TFM - Anexo de Prácticas

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3.2.1 Visión práctica del problema

```
# Calculo la media
y <- c(4, 6, 7)
mean(y)
```

```
## [1] 5.666667
```

```
# Calculo la media, pero hay un dato faltante
y <- c(4, 6, NA)
mean(y)
```

```
## [1] NA
```

```
# Utilizando el argumento na.rm=TRUE
y <- c(4, 6, NA)
mean(y, na.rm=TRUE)
```

```
## [1] 5
```

```
# Verifico cual es el directorio de trabajo
getwd()
```

```
## [1] "/Users/MacMini/UOC - M0.168 TFM"
```

```
# Defino directorio de trabajo
setwd("~/UOC - M0.168 TFM")

# Quito todas las variables de ambiente
rm(list=ls())

# Primer vistazo de los contenidos del fichero
readLines("HOC.csv", n=5)
```

```
## [1]
"\"\",\"surgery\",\"Age\",\"Hospital_Number\",\"rectal_temp\",\"pulse\",\
"resp_rate\",\"extremities_temp\",\"peripheral_pulse\",\"mucous_membranes
\",\"capillary_refill_time\",\"pain\",\"peristalsis\",\"abdominal_distens
ion\",\"nasogastric_tube\",\"nasogastric_reflux\",\"nasogastric_reflux_PH
\",\"rectal_examination_feces\",\"abdomen\",\"packed_cell_volume\",\"tota
l_protein\",\"abdominocentesis_appearance\",\"abdomcentesis_total_protein
\",\"outcome\",\"surgical_lesion\",\"type_of_lesion_1\",\"type_of_lesion_
2\",\"type_of_lesion_3\",\"cp_data\""
## [2]
"\"1\",2,1,530101,38.5,66,28,3,3,NA,2,5,4,4,NA,NA,NA,3,5,45,8.4,NA,NA,2,2
,11300,0,0,2"
## [3]
"\"2\",1,1,534817,39.2,88,20,NA,NA,4,1,3,4,2,NA,NA,NA,4,2,50,85,2,2,3,2,2
208,0,0,2"
## [4]
"\"3\",2,1,530334,38.3,40,24,1,1,3,1,3,3,1,NA,NA,NA,1,1,33,6.7,NA,NA,1,2,
0,0,0,1"
## [5]
"\"4\",1,9,5290409,39.1,164,84,4,1,6,2,2,4,4,1,2,5,3,NA,48,7.2,3,5.3,2,1,
2208,0,0,1"
```

```
# Ahora leo el fichero .csv y lo cargo
HOC <- read.table("HOC.csv", sep=",", dec=".",header=TRUE,
stringsAsFactors=FALSE)
names(HOC)
```

```
##  [1] "X"                          "surgery"
##  [3] "Age"                        "Hospital_Number"
##  [5] "rectal_temp"                "pulse"
##  [7] "resp_rate"                  "extremities_temp"
##  [9] "peripheral_pulse"           "mucous_membranes"
## [11] "capillary_refill_time"      "pain"
## [13] "peristalsis"                "abdominal_distension"
## [15] "nasogastric_tube"           "nasogastric_reflux"
## [17] "nasogastric_reflux_PH"      "rectal_examination_feces"
## [19] "abdomen"                    "packed_cell_volume"
## [21] "total_protein"              "abdominocentesis_appearance"
## [23] "abdomcentesis_total_protein" "outcome"
## [25] "surgical_lesion"            "type_of_lesion_1"
## [27] "type_of_lesion_2"           "type_of_lesion_3"
## [29] "cp_data"
```

```
# Verifico estructura del dataframe
str(HOC)
```

```
## 'data.frame':    300 obs. of  29 variables:
##  $ X                          : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ surgery                    : int  2 1 2 1 2 2 1 1 2 2 ...
##  $ Age                        : int  1 1 1 9 1 1 1 1 1 9 ...
##  $ Hospital_Number            : int  530101 534817 530334 5290409
```

```
530255 528355 526802 529607 530051 5299629 ...
##  $ rectal_temp                : num  38.5 39.2 38.3 39.1 37.3 NA 37.9
NA NA 38.3 ...
##  $ pulse                      : int  66 88 40 164 104 NA 48 60 80 90
...
##  $ resp_rate                  : int  28 20 24 84 35 NA 16 NA 36 NA ...
##  $ extremities_temp           : int  3 NA 1 4 NA 2 1 3 3 1 ...
##  $ peripheral_pulse           : int  3 NA 1 1 NA 1 1 NA 4 NA ...
##  $ mucous_membranes           : int  NA 4 3 6 6 3 1 NA 3 1 ...
##  $ capillary_refill_time      : int  2 1 1 2 2 1 1 1 1 1 ...
##  $ pain                       : int  5 3 3 2 NA 2 3 NA 4 5 ...
##  $ peristalsis                : int  4 4 3 4 NA 3 3 4 4 3 ...
##  $ abdominal_distension       : int  4 2 1 4 NA 2 3 2 4 1 ...
##  $ nasogastric_tube           : int  NA NA NA 1 NA 2 1 2 2 2 ...
##  $ nasogastric_reflux         : int  NA NA NA 2 NA 1 1 1 1 1 ...
##  $ nasogastric_reflux_PH      : num  NA NA NA 5 NA NA NA NA NA NA ...
##  $ rectal_examination_feces   : int  3 4 1 3 NA 3 3 3 3 3 ...
##  $ abdomen                    : int  5 2 1 NA NA 3 5 4 5 NA ...
##  $ packed_cell_volume         : num  45 50 33 48 74 NA 37 44 38 40 ...
##  $ total_protein              : num  8.4 85 6.7 7.2 7.4 NA 7 8.3 6.2
6.2 ...
##  $ abdominocentesis_appearance: int  NA 2 NA 3 NA NA NA NA NA 1 ...
##  $ abdomcentesis_total_protein: num  NA 2 NA 5.3 NA NA NA NA NA 2.2
...
##  $ outcome                    : int  2 3 1 2 2 1 1 2 3 1 ...
##  $ surgical_lesion            : int  2 2 2 1 2 2 1 1 1 2 ...
##  $ type_of_lesion_1           : int  11300 2208 0 2208 4300 0 3124
2208 3205 0 ...
##  $ type_of_lesion_2           : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ type_of_lesion_3           : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ cp_data                    : int  2 2 1 1 2 2 2 2 2 1 ...
```

```
# Guardo el dataset HOC para generar el fichero HOC.rds
# (a efectos de reproducibilidad posterior)
saveRDS(HOC, "HOC.rds")

# Apertura del dataset HOC
# (Descomentar la línea siguiente si fuera necesario abrirlo para
reproducibilidad posterior)
# HOC <- readRDS("HOC.rds")
```

3.2.2 Listwise Deletion

```
# Genero modelo de regresión lineal
fit<-lm(pulse ~ type_of_lesion_1, data=HOC)

# Se borran los registros con datos faltantes al utilizar el argumento
```

```
'na.action = na.omit'
fit <- lm(pulse ~ type_of_lesion_1, data=HOC, na.action = na.omit)
coef(fit)
```

```
##      (Intercept) type_of_lesion_1
##     7.037461e+01     4.271436e-04
```

```
# Verificar cuantos registros fueron eliminados
eliminados <- na.action(fit)
naprint(eliminados)
```

```
## [1] "24 observations deleted due to missingness"
```

```
# Más registros con valores faltantes si agrego la variable
"abdominal_distension" como predictora
fit2 <- lm(pulse ~ type_of_lesion_1 + abdominal_distension, data=HOC)
naprint(na.action(fit2))
```

```
## [1] "71 observations deleted due to missingness"
```

3.2.3 Pairwise Deletion

```
colMeans(HOC, na.rm = TRUE)
```

```
##                             X                        surgery
##                  1.505000e+02                  1.397993e+00
##                           Age                Hospital_Number
##                  1.640000e+00                  1.085889e+06
##                   rectal_temp                          pulse
##                  3.816792e+01                  7.191304e+01
##                     resp_rate              extremities_temp
##                  3.041736e+01                  2.348361e+00
##              peripheral_pulse              mucous_membranes
##                  2.017316e+00                  2.853755e+00
##         capillary_refill_time                          pain
##                  1.305970e+00                  2.951020e+00
##                   peristalsis         abdominal_distension
##                  2.917969e+00                  2.266393e+00
##              nasogastric_tube           nasogastric_reflux
##                  1.755102e+00                  1.582474e+00
##         nasogastric_reflux_PH     rectal_examination_feces
##                  4.707547e+00                  2.757576e+00
##                       abdomen           packed_cell_volume
##                  3.692308e+00                  4.629520e+01
##                 total_protein abdominocentesis_appearance
##                  2.445693e+01                  2.037037e+00
## abdomcentesis_total_protein                       outcome
##                  3.019608e+00                  1.551839e+00
##               surgical_lesion             type_of_lesion_1
```

```
##                1.363333e+00                3.657880e+03
##            type_of_lesion_2            type_of_lesion_3
##                9.022667e+01                7.363333e+00
##                     cp_data
##                1.670000e+00

a <- cor(HOC, use = "pair")

# Visualizo sólo las 6 primeras filas
head(a)

##                             X     surgery         Age Hospital_Number
## X                1.000000000 -0.09275015 -0.05348758    -0.009961148
## surgery         -0.092750153  1.00000000 -0.08931879    -0.126043799
## Age             -0.053487583 -0.08931879  1.00000000     0.697433955
## Hospital_Number -0.009961148 -0.12604380  0.69743396     1.000000000
## rectal_temp      0.014783271  0.04068010  0.19684404     0.144420722
## pulse           -0.049863144 -0.18688550  0.52983820     0.380078482
##                 rectal_temp       pulse   resp_rate extremities_temp
## X                0.01478327 -0.04986314 -0.01735362       0.03070778
## surgery          0.04068010 -0.18688550 -0.20142323      -0.11647364
## Age              0.19684404  0.52983820  0.41227590      -0.05673518
## Hospital_Number  0.14442072  0.38007848  0.27397575      -0.06116699
## rectal_temp      1.00000000  0.21926017  0.26918132       0.09652555
## pulse            0.21926017  1.00000000  0.47039707       0.33504101
##                 peripheral_pulse mucous_membranes
capillary_refill_time
## X                    0.034791682     -0.070219369           -
0.10023742
## surgery             -0.238054131     -0.187695693           -
0.08742574
## Age                  0.030656059     -0.006628693           -
0.01586790
## Hospital_Number      0.009016445     -0.031190330
0.04499351
## rectal_temp          0.093773772      0.051793906
0.13932397
## pulse                0.533369102      0.483060063
0.39848128
##                         pain peristalsis abdominal_distension
## X                0.004712395 -0.11891225          -0.03506056
## surgery         -0.316086444 -0.28588936          -0.24713695
## Age              0.034857959 -0.03954913           0.09637696
## Hospital_Number  0.097597480 -0.01735768           0.06792270
## rectal_temp     -0.088079389  0.04698099           0.04965014
## pulse            0.307522021  0.33530047           0.42333034
##                 nasogastric_tube nasogastric_reflux
nasogastric_reflux_PH
## X                    0.02455320         0.01452943
0.066097812
```

```
## surgery              -0.15051000        -0.12867267
0.175800531
## Age                   0.09218690        -0.07147698
0.028004041
## Hospital_Number      -0.01610032        -0.03093299          -
0.005577291
## rectal_temp          -0.14263271         0.01446057
0.228305910
## pulse                 0.05980760         0.23402363
0.005795796
##                 rectal_examination_feces      abdomen
packed_cell_volume
## X                           -0.06404337 -0.001536589        -
0.09246395
## surgery                     -0.24886861 -0.393516084        -
0.04203374
## Age                         -0.08634740 -0.094955534        -
0.14741539
## Hospital_Number             -0.09923886  0.008340622        -
0.09305766
## rectal_temp                  0.02899817 -0.037589873
0.06537316
## pulse                        0.26670718  0.274881266
0.40609021
##                 total_protein abdominocentesis_appearance
## X                  0.02619737                  0.02574511
## surgery           -0.04482801                 -0.21259132
## Age               -0.11937987                 -0.07770150
## Hospital_Number   -0.22978938                 -0.16010906
## rectal_temp       -0.06225120                 -0.07826784
## pulse             -0.09159872                  0.36204924
##                 abdomcentesis_total_protein      outcome
surgical_lesion
## X                           -0.06034290  0.029697349     -
0.02524883
## surgery                      0.03513254 -0.117619377
0.60502302
## Age                         -0.05876734 -0.004083472     -
0.04393995
## Hospital_Number             -0.04098076 -0.004376518     -
0.10139308
## rectal_temp                  0.01127046 -0.057082020
0.01955315
## pulse                        0.03144616  0.313215253     -
0.26633548
##                 type_of_lesion_1 type_of_lesion_2 type_of_lesion_3
## X                     0.14238933     -0.010672090       0.05308885
## surgery              -0.16394008     -0.098594360      -0.04710089
## Age                   0.02296642      0.017915483       0.19611614
## Hospital_Number       0.14548573     -0.050252610      -0.02087546
```

```
## rectal_temp           0.06270311     -0.062728167       0.02939493
## pulse                 0.07951079     -0.001454538       0.10146572
##                       cp_data
## X                  0.007244350
## surgery            0.005826918
## Age               -0.080481522
## Hospital_Number   -0.097457068
## rectal_temp       -0.066317467
## pulse             -0.119113065
```

```
b <- cov(HOC, use = "pair")

# Visualizo sólo las 6 primeras filas
head(b)
```

```
##                              X       surgery           Age
Hospital_Number
## X                 7.525000e+03 -3.951224e+00 -1.008696e+01   -
1.321897e+06
## surgery          -3.951224e+00  2.403986e-01 -9.535140e-02   -
9.467934e+04
## Age              -1.008696e+01 -9.535140e-02  4.726154e+00
2.319487e+06
## Hospital_Number -1.321897e+06 -9.467934e+04  2.319487e+06
2.340291e+12
## rectal_temp       9.420607e-01  1.473401e-02  3.193863e-01
1.667279e+05
## pulse            -1.255605e+02 -2.631387e+00  3.292838e+01
1.590550e+07
##                   rectal_temp         pulse     resp_rate
extremities_temp
## X                9.420607e-01 -1.255605e+02 -2.675143e+01
2.767658e+00
## surgery          1.473401e-02 -2.631387e+00 -1.748651e+00    -
6.035098e-02
## Age              3.193863e-01  3.292838e+01  1.605487e+01    -
1.176550e-01
## Hospital_Number 1.667279e+05  1.590550e+07  7.482344e+06    -
9.241454e+04
## rectal_temp      5.362467e-01  4.621599e+00  3.553247e+00
7.495770e-02
## pulse            4.621599e+00  8.197088e+02  2.440669e+02
9.899851e+00
##                  peripheral_pulse mucous_membranes
capillary_refill_time
## X                    3.125711e+00    -9.828330e+00         -
4.130080e+00
## surgery             -1.226505e-01    -1.503194e-01         -2.058517e-
02
## Age                  6.113307e-02    -2.095489e-02         -1.520487e-
```

```
02
## Hospital_Number     1.288242e+04    -6.927985e+04
3.083278e+04
## rectal_temp         6.764690e-02     6.435709e-02          4.614570e-
02
## pulse               1.524186e+01     2.213819e+01
5.194071e+00
##                           pain   peristalsis abdominal_distension
## X                5.284209e-01 -1.007999e+01        -3.199622e+00
## surgery         -2.041928e-01 -1.368689e-01        -1.298847e-01
## Age              9.287387e-02 -7.916667e-02         1.976658e-01
## Hospital_Number  1.775179e+05 -2.265648e+04         1.045943e+05
## rectal_temp     -7.944724e-02  3.422192e-02         3.637186e-02
## pulse            1.120930e+01  9.339338e+00         1.260839e+01
##                 nasogastric_tube nasogastric_reflux
nasogastric_reflux_PH
## X                   1.375092e+00       1.007211e+00
1.145831e+01
## surgery            -4.789849e-02      -5.124676e-02
1.666183e-01
## Age                 1.105181e-01      -8.610651e-02
1.184325e-01
## Hospital_Number    -1.440225e+04      -3.268155e+04         -
1.684099e+04
## rectal_temp        -6.786950e-02       8.977667e-03
3.552128e-01
## pulse               1.031962e+00       4.827542e+00
3.400000e-01
##                 rectal_examination_feces       abdomen
packed_cell_volume
## X                         -7.045993e+00 -2.035699e-01      -
8.392053e+01
## surgery                   -1.530353e-01 -2.889503e-01      -
2.156409e-01
## Age                       -2.067374e-01 -1.665958e-01      -
3.430805e+00
## Hospital_Number           -1.659386e+05  1.217909e+04      -
1.450103e+06
## rectal_temp                2.451369e-02 -4.364802e-02
4.965554e-01
## pulse                      8.991557e+00  1.021440e+01
1.189696e+02
##                 total_protein abdominocentesis_appearance
## X                6.265164e+01                1.790492e+00
## surgery         -6.035438e-01               -7.889126e-02
## Age             -7.228645e+00               -1.481481e-01
## Hospital_Number -9.504629e+06               -1.989880e+05
## rectal_temp     -1.279962e+00               -5.349985e-02
## pulse           -7.172957e+01                8.362392e+00
##                 abdomcentesis_total_protein       outcome
```

```
surgical_lesion
## X                            -1.009390e+01  1.902157e+00   -
1.055184e+00
## surgery                       3.232673e-02 -4.251307e-02
1.430159e-01
## Age                          -2.500485e-01 -6.554286e-03   -
4.602007e-02
## Hospital_Number              -1.037371e+05 -4.942812e+03   -
7.472689e+04
## rectal_temp                   1.949566e-02 -3.068458e-02
7.029289e-03
## pulse                         1.795176e+00  6.726277e+00   -
3.694704e+00
##                  type_of_lesion_1 type_of_lesion_2 type_of_lesion_3
## X                    6.669378e+04    -6.013512e+02     5.873428e+02
## surgery             -4.347362e+02    -3.145263e+01    -2.950226e+00
## Age                  2.695888e+02     2.529926e+01     5.437538e+01
## Hospital_Number      1.201738e+09    -4.993660e+07    -4.072922e+06
## rectal_temp          2.347719e+02    -3.207523e+01     3.069339e+00
## pulse                1.213215e+04    -2.818277e+01     3.862694e+02
##                        cp_data
## X                   2.959866e-01
## surgery             1.346771e-03
## Age                -8.240803e-02
## Hospital_Number -7.022111e+04
## rectal_temp        -2.339435e-02
## pulse              -1.614862e+00
```

3.2.4 Imputación de la media

```
# Cargo librería MICE
library("mice")

# Visualizo el patrón de datos faltantes
c <- md.pattern(HOC)

# Visualizo sólo las 6 primeras filas
head(c)
```

```
##    X Age Hospital_Number surgical_lesion type_of_lesion_1
type_of_lesion_2
##  6 1   1               1               1                 1
1
##  1 1   1               1               1                 1
1
##  1 1   1               1               1                 1
1
```

```
## 15 1   1               1               1               1
1
##  1 1   1               1               1               1
1
##  5 1   1               1               1               1
1
##    type_of_lesion_3 cp_data surgery outcome pulse packed_cell_volume
##  6                1       1       1       1     1                  1
##  1                1       1       1       1     1                  1
##  1                1       1       1       1     1                  1
## 15                1       1       1       1     1                  1
##  1                1       1       1       1     1                  1
##  5                1       1       1       1     1                  1
##    capillary_refill_time total_protein peristalsis mucous_membranes
pain
##  6                     1             1           1                1
1
##  1                     1             1           1                1
1
##  1                     1             1           1                1
1
## 15                     1             1           1                1
1
##  1                     1             1           1                1
1
##  5                     1             1           1                1
1
##    extremities_temp abdominal_distension resp_rate rectal_temp
##  6                1                    1         1           1
##  1                1                    1         0           1
##  1                1                    1         1           1
## 15                1                    1         1           1
##  1                1                    1         1           1
##  5                1                    1         1           1
##    peripheral_pulse rectal_examination_feces nasogastric_tube
##  6                1                        1                1
##  1                1                        1                1
##  1                1                        1                0
## 15                1                        1                1
##  1                1                        0                1
##  5                1                        1                1
##    nasogastric_reflux abdomen abdominocentesis_appearance
##  6                  1       1                           1
##  1                  1       1                           1
##  1                  1       1                           1
## 15                  1       1                           1
##  1                  1       1                           1
##  5                  1       0                           1
##    abdomcentesis_total_protein nasogastric_reflux_PH
##  6                           1                    1 0
```

```
##  1                            1                    1 1
##  1                            1                    1 1
## 15                            1                    0 1
##  1                            1                    1 1
##  5                            1                    1 1
```

