      0.60   130.14 13.19   66.00  228.88        68
142    AVENA      1.30   150.18  1.08   49.58  168.59       140
```

```r
datos$SELENIO[out_ind]<-NA

summary(datos)
```

```
   VARIEDAD    MANGANESO        CALORIAS         FIBRA           SELENIO     
 AVENA:61   Min.   :0.580   Min.   :118.1   Min.   : 0.720   Min.   :18.20  
CEBADA:40   1st Qu.:1.040   1st Qu.:148.1   1st Qu.: 4.180   1st Qu.:19.17  
TRIGO :72   Median :1.110   Median :150.8   Median : 7.970   Median :24.77  
            Mean   :1.056   Mean   :163.6   Mean   : 7.931   Mean   :25.43  
            3rd Qu.:1.290   3rd Qu.:195.2   3rd Qu.: 8.190   3rd Qu.:26.17  
            Max.   :1.350   Max.   :200.4   Max.   :15.210   Max.   :37.92  
            NA's   :3                                        NA's   :3      
    FOSFORO        N_MUESTRA     
 Min.   :105.9   Min.   :  1.0  
 1st Qu.:121.9   1st Qu.: 43.0  
 Median :164.5   Median : 85.0  
 Mean   :162.3   Mean   : 85.3  
 3rd Qu.:177.4   3rd Qu.:128.0  
 Max.   :255.2   Max.   :170.0  
```

## Estudio Multivariante

```r
library(dbscan)
```

```
Warning: package 'dbscan' was built under R version 4.3.3
```

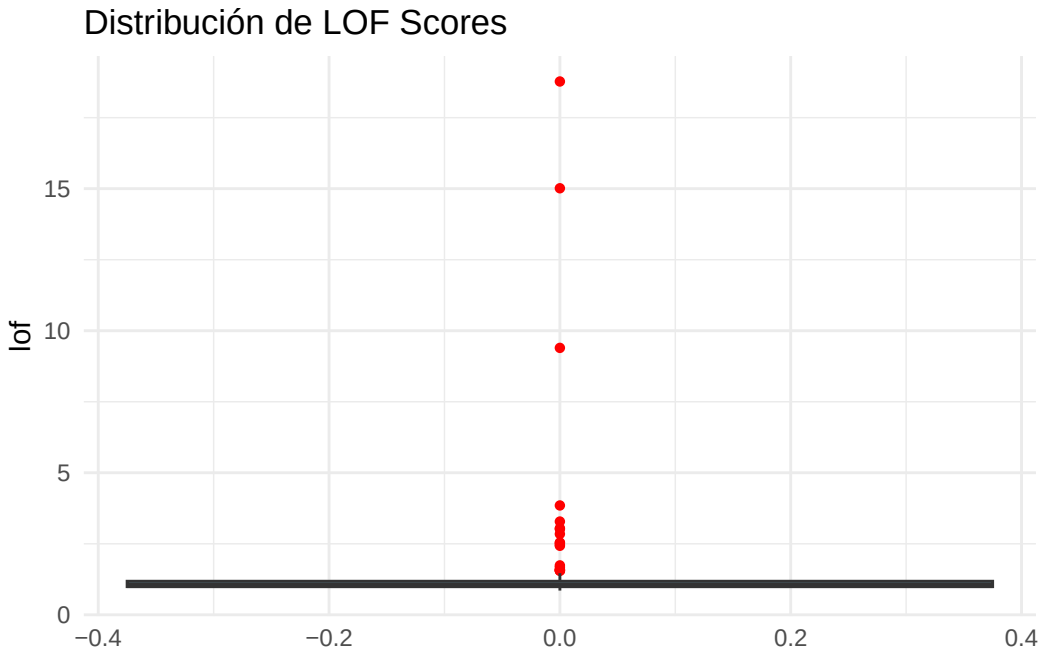
```
Attaching package: 'dbscan'
```

```
The following object is masked from 'package:stats':