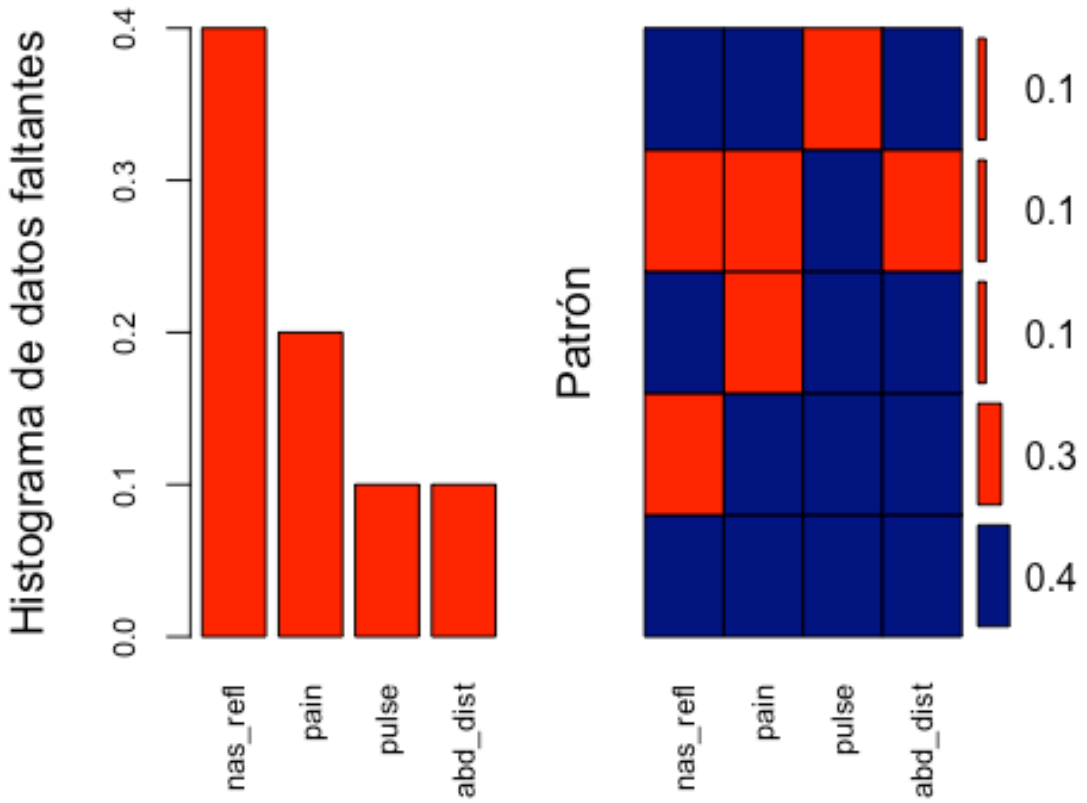
```
# Generación de subsample mediante paquete DPLYR
library("dplyr")
subsample <- slice(HOC,1:10) %>% select(pulse, abdominal_distension, pain
, nasogastric_reflux)

# Visualización de subsample
subsample
```

```
##    pulse abdominal_distension pain nasogastric_reflux
## 1     66                    4    5                 NA
## 2     88                    2    3                 NA
## 3     40                    1    3                 NA
## 4    164                    4    2                  2
## 5    104                   NA   NA                 NA
## 6     NA                    2    2                  1
## 7     48                    3    3                  1
## 8     60                    2   NA                  1
## 9     80                    4    4                  1
## 10    90                    1    5                  1
```

```
# Genero el patrón de datos faltantes de subsample
pattern <- md.pattern(subsample)

# Abrevio los nombres de las variables de subsample
names(subsample) <- c("pulse","abd_dist","pain", "nas_refl")

# Visualizo el patrón de datos faltantes de subsample
pattern
```

```
##   pulse abdominal_distension pain nasogastric_reflux
## 4     1                    1    1                 1 0
## 1     0                    1    1                 1 1
## 1     1                    1    0                 1 1
## 3     1                    1    1                 0 1
## 1     1                    0    0                 0 3
##       1                    1    2                 4 8
```

```
# Cargo librería VIM
library(VIM)

# Ilustración 12: Visualización de patrón de valores faltantes en
subsample, mediante paquete VIM
aggr_plot <- aggr(subsample, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(subsample), cex.axis=.8, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##  Variable Count
##  nas_refl   0.4
##      pain   0.2
##     pulse   0.1
##  abd_dist   0.1
```

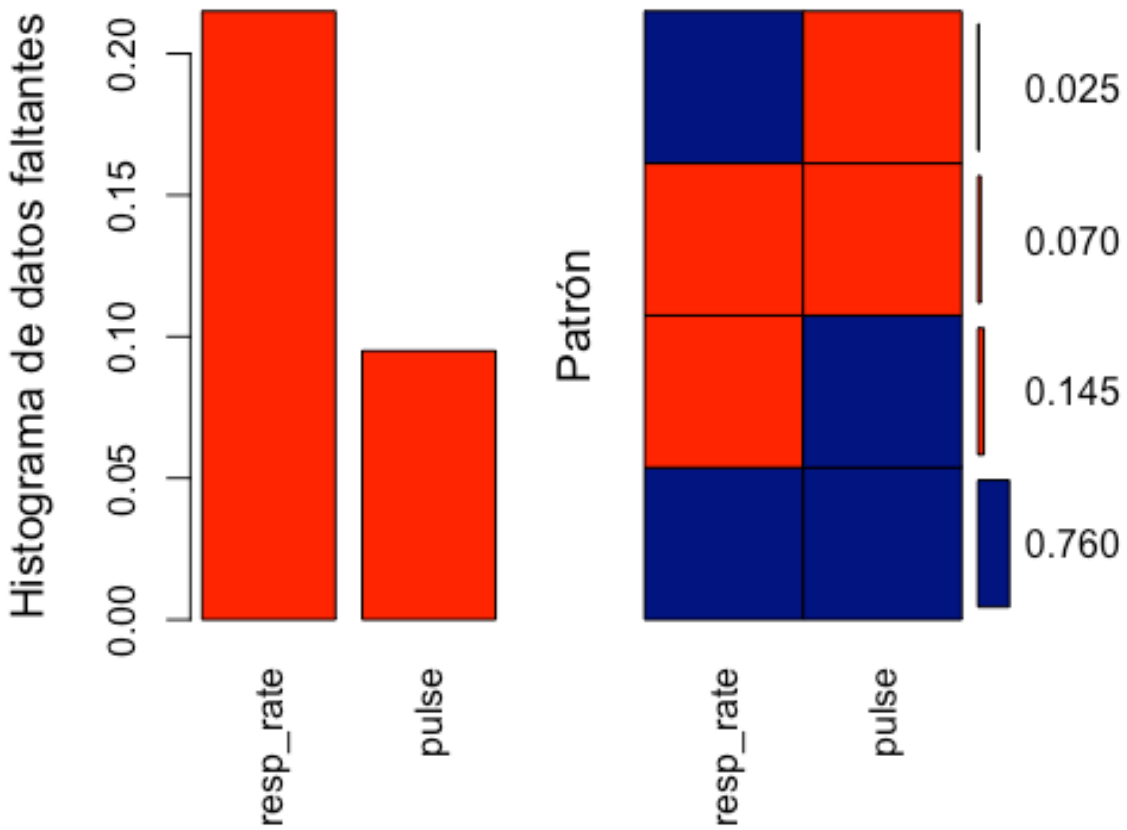
```
# Copia de seguridad del dataset HOC
HOC_bak <- HOC

# Imputar la media al dataset HOC
HOC_mean_imp <- mice(HOC, method="mean", m=1, maxit=1)
```

```
##
##  iter imp variable
##   1   1  surgery  rectal_temp  pulse  resp_rate  extremities_temp
peripheral_pulse  mucous_membranes  capillary_refill_time  pain
peristalsis  abdominal_distension  nasogastric_tube  nasogastric_reflux
nasogastric_reflux_PH  rectal_examination_feces  abdomen
packed_cell_volume  total_protein  abdominocentesis_appearance
abdomcentesis_total_protein  outcome
```

```r
# Generación de subsample2 mediante paquete DPLYR
subsample2 <- slice(HOC,1:200) %>% select(pulse, resp_rate)

# Visualizo subsample2 (Sólo las 6 primeras filas)
head(subsample2)
```

```
##   pulse resp_rate
## 1    66        28
## 2    88        20
## 3    40        24
## 4   164        84
## 5   104        35
## 6    NA        NA
```

```r
# Ilustración 13: Visualización de patrón de valores faltantes en
subsample2, mediante paquete VIM
aggr_plot <- aggr(subsample2, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(subsample2), cex.axis=1, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##   Variable Count
```

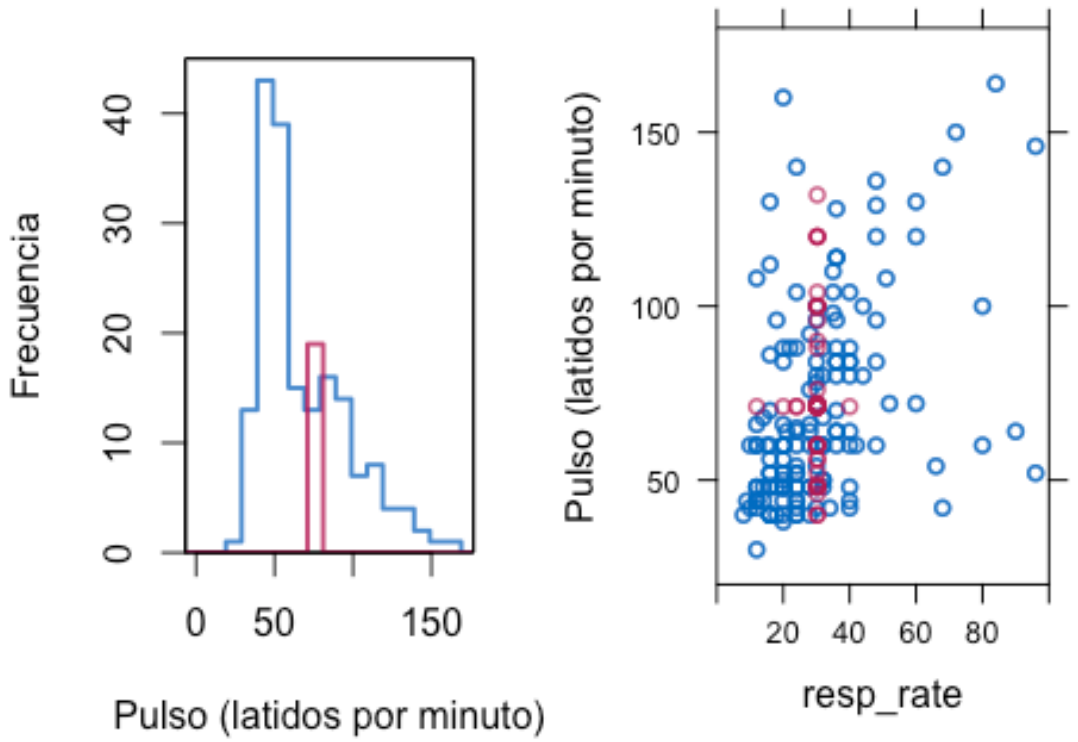
```
##  resp_rate 0.215
##      pulse 0.095
```

```
# Imputar la media al dataset subsample2
imp <- mice(subsample2, method="mean", m=1, maxit=1)
```

```
##
##  iter imp variable
##   1   1  pulse  resp_rate
```

```
# Cargo librería lattice
library(lattice)

# Ilustración 14
lwd <- 1.5
par(mfrow=c(1,2))
breaks <- seq(-20, 200, 10)
nudge <- 1
x <- matrix(c(breaks-nudge, breaks+nudge), ncol=2)
obs <- subsample2[,"pulse"]
mis  <- imp$imp$pulse[,1]
fobs <- c(hist(obs, breaks, plot=FALSE)$counts, 0)
fmis <- c(hist(mis, breaks, plot=FALSE)$counts, 0)
y <- matrix(c(fobs, fmis), ncol=2)
matplot(x, y, type="s",
        col=c(mdc(4),mdc(5)), lwd=2, lty=1,
        xlim = c(0, 170), ylim = c(0,45), yaxs = "i",
        xlab="Pulso (latidos por minuto)",
        ylab="Frecuencia")
box()

tp <- xyplot(imp, pulse~resp_rate, na.groups=ici(imp),
       ylab="Pulso (latidos por minuto)", xlab="resp_rate",
       cex = 0.75, lex=lwd,
       ylim = c(20, 180), xlim = c(0,100))
print(tp, newpage = FALSE, position = c(0.48,0.045,1,0.95))

# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

```
##     pulse resp_rate
##    "mean"    "mean"
```

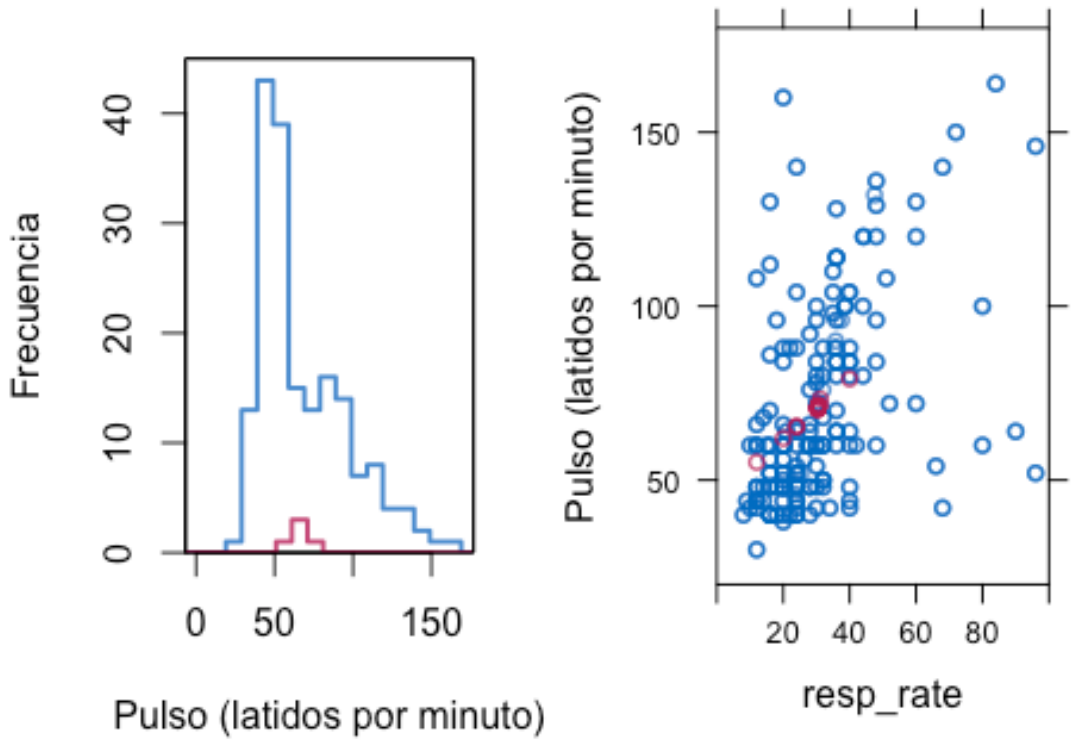


3.2.5 Imputación mediante regresión

```
# Defino modelo y predicciones para subsample2
fit <- lm(pulse ~ resp_rate, data=subsample2)
pred <- predict(fit, newdata=ic(subsample2))

# Imputación alternativa utilizando MICE
imp <- mice(subsample2[,1:2], method="norm.predict", m=1, maxit=3,seed=1)

##
##  iter imp variable
##    1   1  pulse  resp_rate
##    2   1  pulse  resp_rate
##    3   1  pulse  resp_rate

# Ilustración 15
par(mfrow = c(1,2))
fmis <- c(hist(pred, breaks, plot=FALSE)$counts, 0)
y <- matrix(c(fobs, fmis), ncol=2)
matplot(x, y, type="s",
```

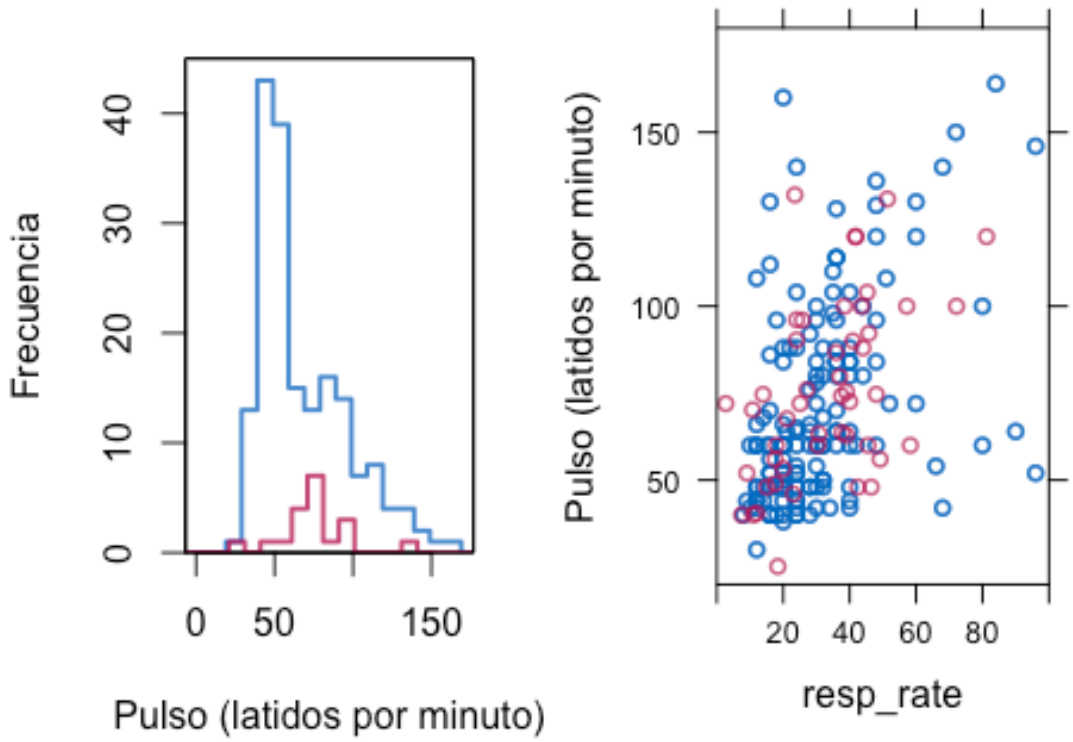
```
        col=c(mdc(4),mdc(5)), lwd=2, lty=1,
        xlim = c(0, 170), ylim = c(0,45), yaxs = "i",
        xlab="Pulso (latidos por minuto)",
        ylab="Frecuencia")
box()

tp <- xyplot(imp, pulse~resp_rate,
      ylab="Pulso (latidos por minuto)", xlab="resp_rate",
       cex = 0.75, lex=lwd,
       ylim = c(20, 180), xlim = c(0,100))
print(tp, newpage = FALSE, position = c(0.48,0.045,1,0.95))

# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

```
##          pulse      resp_rate
## "norm.predict" "norm.predict"
```



3.2.6 Imputación mediante regresión estocástica

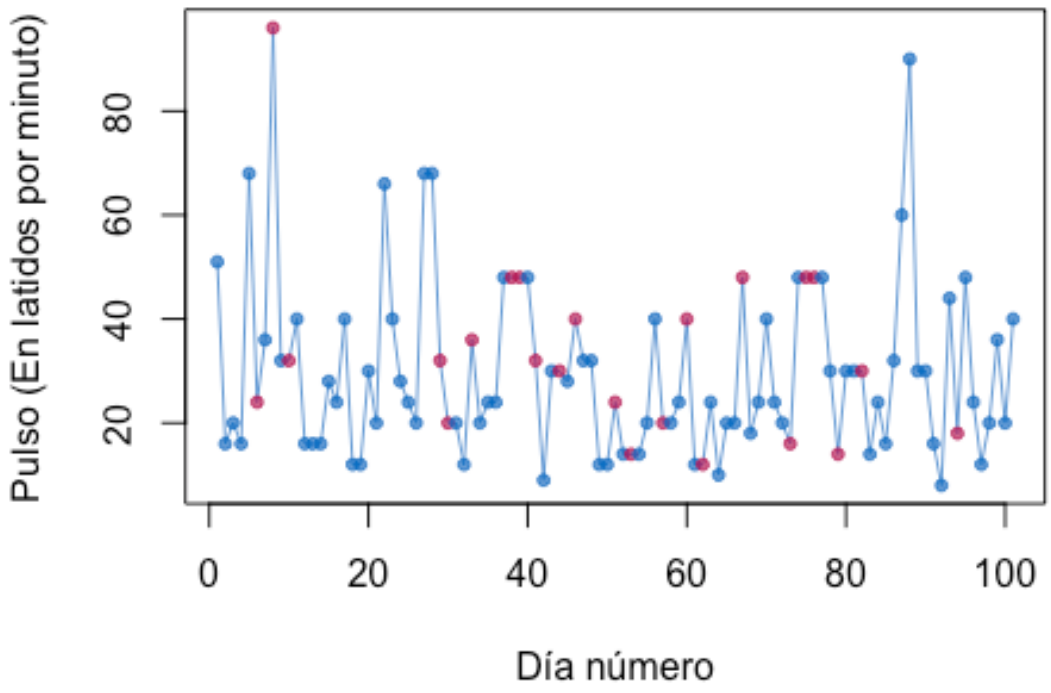
```
# Realizo la imputación mediante regresión estocástica, utilizando el
paquete MICE:
imp <- mice(subsample2[,1:2],method="norm.nob",m=1,maxit=1,seed=1)

##
##  iter imp variable
##   1   1  pulse  resp_rate

# Ilustración 16
par(mfrow = c(1,2))
mis  <- imp$imp$pulse[,1]
fmis <- c(hist(mis, breaks, plot=FALSE)$counts, 0)
y <- matrix(c(fobs, fmis), ncol=2)
matplot(x, y, type="s",
        col=c(mdc(4),mdc(5)), lwd=2, lty=1,
        xlim = c(0, 170), ylim = c(0,45), yaxs = "i",
        xlab="Pulso (latidos por minuto)",
        ylab="Frecuencia")
box()

tp <- xyplot(imp, pulse~resp_rate, na.groups=ici(imp),
       ylab="Pulso (latidos por minuto)", xlab="resp_rate",
       cex = 0.75, lex=lwd,
       ylim = c(20, 180), xlim = c(0,100))
print(tp, newpage = FALSE, position = c(0.48,0.045,1,0.95))

# Verificación del modelo de imputación empleado en cada variable
imp$meth

##      pulse  resp_rate
## "norm.nob" "norm.nob"
```



3.2.7 Imputación mediante LOCF y BOFC

```
# LOCF y BOCF
par(mfrow=c(1,1))
Pu <- subsample2$resp_rate
locf <- function(x) {
  a <- x[1]
  for (i in 2:length(x)) {
    if (is.na(x[i])) x[i] <- a
    else a <- x[i]
  }
  return(x)
}
Pul <- locf(Pu)
colvec <- ifelse(is.na(Pu),mdc(2),mdc(1))

# Ilustración 17
plot(Pul[100:200],col=colvec,type="l",xlab="Día número",ylab="Pulso (En
```

```
latidos por minuto)")
points(Pul[100:200],col=colvec,pch=20,cex=1)
```