    as.dendrogram
```

```r
library(class)
```

```
Warning: package 'class' was built under R version 4.3.3
```

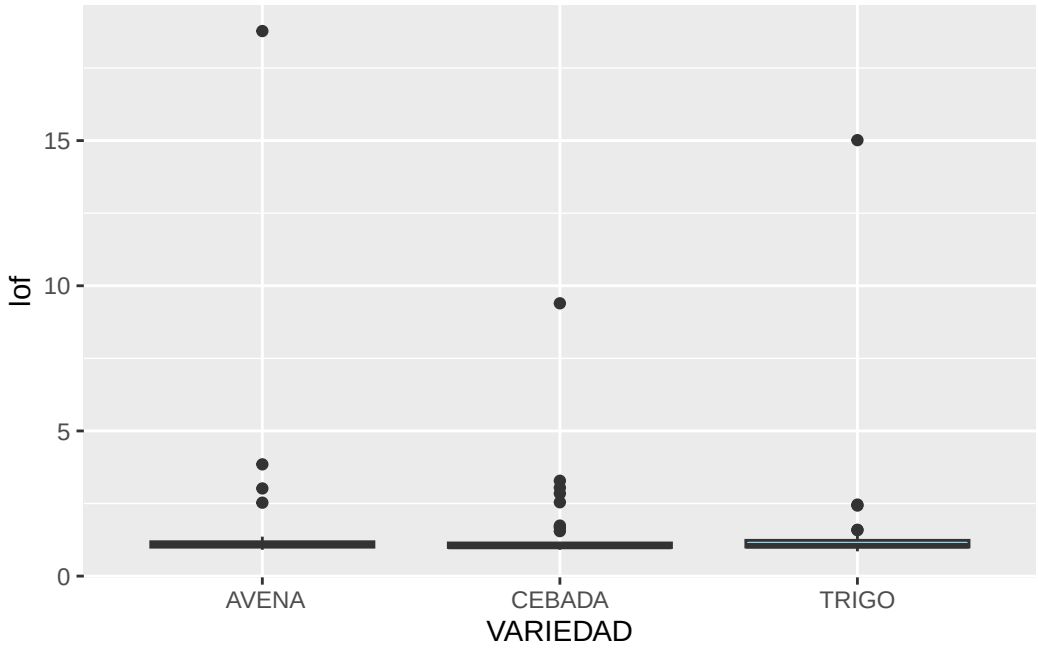
```r
library(ggplot2)

datos <- read.csv("CEREALES.csv")  # import data
datos$VARIEDAD<-factor(datos$VARIEDAD)

####Aplicamos LOF
k<-round(log(nrow(datos)))
lof<-lof(select(datos,-VARIEDAD,-N_MUESTRA),minPts = k)

datos$lof<-lof

ggplot(datos, aes(y = lof)) +
  geom_boxplot(fill = "skyblue", outlier.color = "red", outlier.shape = 16) +
  theme_minimal() +
  labs(title = "Distribución de LOF Scores")
```




```r
datos[lof>5,]
```

```
    VARIEDAD MANGANESO CALORIAS FIBRA SELENIO FOSFORO N_MUESTRA       lof
23     TRIGO      1.11   187.22  7.95   55.22  126.64        23 15.015167
69    CEBADA      0.60   130.14 13.19   66.00  228.88        68  9.395902
142    AVENA      1.30   150.18  1.08   49.58  168.59       140 18.772921
```

```
####Comprobamos las cualitativas
ggplot(datos, aes(x = VARIEDAD, y = lof)) +
  geom_boxplot(fill = "lightblue")
```



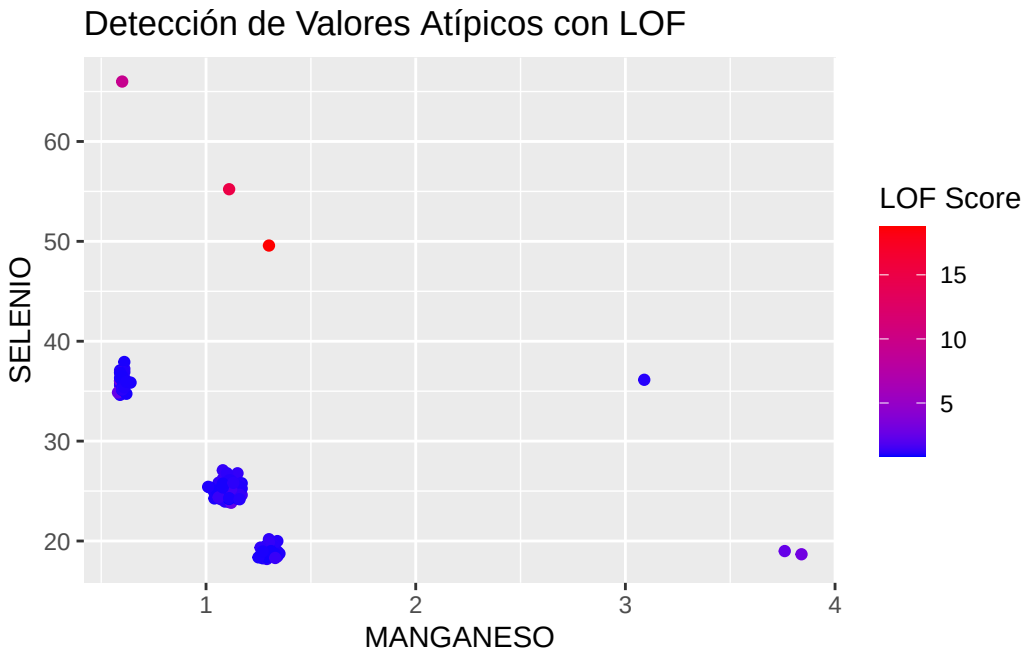

```
###Vamos a ver si son los mismos que los datos que hemos quitado
extreme_values <- boxplot.stats(datos$MANGANESO,coef=3)$out  # extreme values.
ext_ind <- which(datos$MANGANESO %in% c(extreme_values))
datos[ext_ind,]
```

```
    VARIEDAD MANGANESO CALORIAS FIBRA SELENIO FOSFORO N_MUESTRA      lof
61    CEBADA      3.09   130.02 15.04   36.14  232.83        60 1.093118
112    AVENA      3.76   150.18  0.83   18.99  162.01       110 2.529654
127    AVENA      3.84   150.51  0.72   18.67  167.37       125 3.019403
```

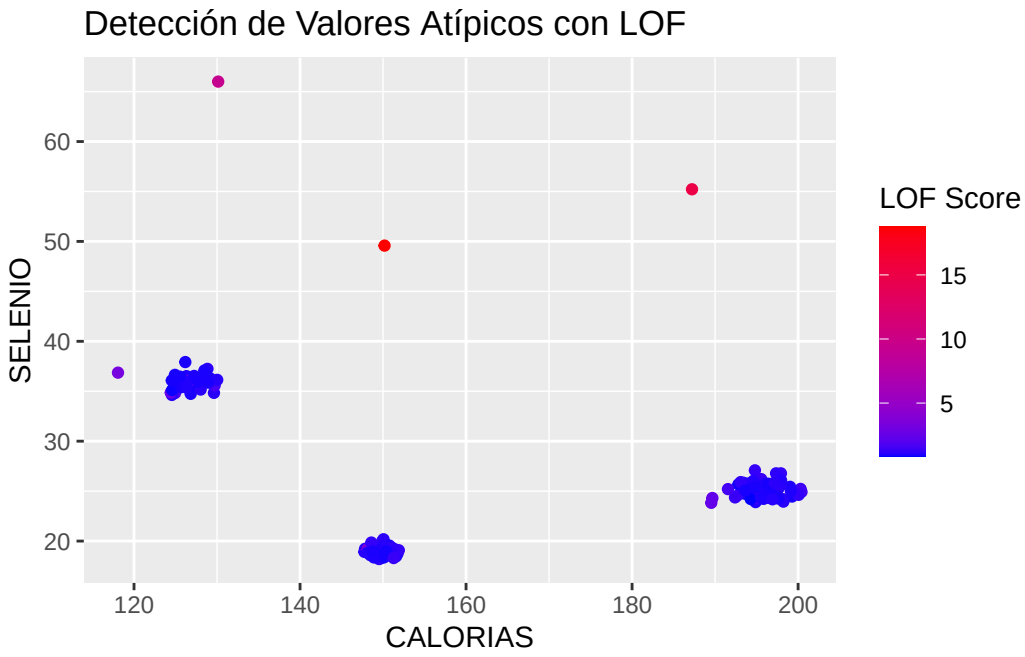
```
outlier_values <- boxplot.stats(datos$SELENIO)$out  # outlier values.
out_ind <- which(datos$SELENIO %in% c(outlier_values))
datos[out_ind,]
```