3.2.8 Imputación múltiple

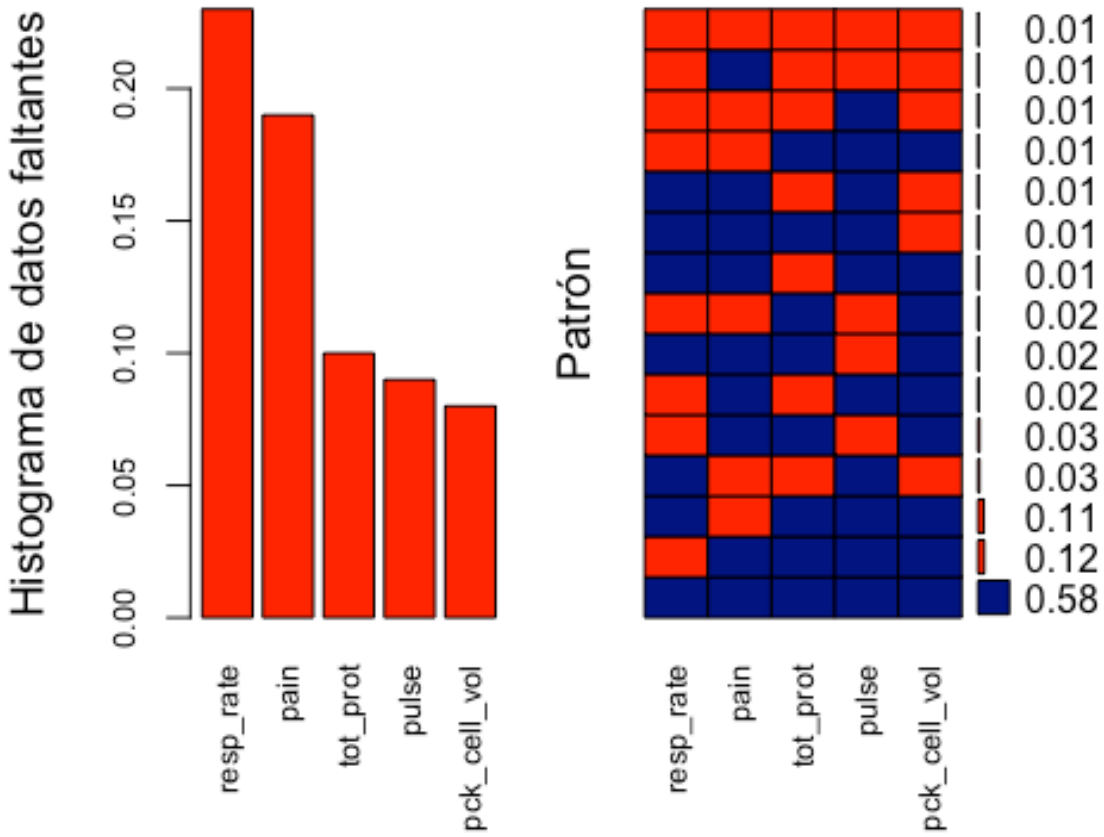
```
# Generación de subsample3 mediante paquete DPLYR
subsample3 <- slice(HOC,1:100) %>% select(pulse, resp_rate, pain,
packed_cell_volume, total_protein)

# Visualizo la estructura del dataset generado
str(subsample)
```

```
## 'data.frame':    10 obs. of  4 variables:
##  $ pulse   : int  66 88 40 164 104 NA 48 60 80 90
##  $ abd_dist: int  4 2 1 4 NA 2 3 2 4 1
##  $ pain    : int  5 3 3 2 NA 2 3 NA 4 5
##  $ nas_refl: int  NA NA NA 2 NA 1 1 1 1 1
```

```r
# Observo el patrón de datos faltantes
pattern3 <- md.pattern(subsample3)
pattern3
```

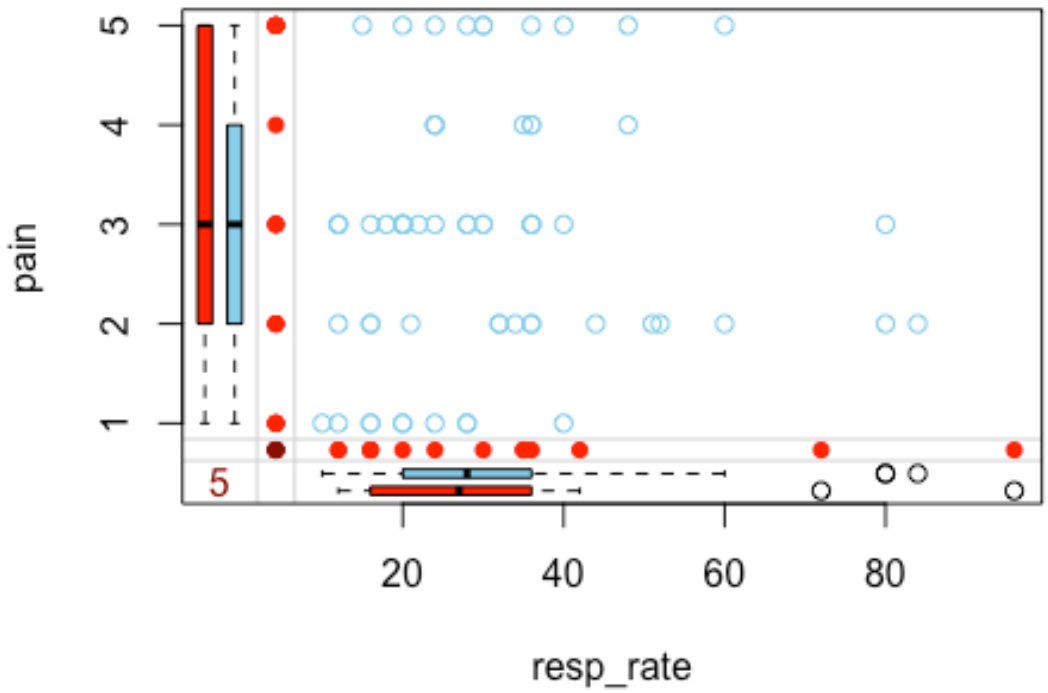
```
##    packed_cell_volume pulse total_protein pain resp_rate
## 58                  1     1             1    1         1  0
##  2                  1     0             1    1         1  1
## 12                  1     1             1    1         0  1
## 11                  1     1             1    0         1  1
##  1                  0     1             1    1         1  1
##  1                  1     1             0    1         1  1
##  3                  1     0             1    1         0  2
##  1                  1     1             1    0         0  2
##  2                  1     1             0    1         0  2
##  1                  0     1             0    1         1  2
##  2                  1     0             1    0         0  3
##  3                  0     1             0    0         1  3
##  1                  0     0             0    1         0  4
##  1                  0     1             0    0         0  4
##  1                  0     0             0    0         0  5
##                     8     9            10   19        23 69
```

```r
# Abrevio los nombres de las variables de subsample3
names(subsample3) <- c("pulse","resp_rate","pain", "pck_cell_vol",
"tot_prot")

# Ilustración 20: Visualización de patrón de valores faltantes en
subsample3, mediante paquete VIM
aggr_plot <- aggr(subsample3, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(subsample3), cex.axis=.8, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##       Variable Count
##     resp_rate  0.23
##          pain  0.19
##      tot_prot  0.10
##         pulse  0.09
##  pck_cell_vol  0.08
```

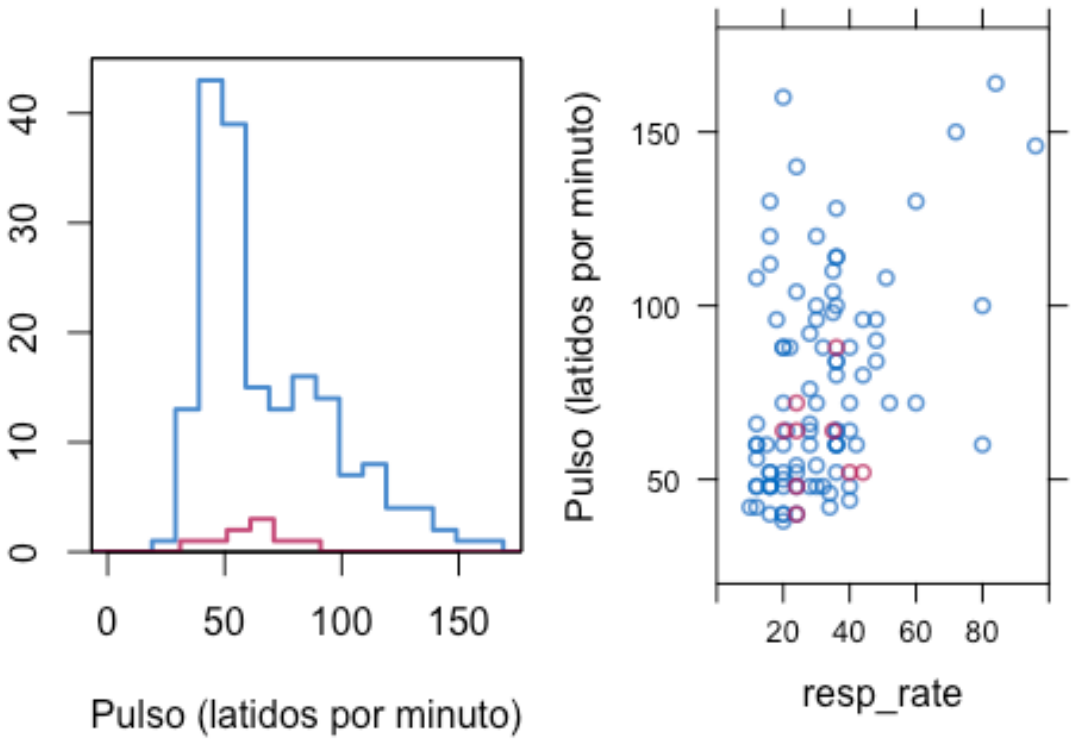
```
# Ilustración 21: Visualización de relación entre valores faltantes de las variables resp_rate y pain del dataframe subsample3, mediante paquete DPLYR y VIM
subsample3 %>% select(resp_rate, pain) %>% marginplot()
```




```
# Imputación múltiple del dataframe subsample3
imp <- mice(subsample3, seed=1, print=FALSE)
fit <- with(imp, lm(pulse ~ resp_rate + pain + pck_cell_vol + tot_prot))
tab <- round(summary(pool(fit)),3)
tab[,c(1:3,5)]

##                  est     se      t Pr(>|t|)
## (Intercept)  -17.543 15.719 -1.116    0.276
## resp_rate      0.855  0.148  5.760    0.000
## pain           1.881  2.010  0.936    0.353
## pck_cell_vol   1.210  0.284  4.268    0.000
## tot_prot       0.153  0.104  1.463    0.153

# Ilustración 22
par(mfrow = c(1,2))
mis  <- imp$imp$pulse[,1]
fmis <- c(hist(mis, breaks, plot=FALSE)$counts, 0)
y <- matrix(c(fobs, fmis), ncol=2)
matplot(x, y, type="s",
        col=c(mdc(4),mdc(5)), lwd=2, lty=1,
        xlim = c(0, 170), ylim = c(0,45), yaxs = "i",
        xlab="Pulso (latidos por minuto)",
        ylab="Frecuencia")
```

```r
box()

tp <- xyplot(imp, pulse ~ resp_rate, subset = .imp==1,
       ylab="Pulso (latidos por minuto)", xlab="resp_rate",
       cex = 0.75, lex=lwd,
       ylim = c(20, 180), xlim = c(0,100))
print(tp, newpage = FALSE, position = c(0.48,0.045,1,0.95))

# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

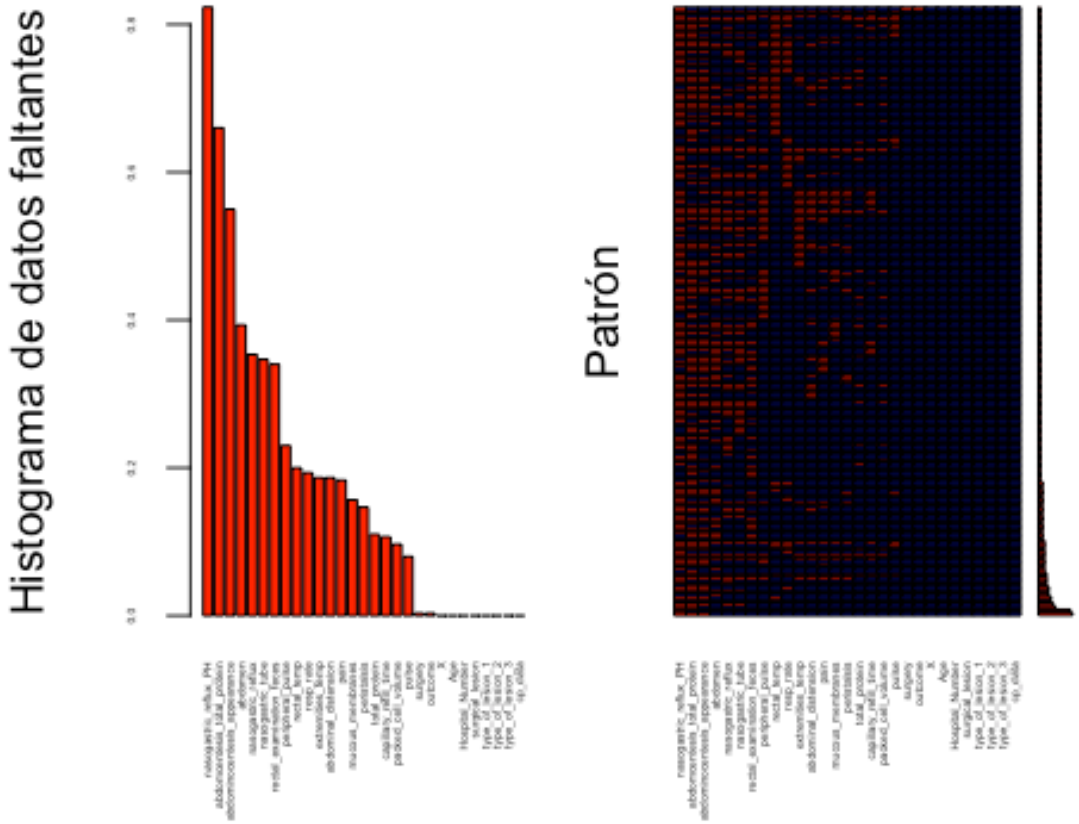
```
##        pulse    resp_rate         pain pck_cell_vol     tot_prot
##        "pmm"        "pmm"        "pmm"        "pmm"        "pmm"
```



4 Imputación múltiple sobre los datasets abordados

4.1 Dataset "HOC"

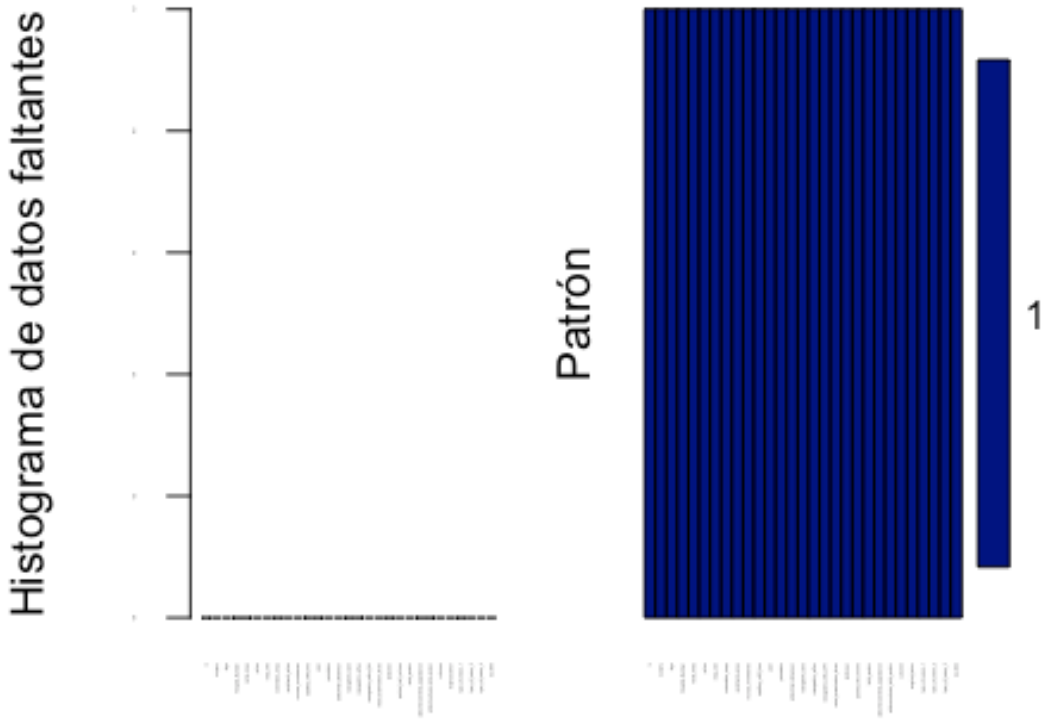
```
# Dataset HOC (Horse-colic)
# Ilustración 23: Visualización de patrón de datos faltantes del dataset HOC
aggr_plot <- aggr(HOC, col=c('navyblue','red'), numbers=TRUE, sortVars=TRUE, labels=names(HOC), cex.axis=.3, gap=3, ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##                       Variable       Count
##        nasogastric_reflux_PH 0.823333333
##  abdomcentesis_total_protein 0.660000000
##  abdominocentesis_appearance 0.550000000
##                      abdomen 0.393333333
##           nasogastric_reflux 0.353333333
##             nasogastric_tube 0.346666667
##     rectal_examination_feces 0.340000000
```

```
##             peripheral_pulse 0.230000000
##                  rectal_temp 0.200000000
##                    resp_rate 0.193333333
##             extremities_temp 0.186666667
##          abdominal_distension 0.186666667
##                         pain 0.183333333
##             mucous_membranes 0.156666667
##                  peristalsis 0.146666667
##                total_protein 0.110000000
##         capillary_refill_time 0.106666667
##            packed_cell_volume 0.096666667
##                         pulse 0.080000000
##                       surgery 0.003333333
##                       outcome 0.003333333
##                             X 0.000000000
##                           Age 0.000000000
##              Hospital_Number 0.000000000
##              surgical_lesion 0.000000000
##             type_of_lesion_1 0.000000000
##             type_of_lesion_2 0.000000000
##             type_of_lesion_3 0.000000000
##                       cp_data 0.000000000
```

```
# Imputación de la media en el dataset HOC
imp <- mice(HOC, method = "mean", seed=1, print=FALSE)

# Imputación efectiva del dataset HOC
HOC_completed = complete(imp)

# Ilustración 24: Visualización de patrón de datos en dataset HOC después
de la imputación efectiva
aggr_plot <- aggr(HOC_completed, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(HOC_completed), cex.axis=.1, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##                      Variable Count
##                             X     0
##                       surgery     0
##                           Age     0
##               Hospital_Number     0
##                   rectal_temp     0
##                         pulse     0
##                     resp_rate     0
##               extremities_temp     0
##               peripheral_pulse     0
##               mucous_membranes     0
##         capillary_refill_time     0
##                          pain     0
##                    peristalsis     0
##           abdominal_distension     0
##               nasogastric_tube     0
##             nasogastric_reflux     0
##          nasogastric_reflux_PH     0
##       rectal_examination_feces     0
##                       abdomen     0
##             packed_cell_volume     0
```

```
##                total_protein     0
##  abdominocentesis_appearance     0
##  abdomcentesis_total_protein     0
##                      outcome     0
##              surgical_lesion     0
##             type_of_lesion_1     0
##             type_of_lesion_2     0
##             type_of_lesion_3     0
##                      cp_data     0
```

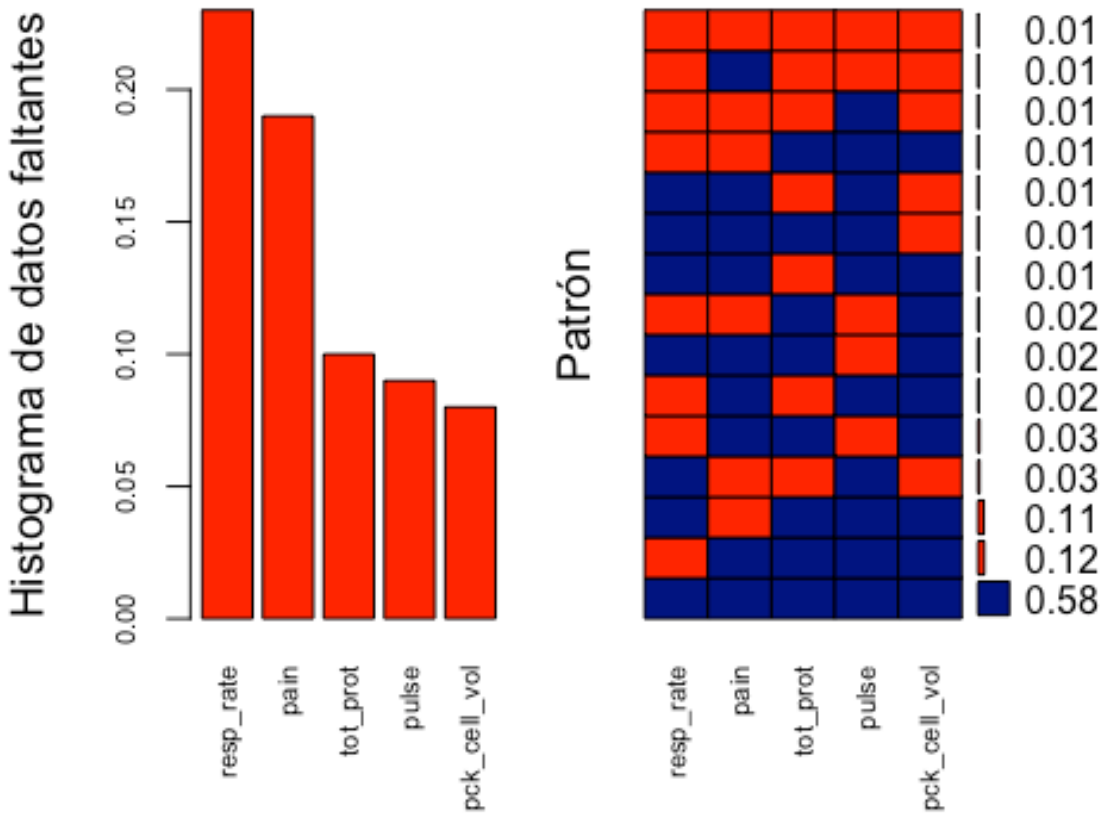
```
# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

```
##                           X                     surgery
##                      "mean"                      "mean"
##                         Age             Hospital_Number
##                      "mean"                      "mean"
##                 rectal_temp                       pulse
##                      "mean"                      "mean"
##                   resp_rate           extremities_temp
##                      "mean"                      "mean"
##            peripheral_pulse           mucous_membranes
##                      "mean"                      "mean"
##       capillary_refill_time                        pain
##                      "mean"                      "mean"
##                  peristalsis       abdominal_distension
##                      "mean"                      "mean"
##            nasogastric_tube         nasogastric_reflux
##                      "mean"                      "mean"
##       nasogastric_reflux_PH   rectal_examination_feces
##                      "mean"                      "mean"
##                     abdomen         packed_cell_volume
##                      "mean"                      "mean"
##               total_protein abdominocentesis_appearance
##                      "mean"                      "mean"
## abdomcentesis_total_protein                     outcome
##                      "mean"                      "mean"
##             surgical_lesion           type_of_lesion_1
##                      "mean"                      "mean"
##            type_of_lesion_2           type_of_lesion_3
##                      "mean"                      "mean"
##                     cp_data
##                      "mean"
```

4.2 Dataset "subsample3"

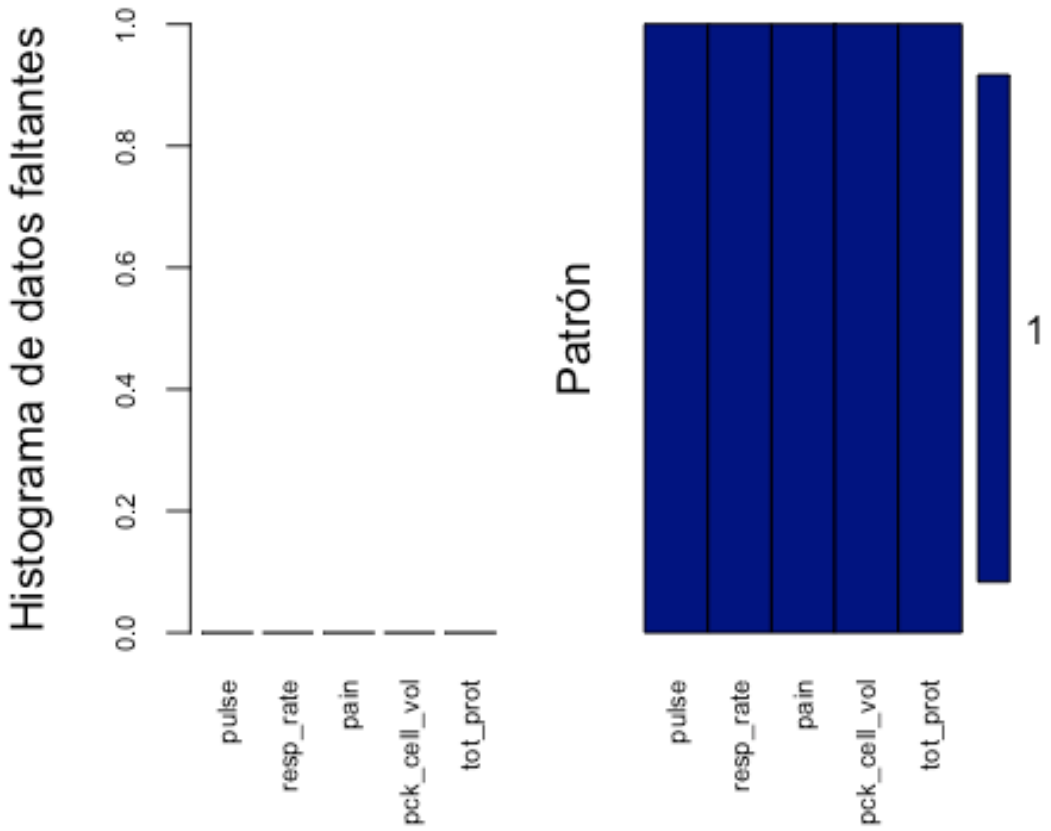
```
# Dataset subsample3 (Muestra del dataset Horse-colic)
# Ilustración 23: Visualización de patrón de datos faltantes del dataset
```

```
HOC
aggr_plot <- aggr(subsample3, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(subsample3), cex.axis=.7, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##       Variable Count
##     resp_rate  0.23
##          pain  0.19
##      tot_prot  0.10
##         pulse  0.09
##  pck_cell_vol  0.08

# Imputación múltiple del dataset subsample3
imp <- mice(subsample3, method = "pmm", seed=1, print=FALSE)

# Imputación efectiva del dataset subsample3
subsample3_completed = complete(imp)

# Ilustración XX: Visualización de patrón de datos en dataset subsample3
después de la imputación efectiva
aggr_plot <- aggr(subsample3_completed, col=c('navyblue','red'),
```

```
numbers=TRUE, sortVars=TRUE, labels=names(subsample3_completed),
cex.axis=.7, gap=3, ylab=c("Histograma de datos faltantes","Patrón"))
```



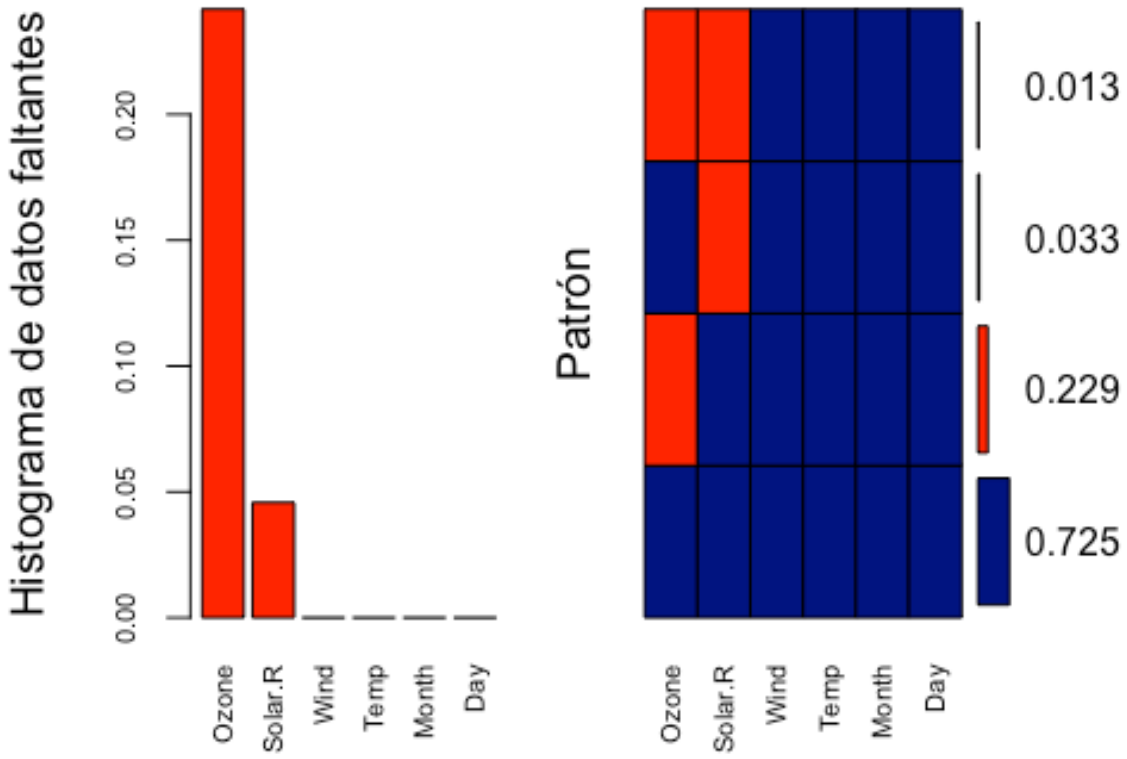

```
##
##  Variables sorted by number of missings:
##      Variable Count
##         pulse     0
##     resp_rate     0
##          pain     0
##  pck_cell_vol     0
##      tot_prot     0

# Verificación del modelo de imputación empleado en cada variable
imp$meth

##        pulse    resp_rate         pain pck_cell_vol     tot_prot
##        "pmm"        "pmm"        "pmm"        "pmm"        "pmm"
```

4.3 Dataset "AIR"

```r
# Cargo librería datasets
library(datasets)

# Dataset AIR (Air Quality)
data(airquality)

# Estructura del dataset
str(airquality)
```

```
## 'data.frame':    153 obs. of  6 variables:
##  $ Ozone  : int  41 36 12 18 NA 28 23 19 8 NA ...
##  $ Solar.R: int  190 118 149 313 NA NA 299 99 19 194 ...
##  $ Wind   : num  7.4 8 12.6 11.5 14.3 14.9 8.6 13.8 20.1 8.6 ...
##  $ Temp   : int  67 72 74 62 56 66 65 59 61 69 ...
##  $ Month  : int  5 5 5 5 5 5 5 5 5 5 ...
##  $ Day    : int  1 2 3 4 5 6 7 8 9 10 ...
```

```r
# Guardo el dataset AIR para generar el fichero AIR.rds
# (a efectos de reproducibilidad posterior)
saveRDS(airquality, "AIR.rds")

# Apertura del dataset AIR
# (Descomentar la línea siguiente  si fuera necesario abrirlo para
reproducibilidad posterior)
# airquality <- readRDS("AIR.rds")

# Ilustración 24: Visualización de patrón de datos faltantes del dataset
AIR
aggr_plot <- aggr(airquality, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(airquality), cex.axis=.7, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```

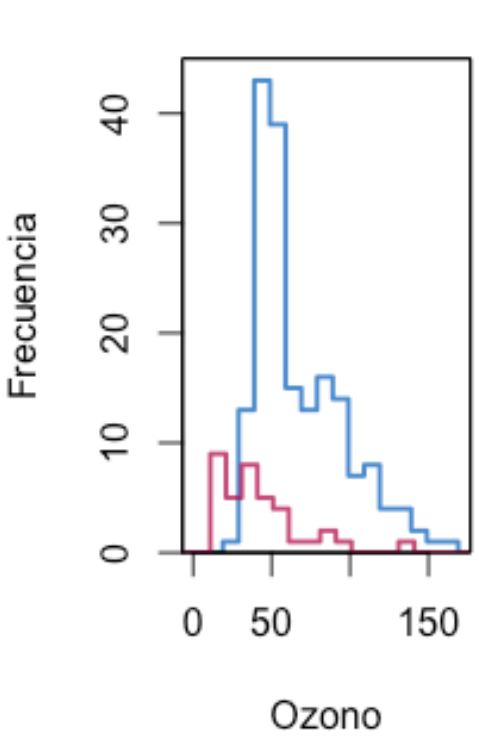


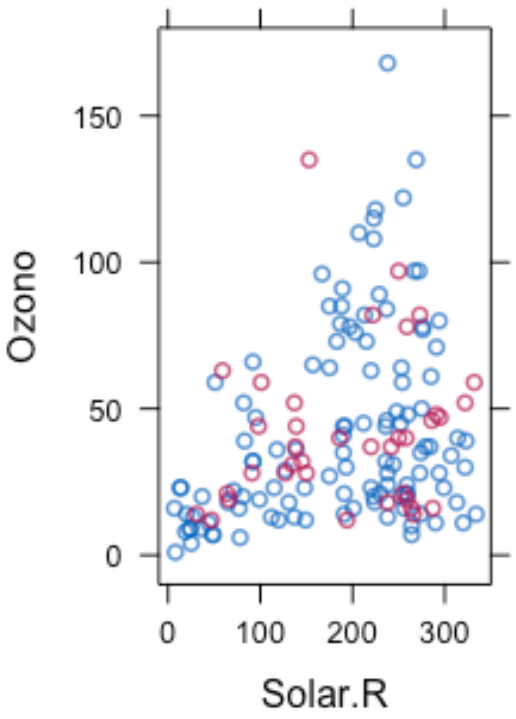

```
##
##  Variables sorted by number of missings:
##  Variable      Count
##     Ozone 0.24183007
##   Solar.R 0.04575163
##      Wind 0.00000000
##      Temp 0.00000000
##     Month 0.00000000
##       Day 0.00000000
```

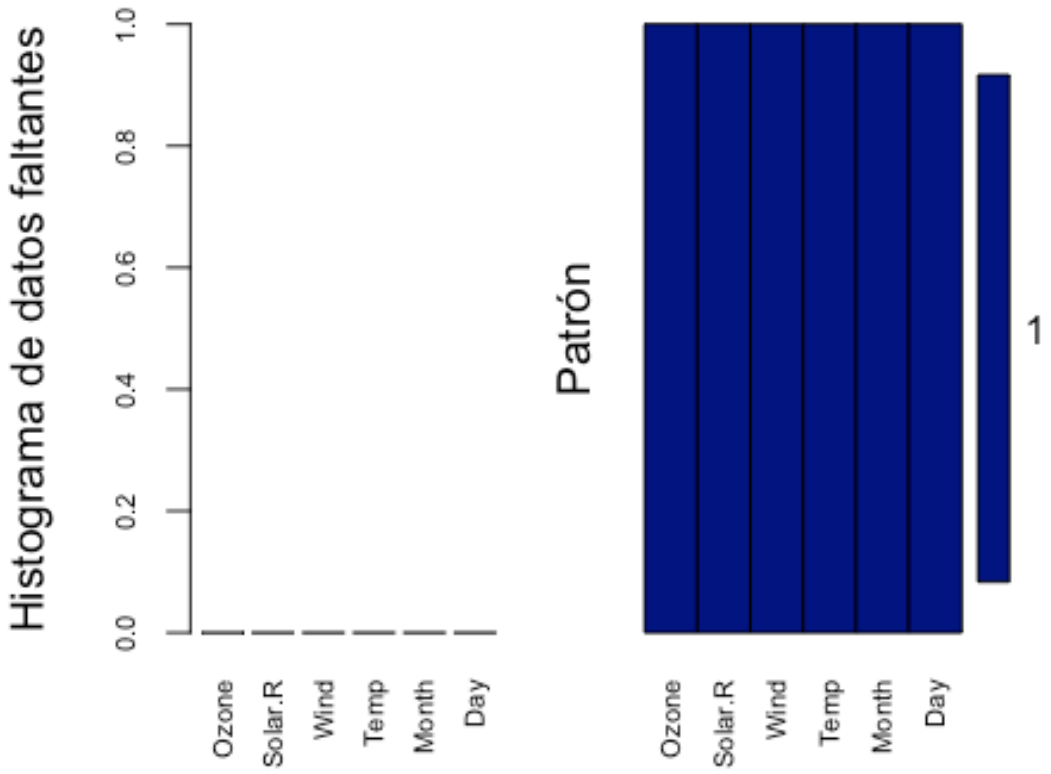
```
# Imputación múltiple del dataframe AIR
imp <- mice(airquality, seed=1, print=FALSE)
fit <- with(imp, lm(Ozone ~ Solar.R + Wind + Temp + Month + Day))
tab <- round(summary(pool(fit)),3)
tab[,c(1:3,5)]
```

```
##                 est     se      t Pr(>|t|)
## (Intercept) -65.713 22.906 -2.869    0.006
## Solar.R       0.055  0.023  2.392    0.020
## Wind         -2.995  0.647 -4.630    0.000
## Temp          1.838  0.262  7.003    0.000
## Month        -2.757  1.704 -1.618    0.118
## Day           0.225  0.212  1.062    0.291
```

```r
# Ilustración XX
par(mfrow = c(1,2))
mis  <- imp$imp$Ozone[,1]
fmis <- c(hist(mis, breaks, plot=FALSE)$counts, 0)
y <- matrix(c(fobs, fmis), ncol=2)
matplot(x, y, type="s",
        col=c(mdc(4),mdc(5)), lwd=2, lty=1,
        xlim = c(0, 170), ylim = c(0,45), yaxs = "i",
        xlab="Ozono",
        ylab="Frecuencia")
box()

tp <- xyplot(imp, Ozone ~ Solar.R, subset = .imp==1,
       ylab="Ozono", xlab="Solar.R",
       cex = 0.75, lex=lwd,
       ylim = c(-10, 180), xlim = c(-10,350))
print(tp, newpage = FALSE, position = c(0.48,0.045,1,0.95))

# Imputación efectiva del dataset AIR
airquality_completed = complete(imp)

# Ilustración XX: Visualización de patrón de datos en dataset AIR después
de la imputación efectiva
aggr_plot <- aggr(airquality_completed, col=c('navyblue','red'),
numbers=TRUE, sortVars=TRUE, labels=names(airquality_completed),
cex.axis=.7, gap=3, ylab=c("Histograma de datos faltantes","Patrón"))
```


Frecuencia
0
10
20
30
40
0
50
150
Ozono


Ozono
0
50
100
150
0
100
200
300
Solar.R




```
##
##  Variables sorted by number of missings:
##  Variable Count
##     Ozone     0
##   Solar.R     0
##      Wind     0
##      Temp     0
##     Month     0
##       Day     0
```

```
# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

```
##   Ozone Solar.R    Wind    Temp   Month     Day
##   "pmm"   "pmm"      ""      ""      ""      ""
```

```
# Comparación de dataset original con dataset imputado
head(airquality)
```

```
##   Ozone Solar.R Wind Temp Month Day
## 1    41     190  7.4   67     5   1
## 2    36     118  8.0   72     5   2
## 3    12     149 12.6   74     5   3
## 4    18     313 11.5   62     5   4
```

```
## 5    NA      NA 14.3   56     5   5
## 6    28      NA 14.9   66     5   6
```

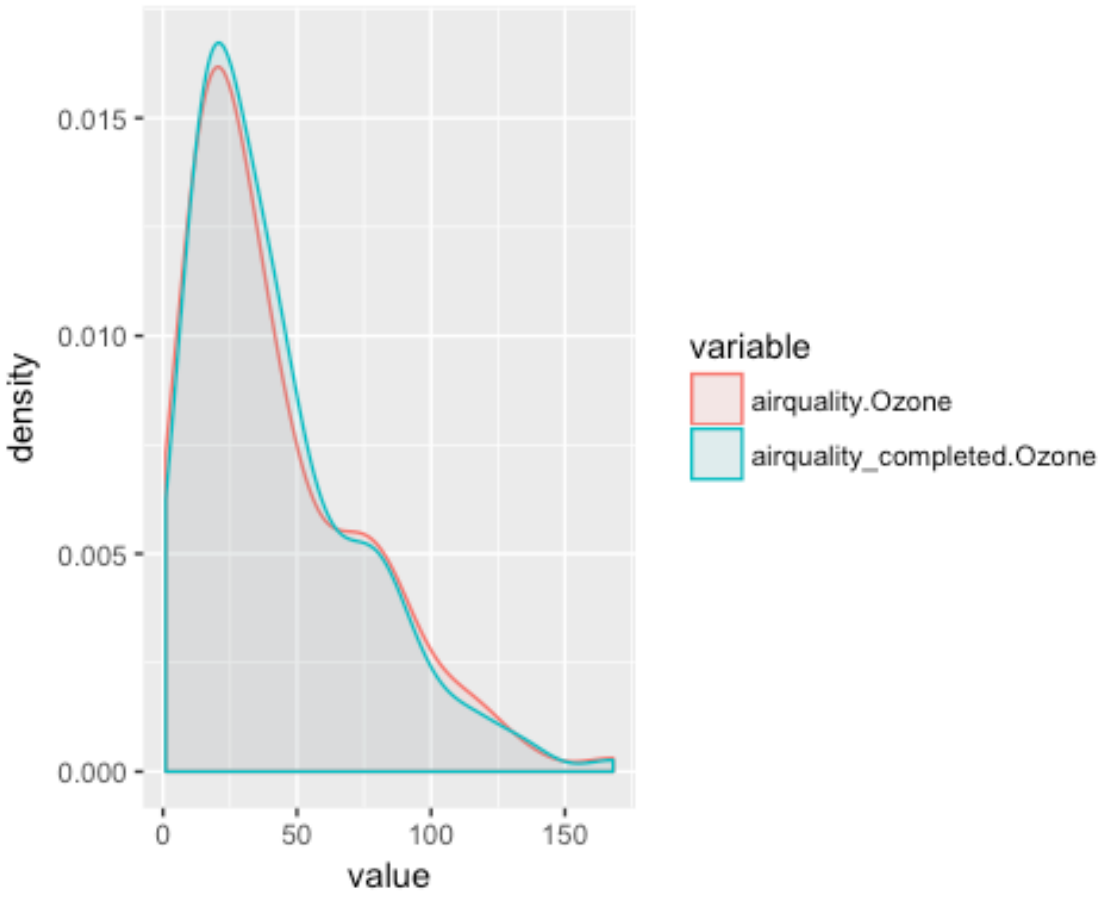
```
head(airquality_completed) # Imputado con Regresión lineal
```

```
##   Ozone Solar.R Wind Temp Month Day
## 1    41     190  7.4   67     5   1
## 2    36     118  8.0   72     5   2
## 3    12     149 12.6   74     5   3
## 4    18     313 11.5   62     5   4
## 5    19     259 14.3   56     5   5
## 6    28     294 14.9   66     5   6
```

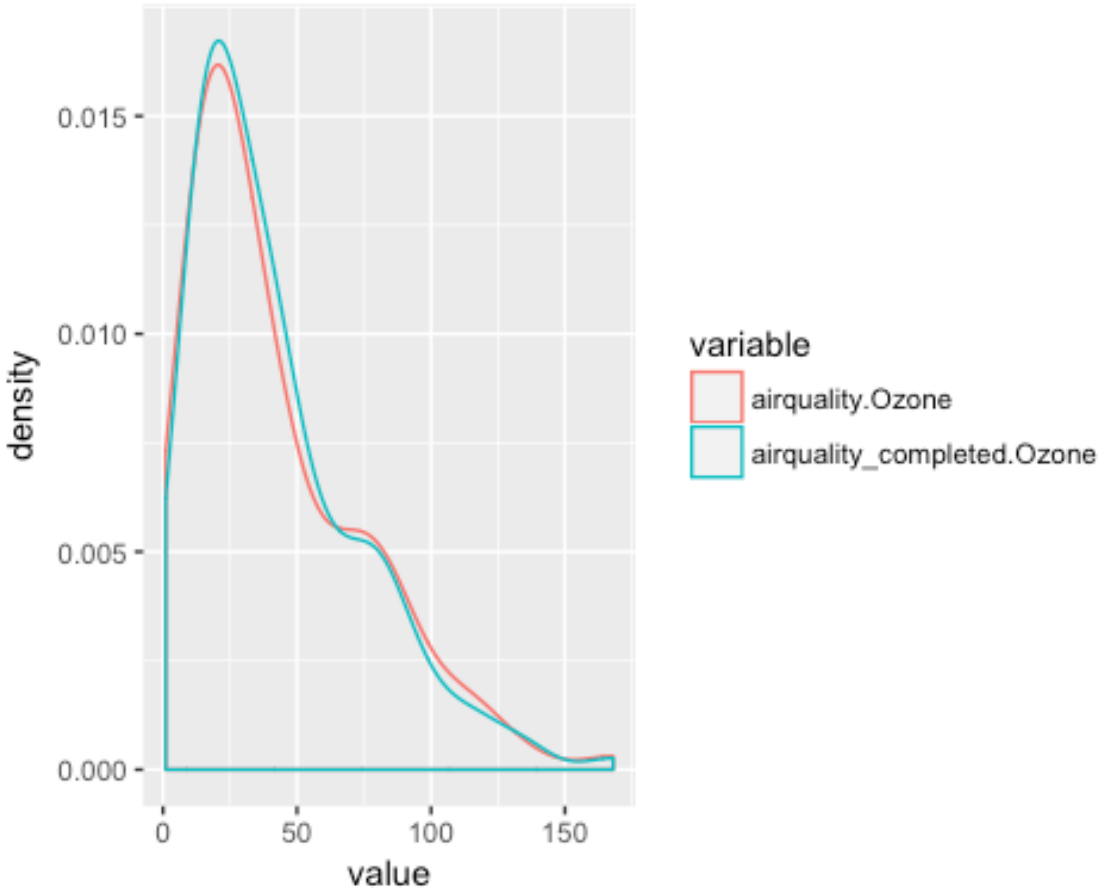
```
# Dataframe con las 2 variables Ozone de los 2 datasets
comp_Ozone <- data.frame(airquality$Ozone, airquality_completed$Ozone)
comp_Ozone <- melt(comp_Ozone)
```

```
## No id variables; using all as measure variables
```