```
    VARIEDAD MANGANESO CALORIAS FIBRA SELENIO FOSFORO N_MUESTRA       lof
23     TRIGO      1.11   187.22  7.95   55.22  126.64        23 15.015167
69    CEBADA      0.60   130.14 13.19   66.00  228.88        68  9.395902
142    AVENA      1.30   150.18  1.08   49.58  168.59       140 18.772921
```

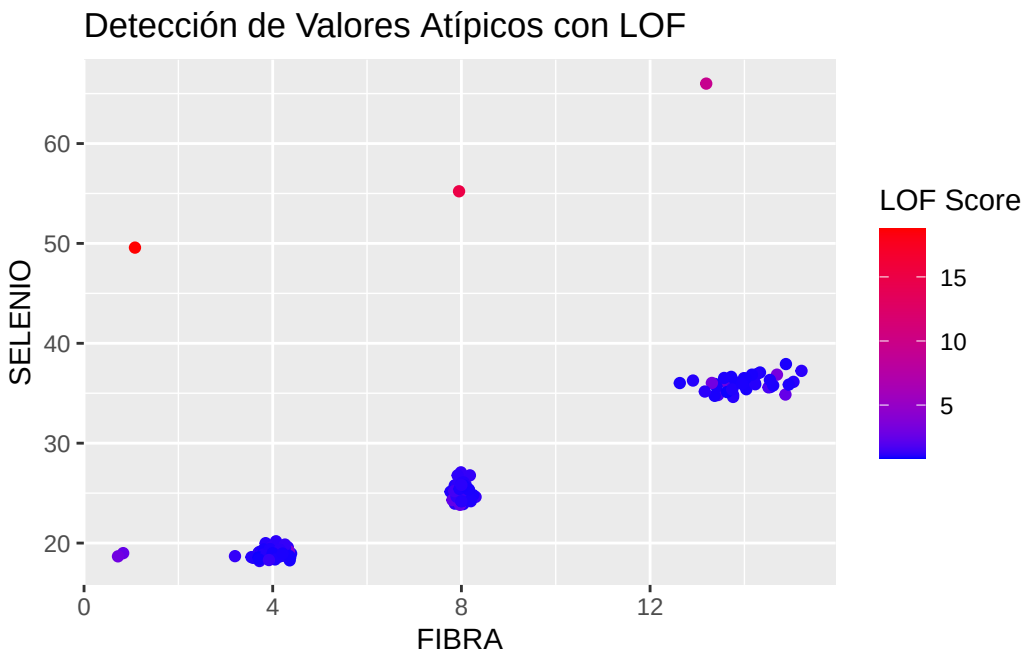
```r
####Comprobamos las cuantitativas
ggplot(datos, aes(x = MANGANESO, y = SELENIO, colour = lof)) +
  geom_point() +
  scale_color_gradient(low = "blue", high = "red", name = "LOF Score") +
  labs(title = "Detección de Valores Atípicos con LOF")
```



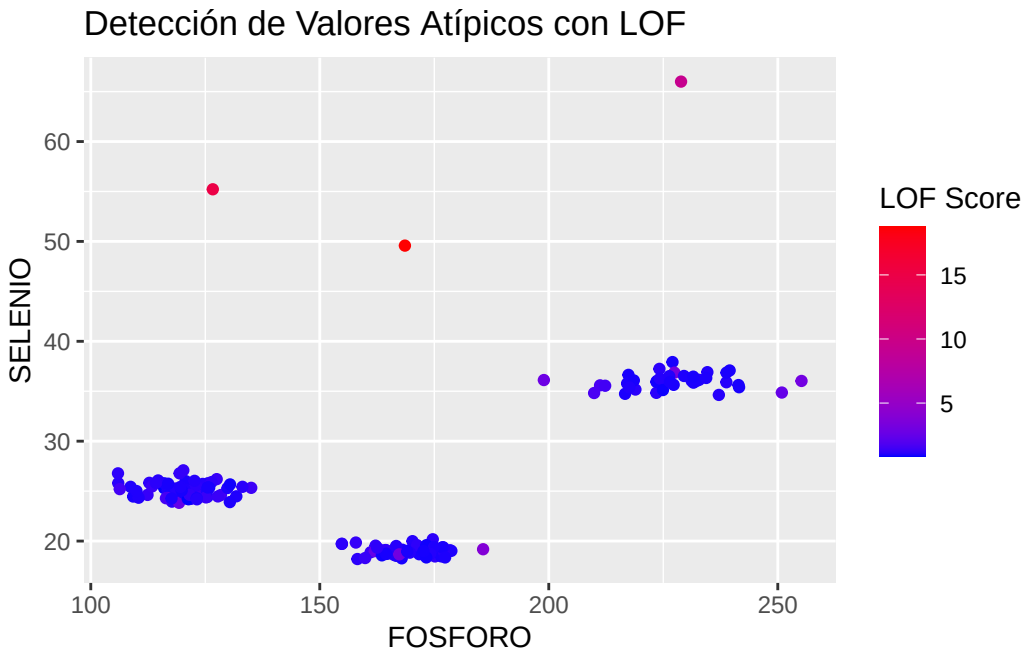

```r
ggplot(datos, aes(x = CALORIAS, y = SELENIO, colour = lof)) +
  geom_point() +
  scale_color_gradient(low = "blue", high = "red", name = "LOF Score") +
  labs(title = "Detección de Valores Atípicos con LOF")
```




```
ggplot(datos, aes(x = FIBRA, y = SELENIO, colour = lof)) +
  geom_point() +
  scale_color_gradient(low = "blue", high = "red", name = "LOF Score") +
  labs(title = "Detección de Valores Atípicos con LOF")
```




```
ggplot(datos, aes(x = FOSFORO, y = SELENIO, colour = lof)) +
  geom_point() +
  scale_color_gradient(low = "blue", high = "red", name = "LOF Score") +
  labs(title = "Detección de Valores Atípicos con LOF")
```


Detección de Valores Atípicos con LOF
SELENIO
FOSFORO
60
50
40
30
20
100
150
200
250
LOF Score
15
10
5