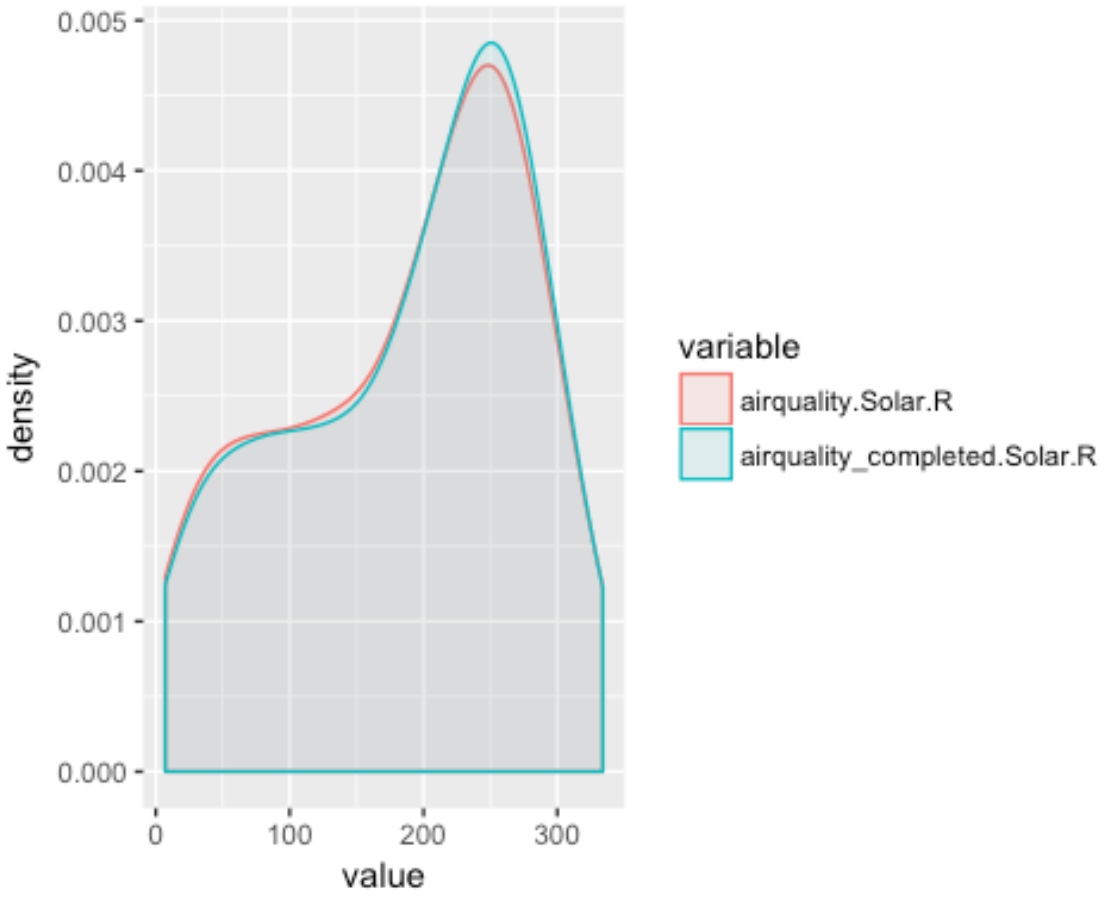
```
# Cargo librería GGPLOT2
library(ggplot2)

# Plot de densidad con las 2 variables Ozone de los 2 datasets
ggplot(comp_Ozone , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```



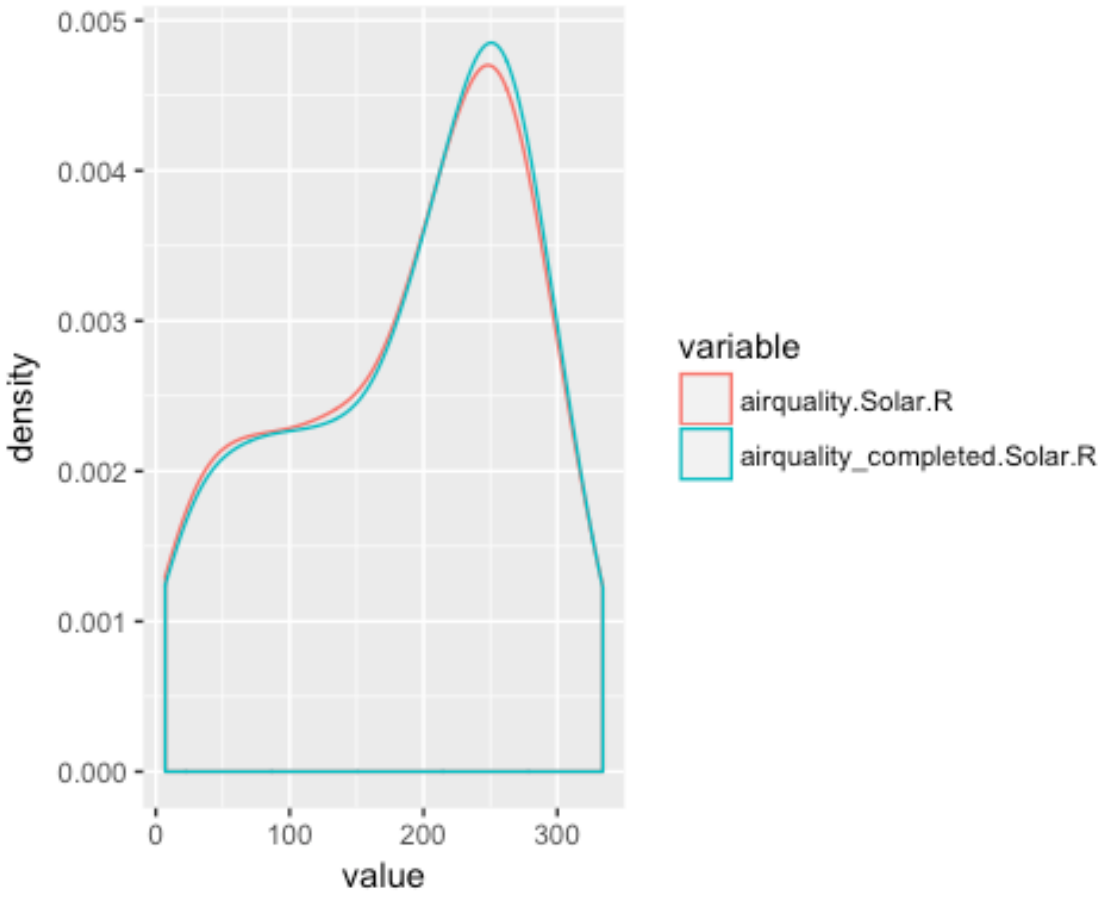

```
ggplot(comp_Ozone , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```



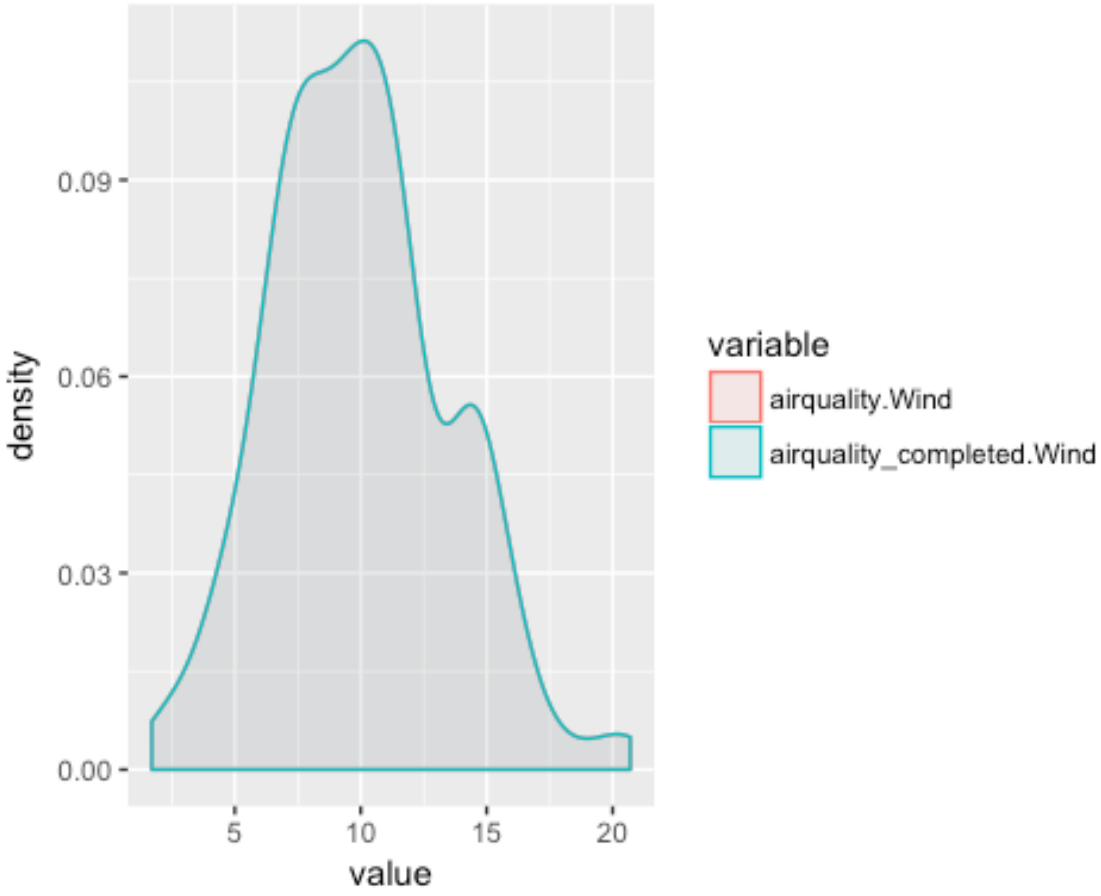

```
# Dataframe con las 2 variables Solar.R de los 2 datasets
comp_Solar.R <- data.frame(airquality$Solar.R,
airquality_completed$Solar.R)
comp_Solar.R <- melt(comp_Solar.R)

## No id variables; using all as measure variables

# Plot de densidad con las 2 variables Solar.R de los 2 datasets
ggplot(comp_Solar.R , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```



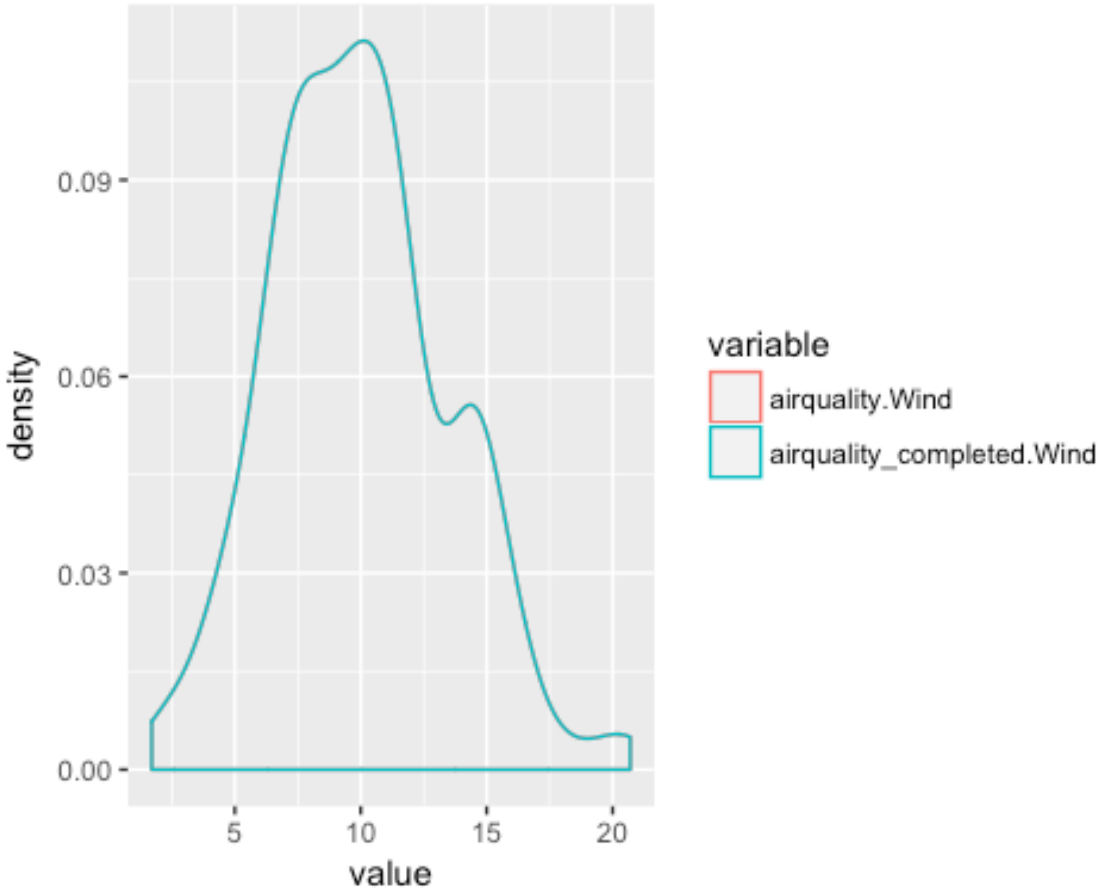

```
ggplot(comp_Solar.R , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```



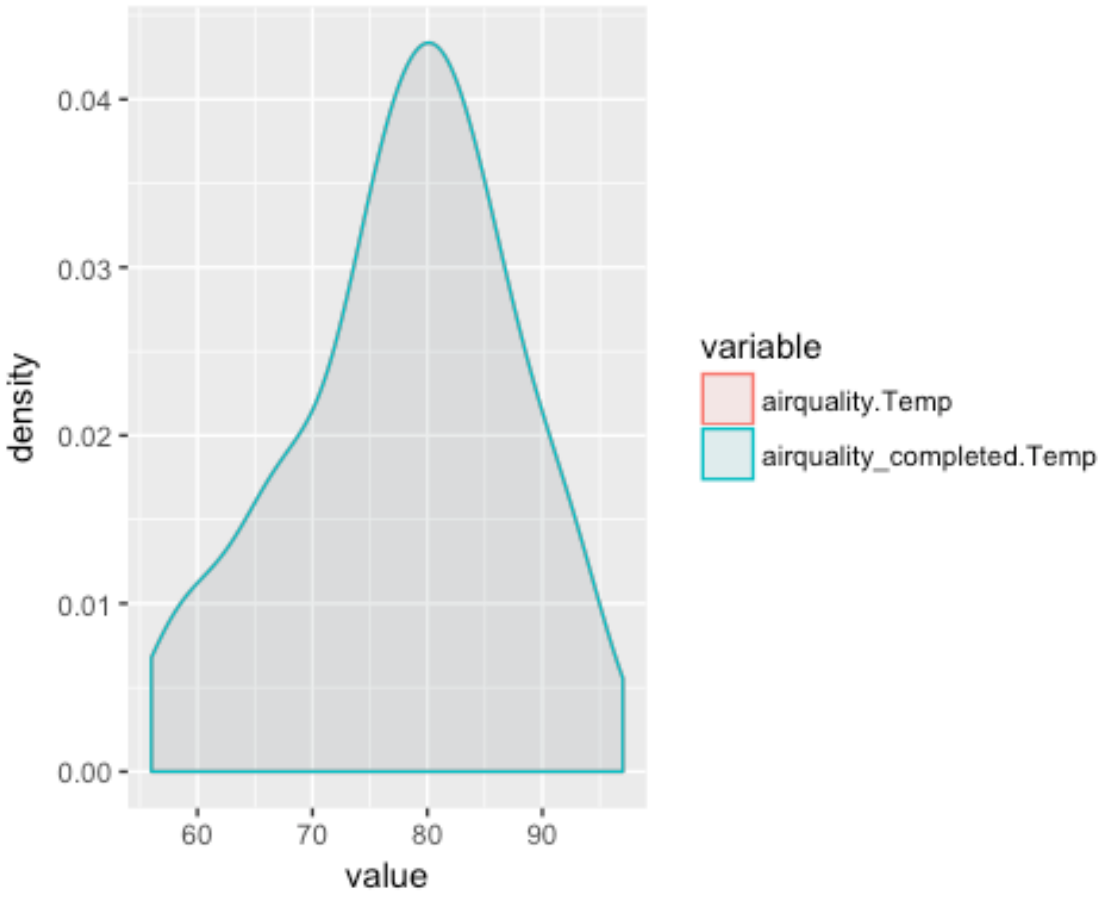

```
# Dataframe con las 2 variables Wind de los 2 datasets
comp_Wind <- data.frame(airquality$Wind, airquality_completed$Wind)
comp_Wind <- melt(comp_Wind)

## No id variables; using all as measure variables

# Plot de densidad con las 2 variables Wind de los 2 datasets (no se
produjeron imputaciones porque Wind no tenía NAs)
ggplot(comp_Wind , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```



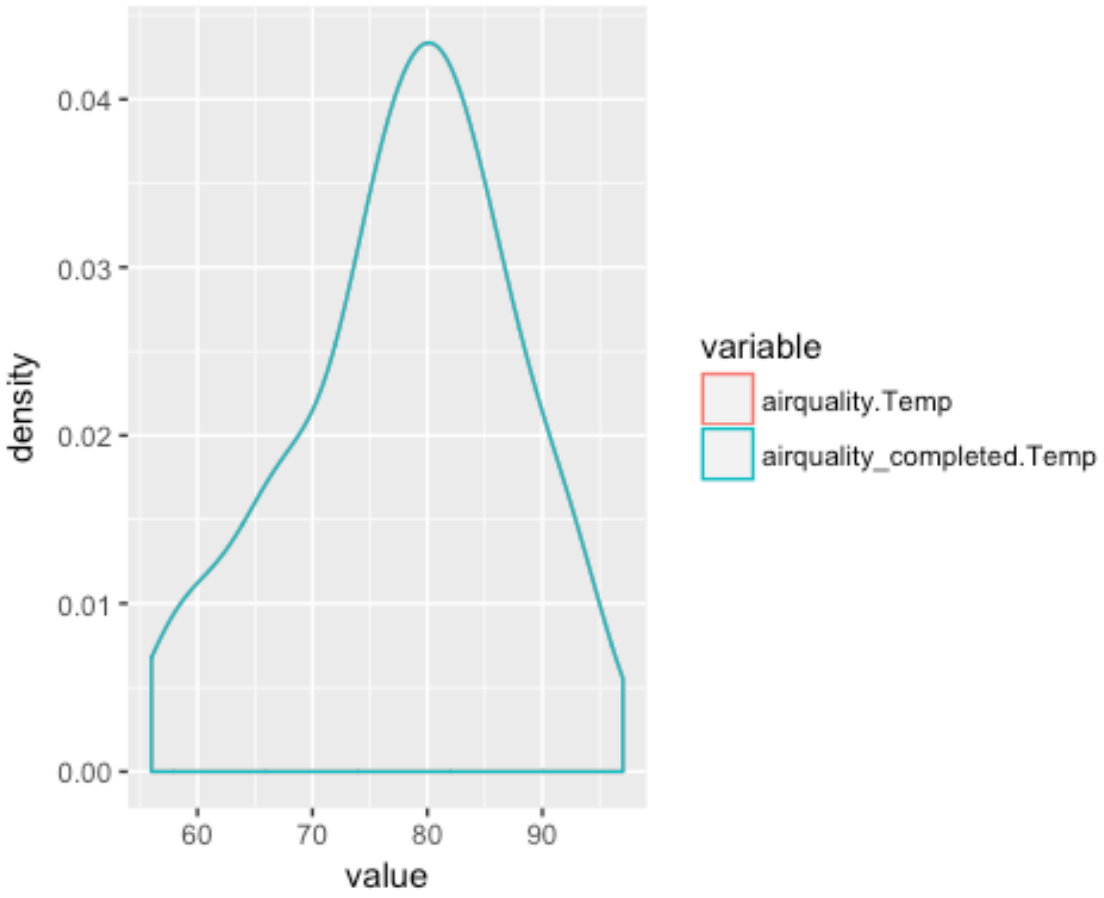

```
ggplot(comp_Wind , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```




```
# Dataframe con las 2 variables Temp de los 2 datasets
comp_Temp <- data.frame(airquality$Temp, airquality_completed$Temp)
comp_Temp <- melt(comp_Temp)

## No id variables; using all as measure variables

# Plot de densidad con las 2 variables Temp de los 2 datasets (no se
produjeron imputaciones porque Wind no tenía NAs)
ggplot(comp_Temp , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```




```
ggplot(comp_Temp , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```



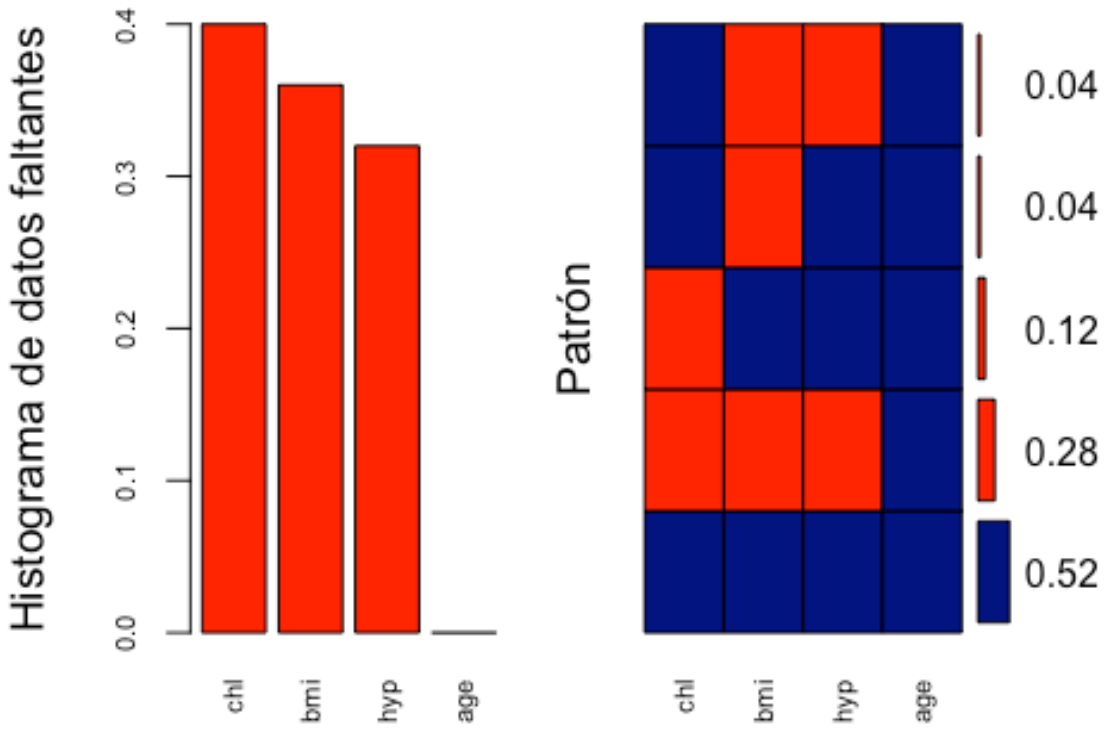
4.4 Dataset "NHAN"

```
# Dataset NHAN (Nhanes)
data(nhanes)

# Estructura del dataset
str(nhanes)
```

```
## 'data.frame':    25 obs. of  4 variables:
##  $ age: num  1 2 1 3 1 3 1 1 2 2 ...
##  $ bmi: num  NA 22.7 NA NA 20.4 NA 22.5 30.1 22 NA ...
##  $ hyp: num  NA 1 1 NA 1 NA 1 1 1 NA ...
##  $ chl: num  NA 187 187 NA 113 184 118 187 238 NA ...
```

```
# Guardo el dataset NHAN para generar el fichero NHAN.rds
# (a efectos de reproducibilidad posterior)
saveRDS(nhanes, "NHAN.rds")

# Apertura del dataset NHAN
# (Descomentar la línea siguiente si fuera necesario abrirlo para
```

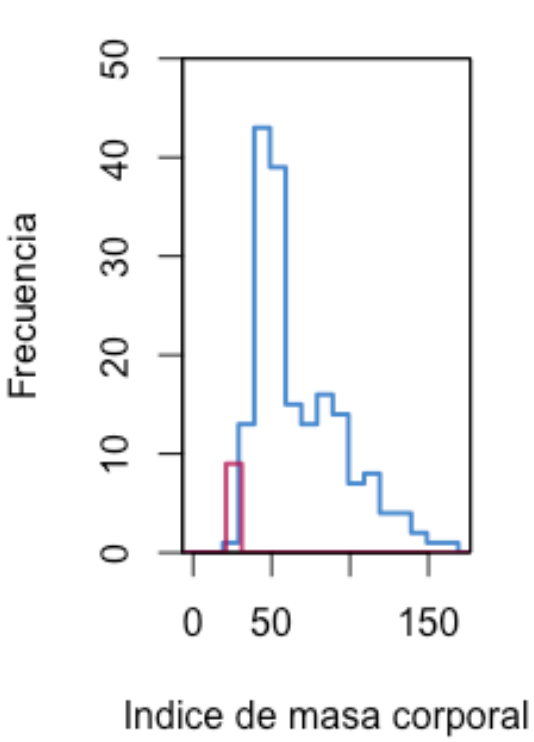
```
reproducibilidad posterior)
# nhanes <- readRDS("NHAN.rds")

# Ilustración 27: Visualización de patrón de datos faltantes del dataset
NHAN
aggr_plot <- aggr(nhanes, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(nhanes), cex.axis=.7, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```

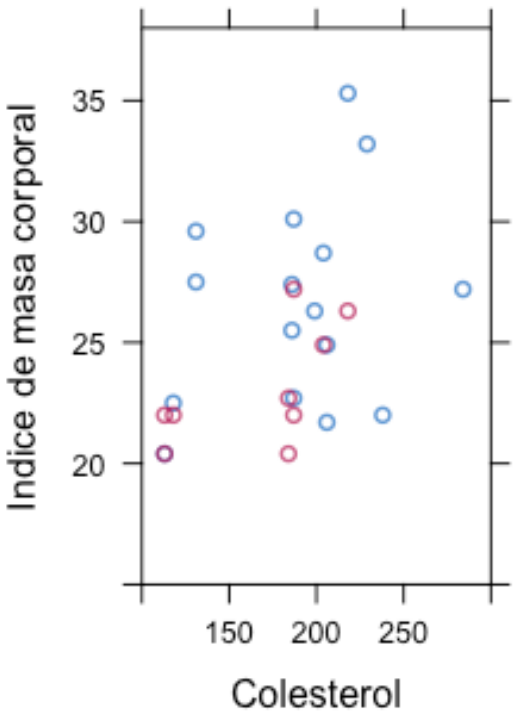


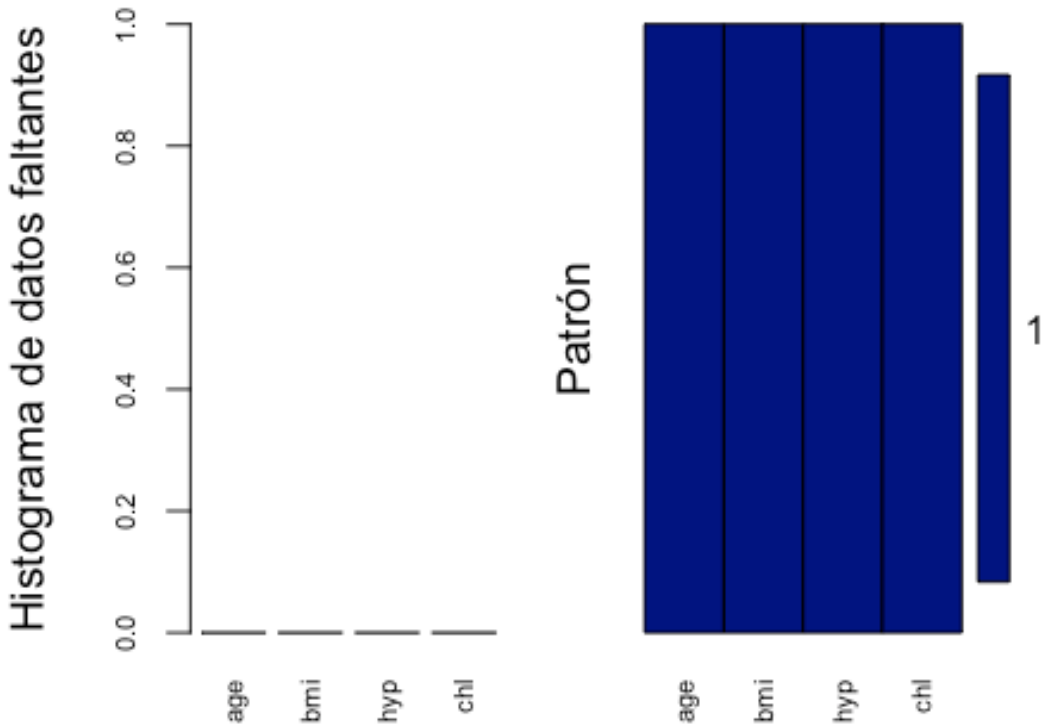

```
##
##  Variables sorted by number of missings:
##  Variable Count
##       chl  0.40
##       bmi  0.36
##       hyp  0.32
##       age  0.00

# Imputación múltiple del dataframe NHAN
imp <- mice(nhanes, seed=5, print=FALSE)
fit <- with(imp, lm(bmi ~ age + hyp + chl))
tab <- round(summary(pool(fit)),3)
tab[,c(1:3,5)]
```

```
##                est    se      t Pr(>|t|)
## (Intercept) 20.594 3.983  5.170    0.002
## age         -3.784 1.318 -2.872    0.024
## hyp          1.604 1.876  0.855    0.408
## chl          0.054 0.022  2.494    0.040
```

```r
# Ilustración XX
par(mfrow = c(1,2))
mis  <- imp$imp$bmi[,1]
fmis <- c(hist(mis, breaks, plot=FALSE)$counts, 0)
y <- matrix(c(fobs, fmis), ncol=2)
matplot(x, y, type="s",
        col=c(mdc(4),mdc(5)), lwd=2, lty=1,
        xlim = c(0, 170), ylim = c(0,50), yaxs = "i",
        xlab="Indice de masa corporal",
        ylab="Frecuencia")
box()

tp <- xyplot(imp, bmi ~ chl, subset = .imp==1,
       ylab="Indice de masa corporal", xlab="Colesterol",
       cex = 0.75, lex=lwd,
       ylim = c(15, 38), xlim = c(100,300))
print(tp, newpage = FALSE, position = c(0.48,0.045,1,0.95))

# Imputación efectiva del dataset NHAN
nhanes_completed = complete(imp)

# Ilustración XX: Visualización de patrón de datos en dataset NHAN
después de la imputación efectiva
aggr_plot <- aggr(nhanes_completed, col=c('navyblue','red'),
numbers=TRUE, sortVars=TRUE, labels=names(nhanes_completed), cex.axis=.7,
gap=3, ylab=c("Histograma de datos faltantes","Patrón"))
```


Frecuencia
0
10
20
30
40
50
0
50
150
Indice de masa corporal


Indice de masa corporal
20
25
30
35
150
200
250
Colesterol




```
##
##  Variables sorted by number of missings:
##  Variable Count
##       age     0
##       bmi     0
##       hyp     0
##       chl     0
```

```
# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

```
##   age   bmi   hyp   chl
##    "" "pmm" "pmm" "pmm"
```

```
# Comparación de dataset original con dataset imputado
head(nhanes)
```

```
##   age  bmi hyp chl
## 1   1   NA  NA  NA
## 2   2 22.7   1 187
## 3   1   NA   1 187
## 4   3   NA  NA  NA
## 5   1 20.4   1 113
## 6   3   NA  NA 184
```

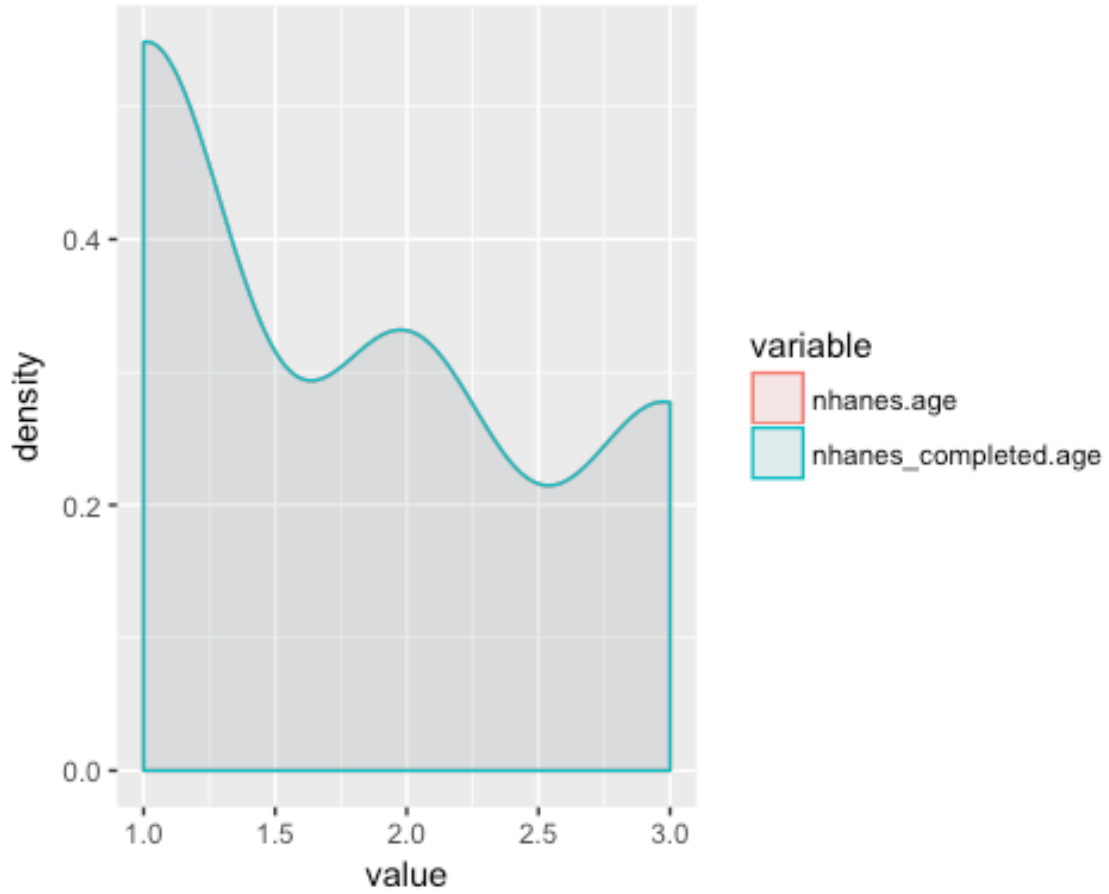
```r
head(nhanes_completed) # Imputado con PMM
```

```
##   age  bmi hyp chl
## 1   1 22.0   1 113
## 2   2 22.7   1 187
## 3   1 27.2   1 187
## 4   3 24.9   2 204
## 5   1 20.4   1 113
## 6   3 20.4   2 184
```

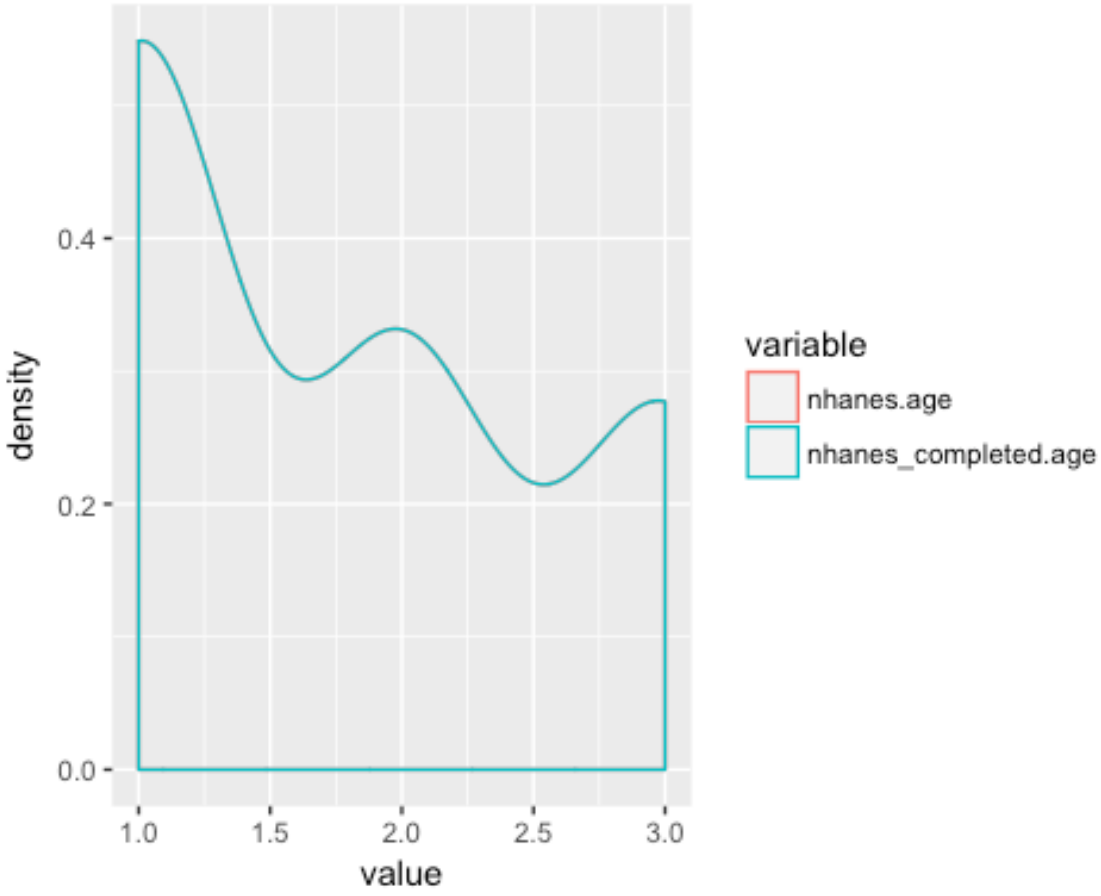
```r
# Dataframe con las 2 variables age de los 2 datasets
comp_age <- data.frame(nhanes$age, nhanes_completed$age)
comp_age <- melt(comp_age)
```

```
## No id variables; using all as measure variables
```

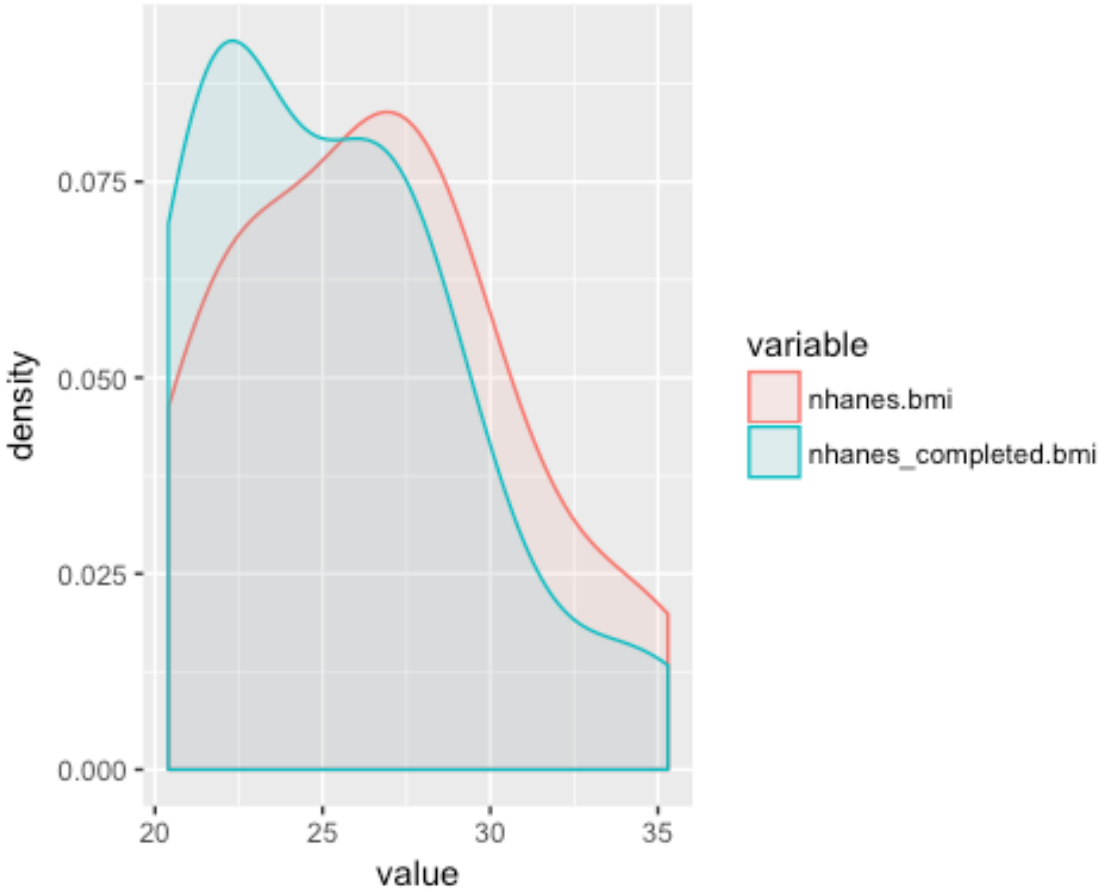
```r
# Cargo librería GGPLOT2
library(ggplot2)

# Plot de densidad con las 2 variables age de los 2 datasets (no se produjeron imputaciones porque hyp no tenía NAs)
ggplot(comp_age, aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable), alpha=0.1)
```



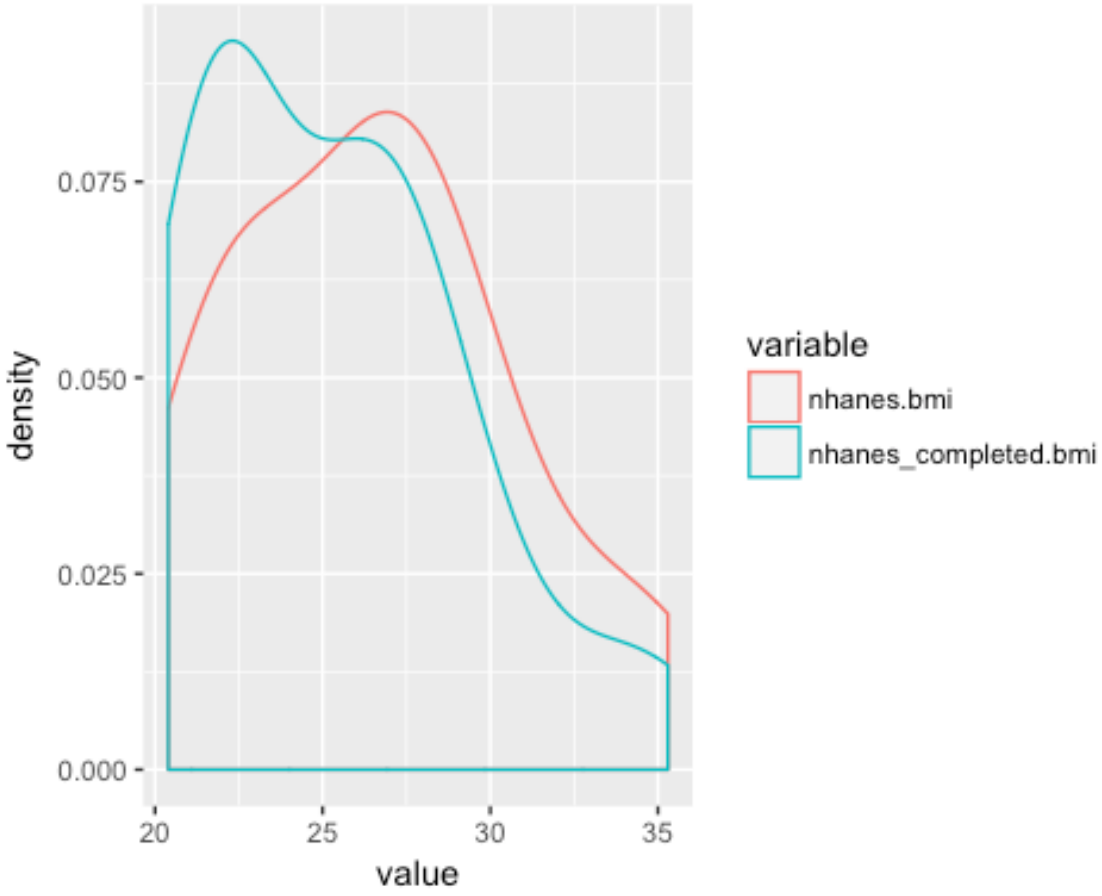
```
ggplot(comp_age, aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```



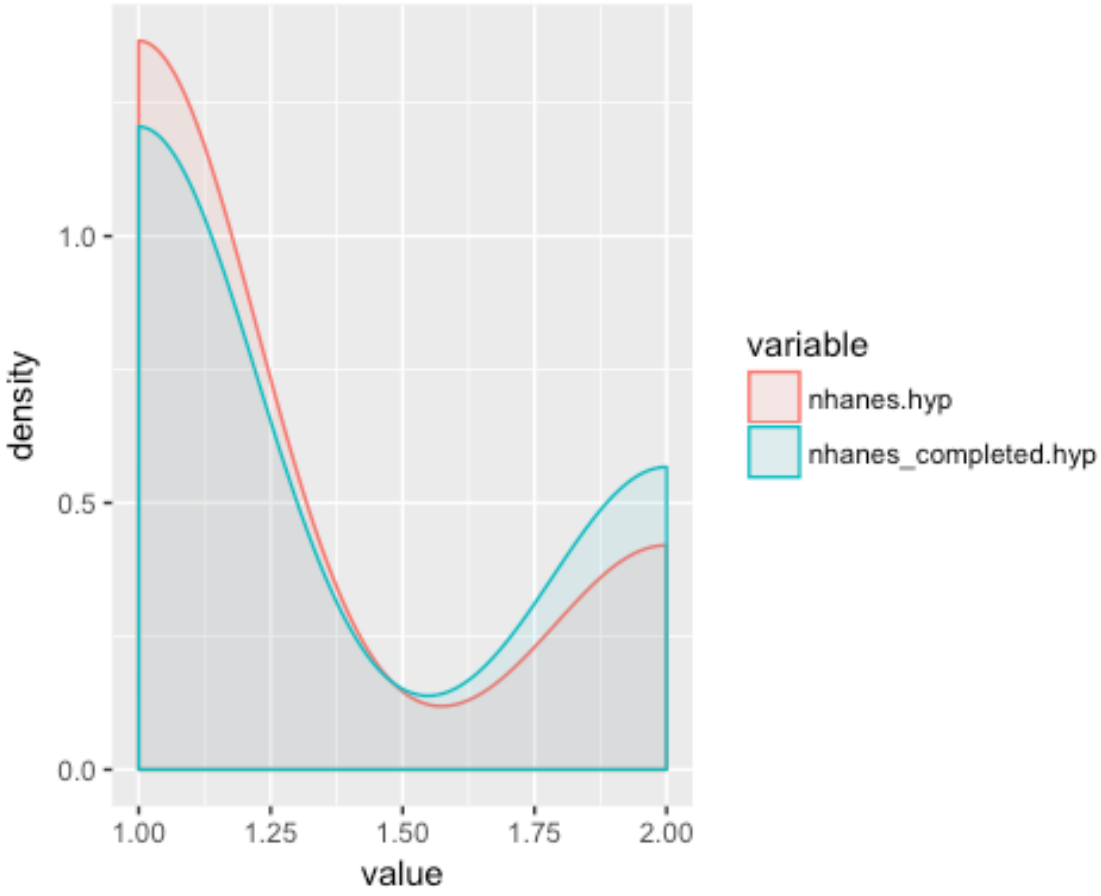

```
# Dataframe con las 2 variables bmi de los 2 datasets
comp_bmi <- data.frame(nhanes$bmi, nhanes_completed$bmi)
comp_bmi <- melt(comp_bmi)

## No id variables; using all as measure variables

# Plot de densidad con las 2 variables bmi de los 2 datasets
ggplot(comp_bmi, aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```



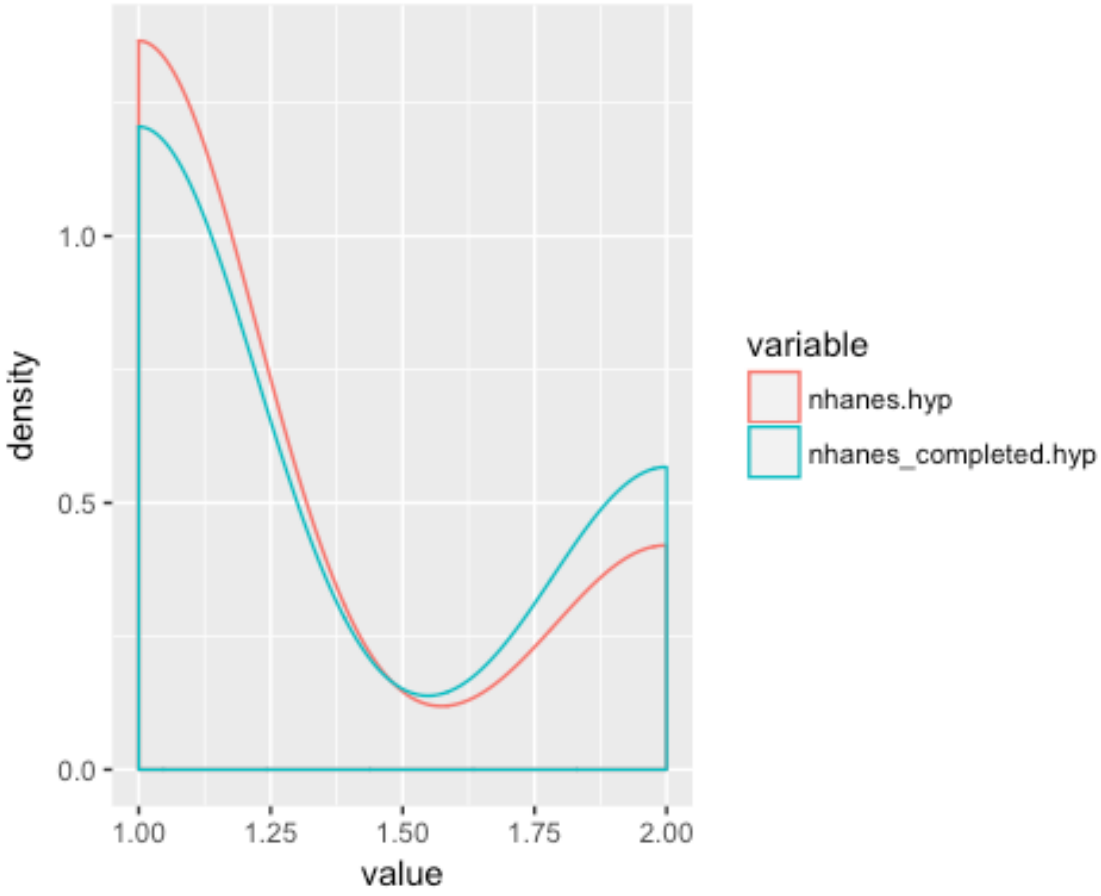

```
ggplot(comp_bmi, aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```



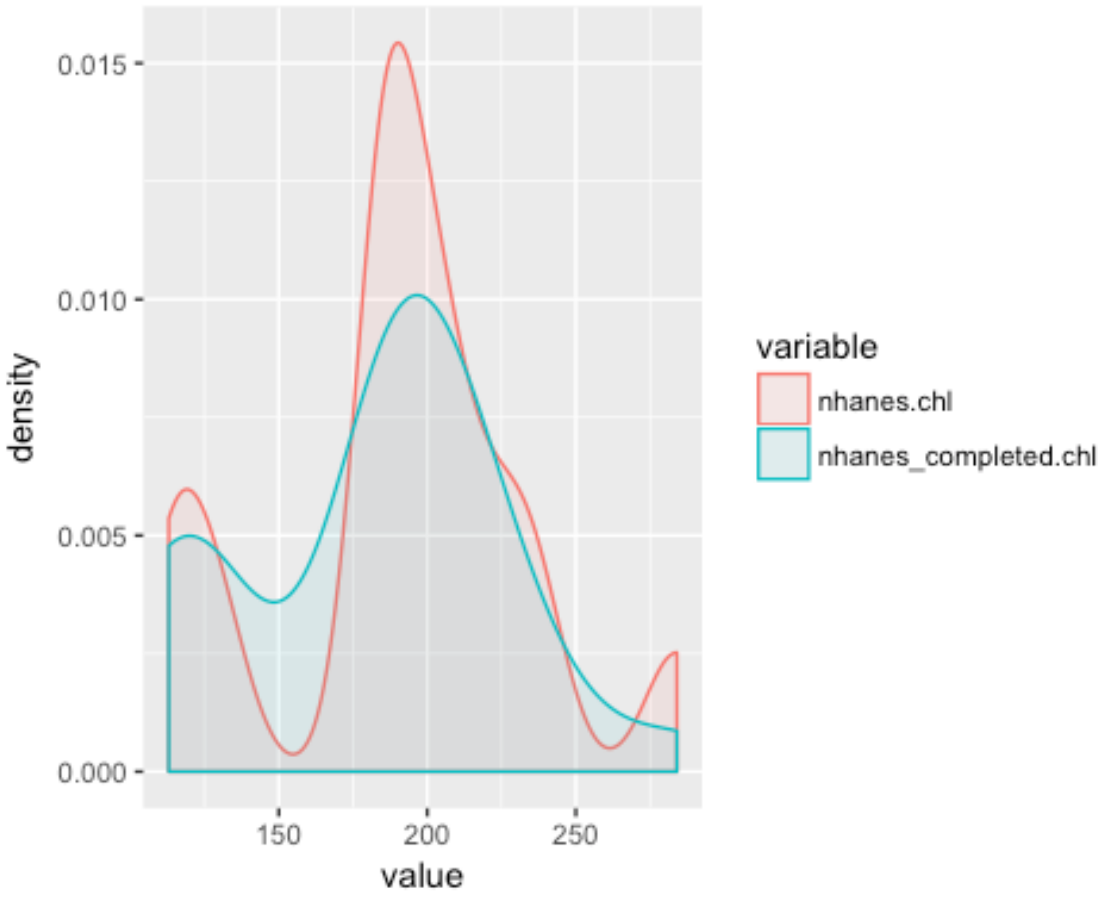

```
# Dataframe con las 2 variables hyp de los 2 datasets
comp_hyp <- data.frame(nhanes$hyp, nhanes_completed$hyp)
comp_hyp <- melt(comp_hyp)

## No id variables; using all as measure variables

# Plot de densidad con las 2 variables hyp de los 2 datasets (no se
produjeron imputaciones porque hyp no tenía NAs)
ggplot(comp_hyp , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```



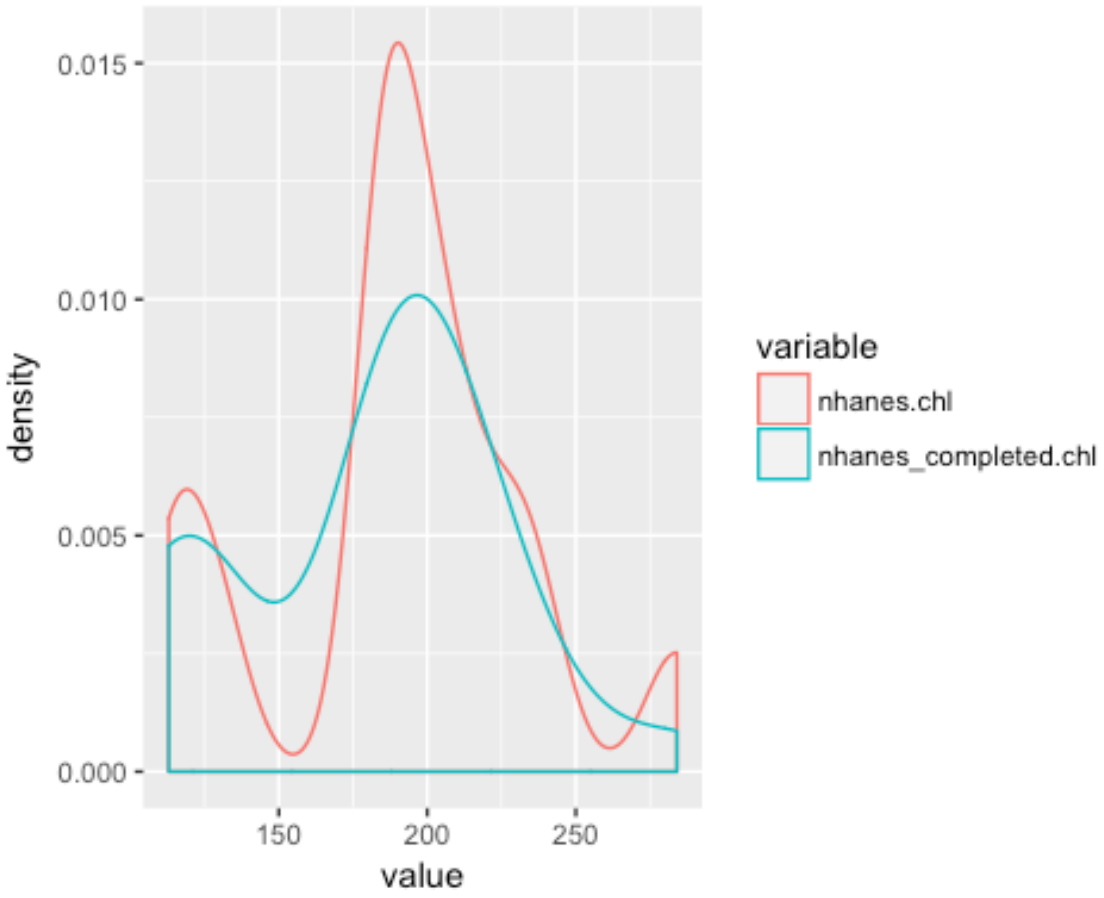

```
ggplot(comp_hyp , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```




```
# Dataframe con las 2 variables chl de los 2 datasets
comp_chl <- data.frame(nhanes$chl, nhanes_completed$chl)
comp_chl <- melt(comp_chl)

## No id variables; using all as measure variables

# Plot de densidad con las 2 variables chl de los 2 datasets (no se
produjeron imputaciones porque Wind no tenía NAs)
ggplot(comp_chl , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```




```
ggplot(comp_chl , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```

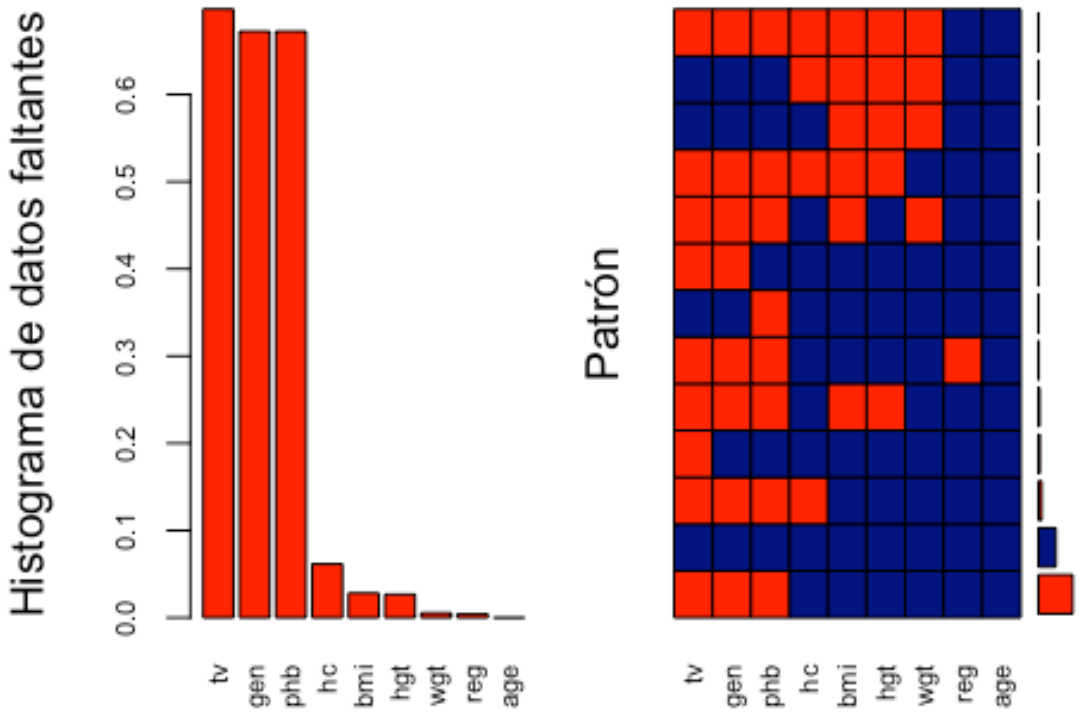


4.5 Dataset "BOYS"

```
# Dataset BOYS
data(boys)

# Estructura del dataset
str(boys)
```

```
## 'data.frame':    748 obs. of  9 variables:
##  $ age: num  0.035 0.038 0.057 0.06 0.062 0.068 0.068 0.071 0.071
0.073 ...
##  $ hgt: num  50.1 53.5 50 54.5 57.5 55.5 52.5 53 55.1 54.5 ...
##  $ wgt: num  3.65 3.37 3.14 4.27 5.03 ...
##  $ bmi: num  14.5 11.8 12.6 14.4 15.2 ...
##  $ hc : num  33.7 35 35.2 36.7 37.3 37 34.9 35.8 36.8 38 ...
##  $ gen: Ord.factor w/ 5 levels "G1"<"G2"<"G3"<..: NA NA NA NA NA NA NA
NA NA NA ...
##  $ phb: Ord.factor w/ 6 levels "P1"<"P2"<"P3"<..: NA NA NA NA NA NA NA
NA NA NA ...
```

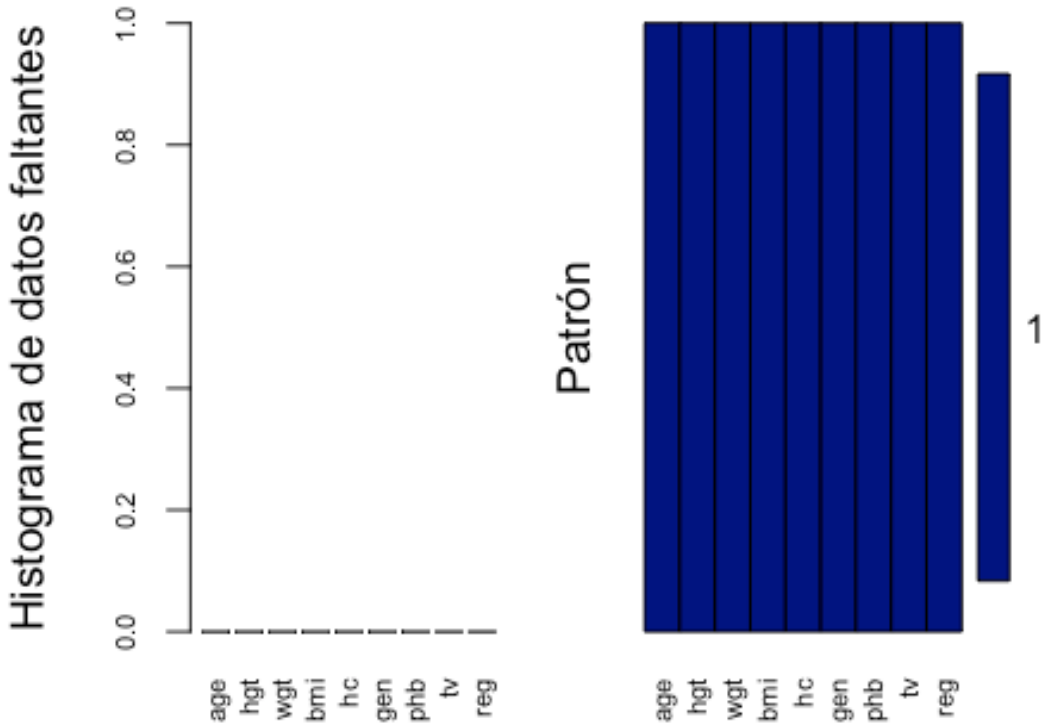
```
##  $ tv : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ reg: Factor w/ 5 levels "north","east",..: 4 4 4 4 4 4 4 3 3 2 ...

# Guardo el dataset BOYS para generar el fichero BOYS.rds
# (a efectos de reproducibilidad posterior)
saveRDS(boys, "BOYS.rds")

# Apertura del dataset BOYS
# (Descomentar la línea siguiente si fuera necesario abrirlo para
reproducibilidad posterior)
# boys <- readRDS("BOYS.rds")

# Ilustración 25: Visualización de patrón de datos faltantes del dataset
BOYS
aggr_plot <- aggr(boys, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(boys), cex.axis=.7, gap=3, ylab=c("Histograma
de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##  Variable       Count
##        tv 0.697860963
##       gen 0.672459893
```

```
##        phb 0.672459893
##         hc 0.061497326
##        bmi 0.028074866
##        hgt 0.026737968
##        wgt 0.005347594
##        reg 0.004010695
##        age 0.000000000
```

```
# Imputación múltiple del dataframe BOYS
imp <- mice(boys, seed=5, print=FALSE)

# Imputación efectiva del dataset BOYS
boys_completed = complete(imp)

# Ilustración XX: Visualización de patrón de datos en dataset BOYS
después de la imputación efectiva
aggr_plot <- aggr(boys_completed, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(boys_completed), cex.axis=.7, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##  Variable Count
```

```
##       age     0
##       hgt     0
##       wgt     0
##       bmi     0
##        hc     0
##       gen     0
##       phb     0
##        tv     0
##       reg     0
```

```
# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

```
##       age       hgt       wgt       bmi        hc       gen       phb
##        ""     "pmm"     "pmm"     "pmm"     "pmm"    "polr"    "polr"
##        tv       reg
##     "pmm" "polyreg"
```

```
# Comparación de dataset original con dataset imputado
head(boys)
```

```
##      age  hgt   wgt   bmi   hc  gen  phb tv   reg
## 3  0.035 50.1 3.650 14.54 33.7 <NA> <NA> NA south
## 4  0.038 53.5 3.370 11.77 35.0 <NA> <NA> NA south
## 18 0.057 50.0 3.140 12.56 35.2 <NA> <NA> NA south
## 23 0.060 54.5 4.270 14.37 36.7 <NA> <NA> NA south
## 28 0.062 57.5 5.030 15.21 37.3 <NA> <NA> NA south
## 36 0.068 55.5 4.655 15.11 37.0 <NA> <NA> NA south
```

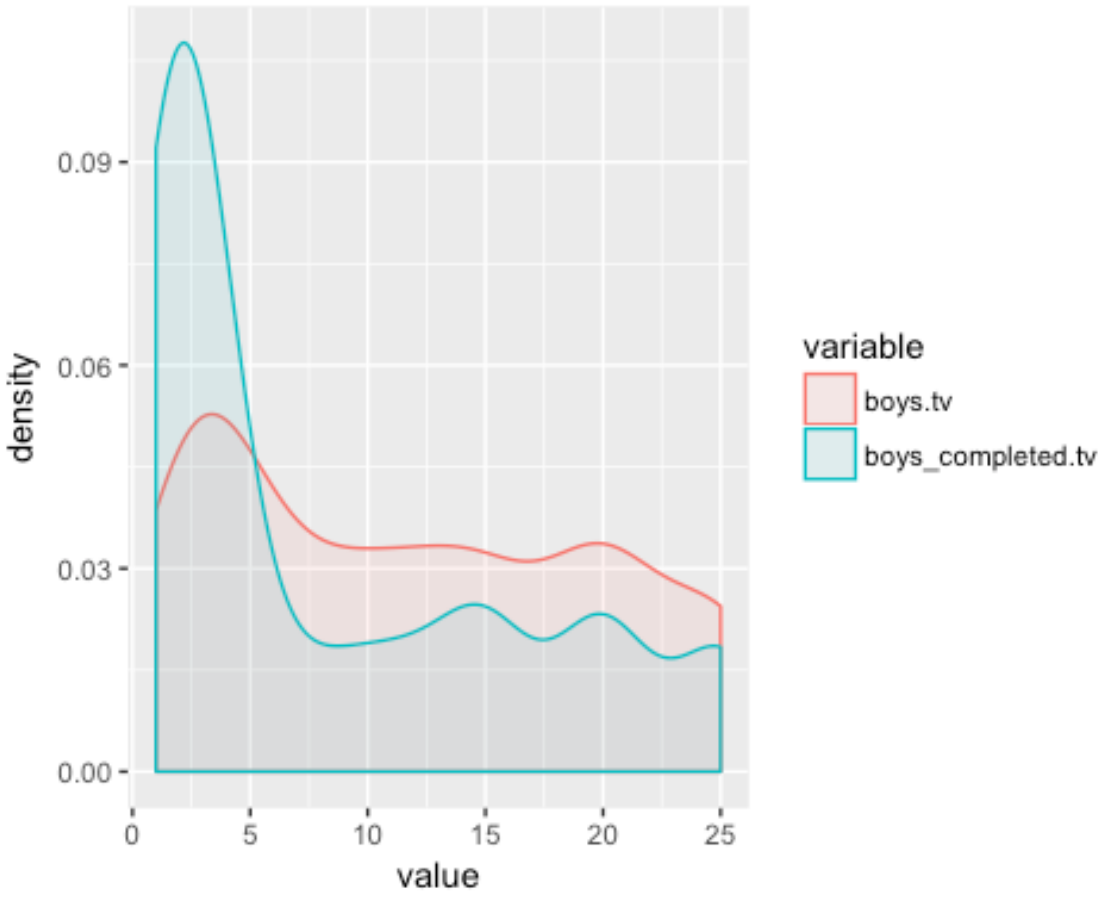
```
head(boys_completed) # Imputado con PMM
```

```
##      age  hgt   wgt   bmi   hc gen phb tv   reg
## 3  0.035 50.1 3.650 14.54 33.7  G1  P2  1 south
## 4  0.038 53.5 3.370 11.77 35.0  G1  P3  2 south
## 18 0.057 50.0 3.140 12.56 35.2  G4  P5  2 south
## 23 0.060 54.5 4.270 14.37 36.7  G2  P1  2 south
## 28 0.062 57.5 5.030 15.21 37.3  G1  P1  2 south
## 36 0.068 55.5 4.655 15.11 37.0  G3  P3  2 south
```

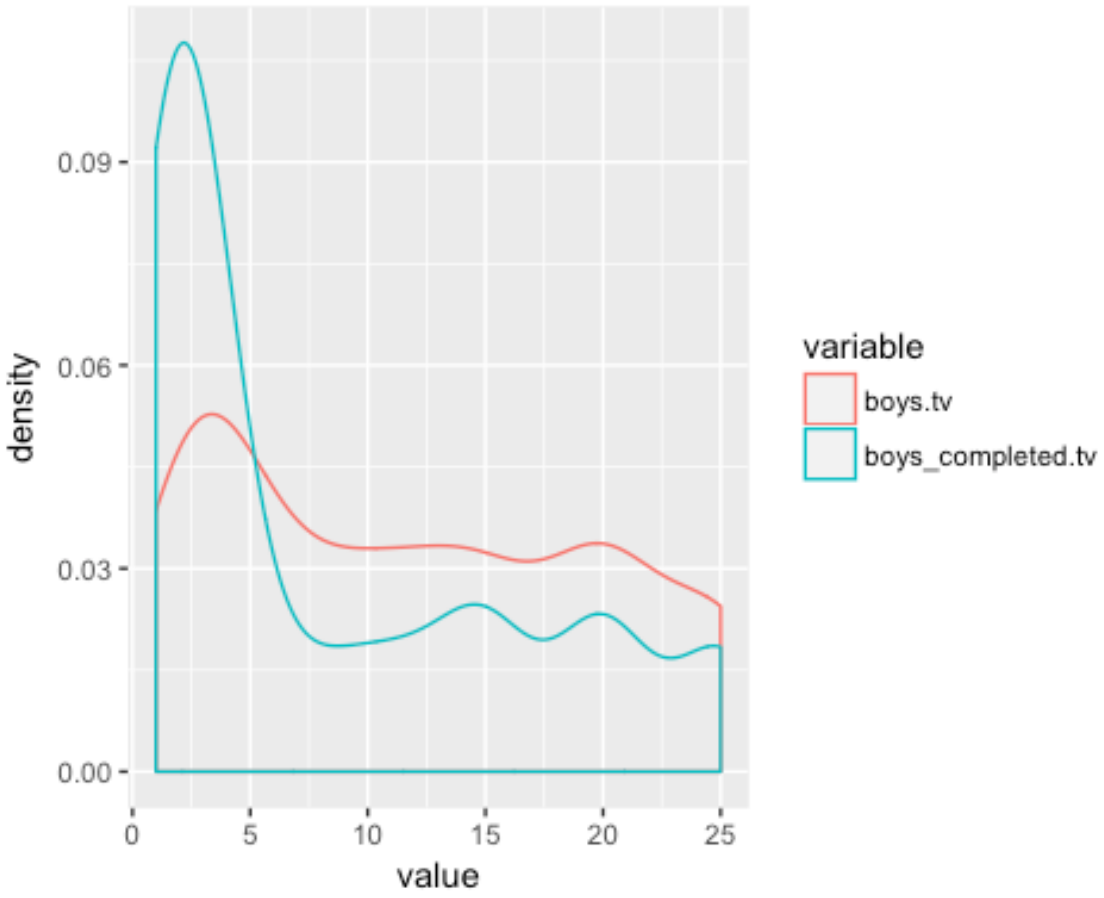
```
# Dataframe con las 2 variables tv de los 2 datasets
comp_tv <- data.frame(boys$tv, boys_completed$tv)
comp_tv <- melt(comp_tv)
```

```
## No id variables; using all as measure variables
```

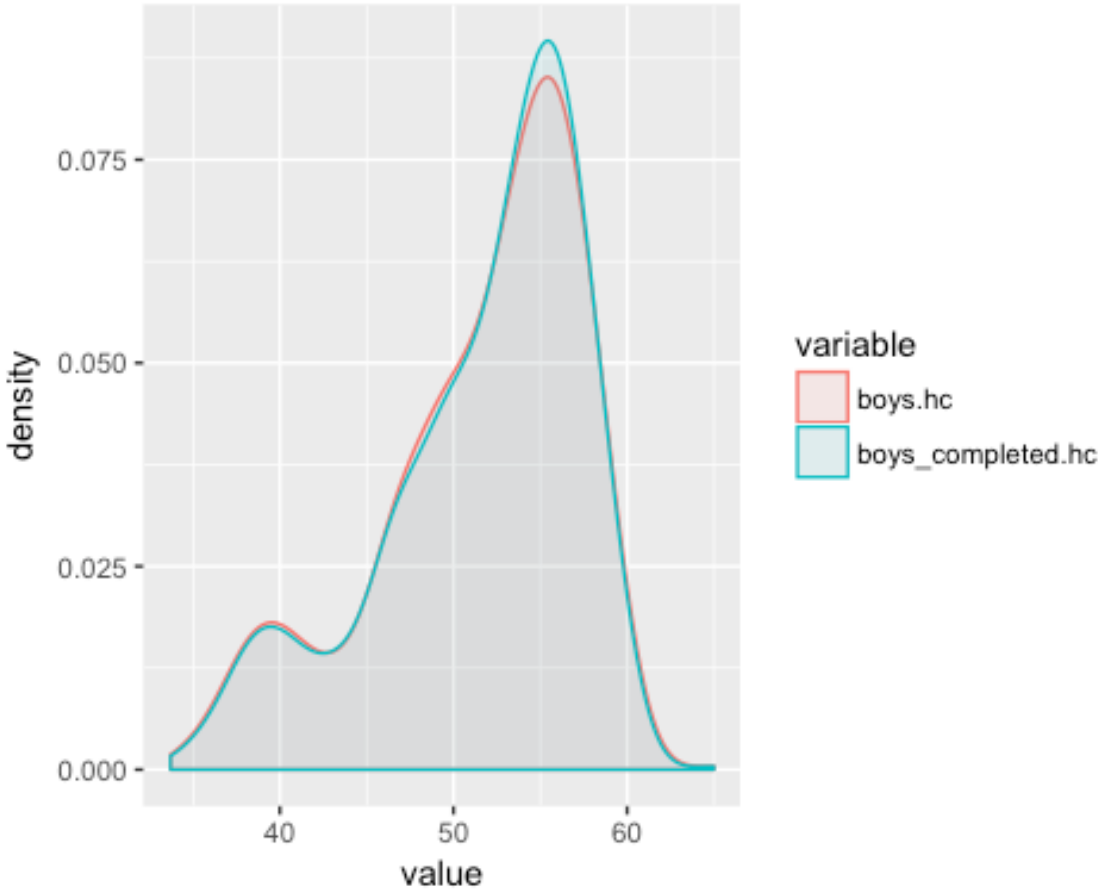
```
# Cargo librería GGPLOT2
library(ggplot2)

# Plot de densidad con las 2 variables tv de los 2 datasets
ggplot(comp_tv, aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```



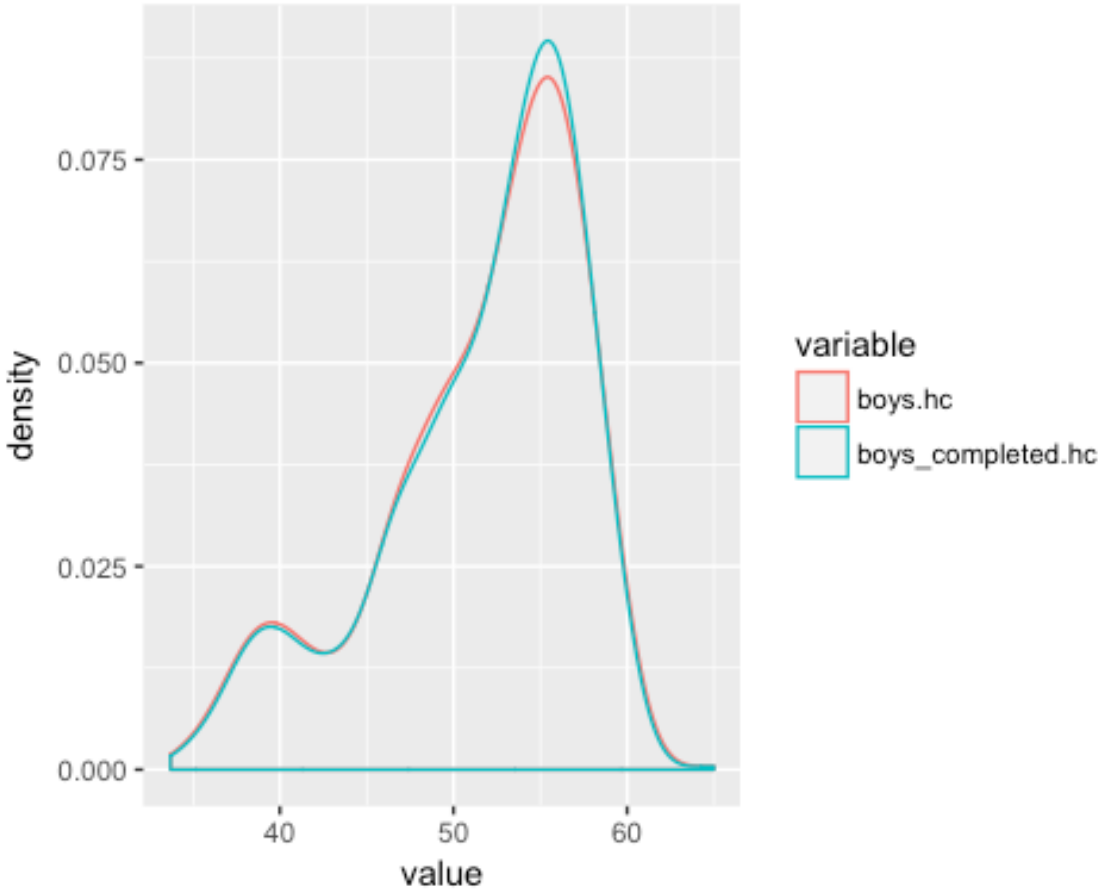

```
ggplot(comp_tv, aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```




```
# Dataframe con las 2 variables hc de los 2 datasets
comp_hc <- data.frame(boys$hc, boys_completed$hc)
comp_hc <- melt(comp_hc)

## No id variables; using all as measure variables

# Plot de densidad con las 2 variables hc de los 2 datasets
ggplot(comp_hc , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable, fill=variable),
alpha=0.1)
```




```
ggplot(comp_hc , aes(x=value)) +
  geom_density(aes(group=variable, colour=variable))
```



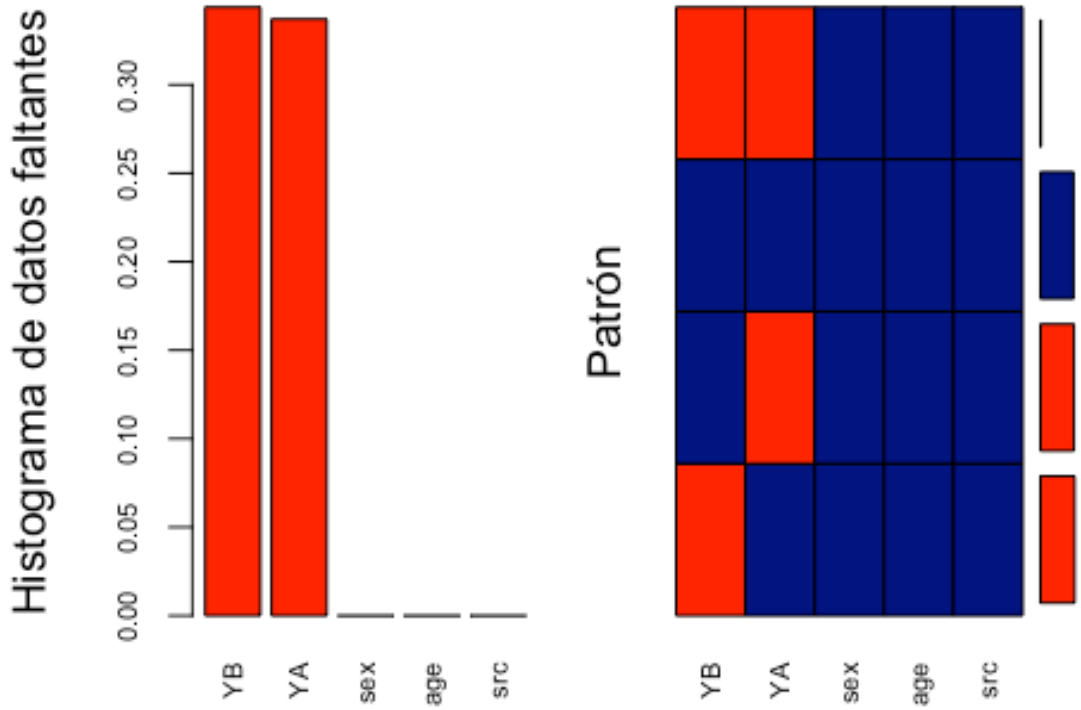
4.6 Dataset "WALK"

```
# Dataset WALK (Walking)
data(walking)

# Estructura del dataset
str(walking)
```

```
## 'data.frame':    890 obs. of  5 variables:
##  $ sex: Factor w/ 2 levels "Male","Female": 1 2 1 1 2 1 2 2 2 2 ...
##  $ age: num  61 69 74 66 72 67 66 66 64 57 ...
##  $ YA : Ord.factor w/ 4 levels "0"<"1"<"2"<"3": 2 2 1 1 3 1 1 2 1 1
...
##  $ YB : Ord.factor w/ 4 levels "0"<"1"<"2"<"3": NA NA NA NA NA NA NA
NA NA NA ...
##  $ src: Factor w/ 3 levels "A","B","E": 1 1 1 1 1 1 1 1 1 1 ...
```

```
# Guardo el dataset WALK para generar el fichero WALK.rds
# (a efectos de reproducibilidad posterior)
saveRDS(walking, "WALK.rds")
```

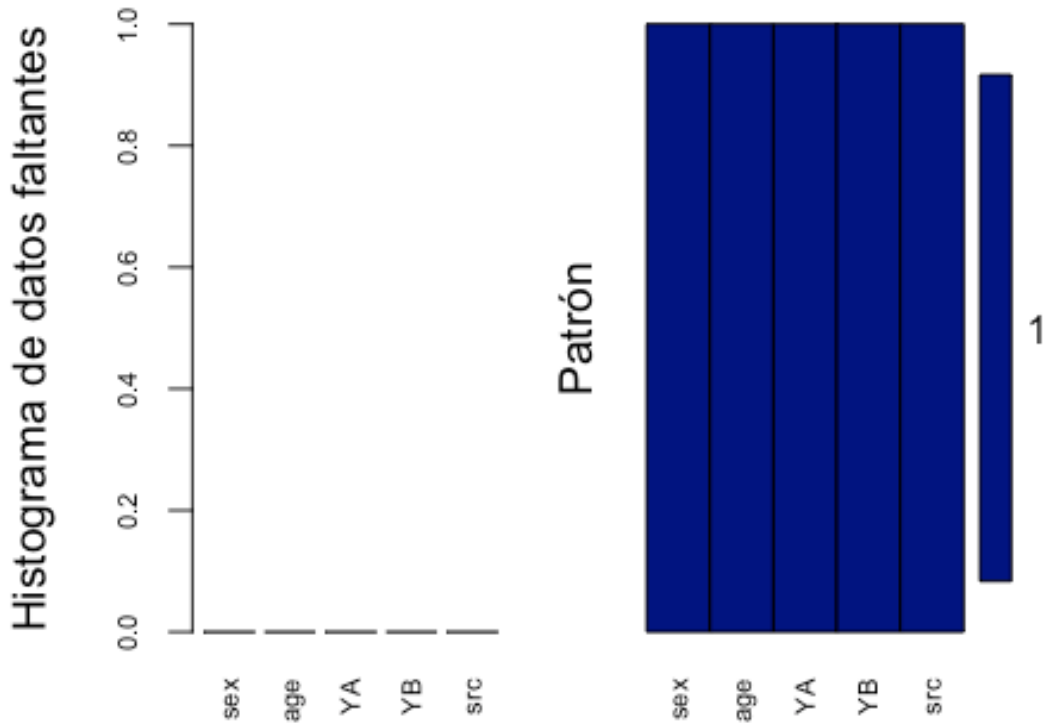
```r
# Apertura del dataset WALK
# (Descomentar la línea siguiente si fuera necesario abrirlo para reproducibilidad posterior)
# walking <- readRDS("WALK.rds")

# Ilustración 26: Visualización de patrón de datos faltantes del dataset WALK
aggr_plot <- aggr(walking, col=c('navyblue','red'), numbers=TRUE, sortVars=TRUE, labels=names(walking), cex.axis=.7, gap=3, ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##  Variable     Count
##        YB 0.3438202
##        YA 0.3370787
##       sex 0.0000000
##       age 0.0000000
##       src 0.0000000
```

```r
# Imputación múltiple del dataframe WALK
imp <- mice(walking, seed=5, print=FALSE)
```

```r
# Imputación efectiva del dataset WALK
walking_completed = complete(imp)

# Ilustración XX: Visualización de patrón de datos en dataset WALK
después de la imputación efectiva
aggr_plot <- aggr(walking_completed, col=c('navyblue','red'),
numbers=TRUE, sortVars=TRUE, labels=names(walking_completed),
cex.axis=.7, gap=3, ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##  Variable Count
##       sex     0
##       age     0
##        YA     0
##        YB     0
##       src     0
```

```r
# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

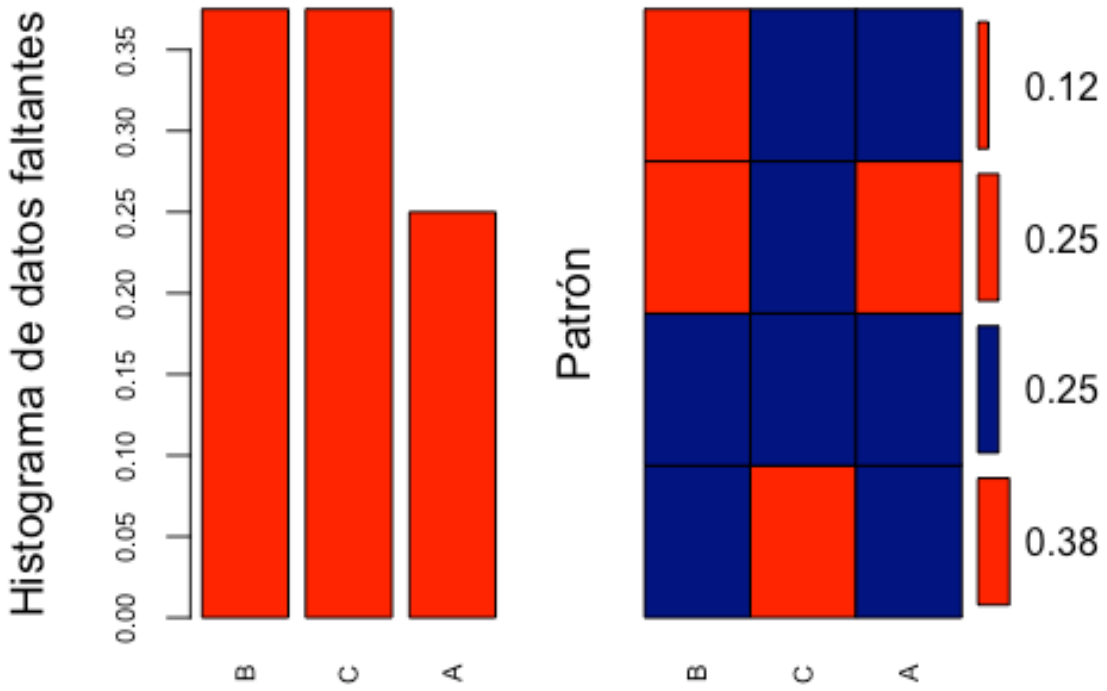
```
##    sex    age     YA     YB    src
##     ""     "" "polr" "polr"     ""
```

4.7 Dataset "PATT"

```
# Dataset PATT
data(pattern4)

# Estructura del dataset
str(pattern4)
```

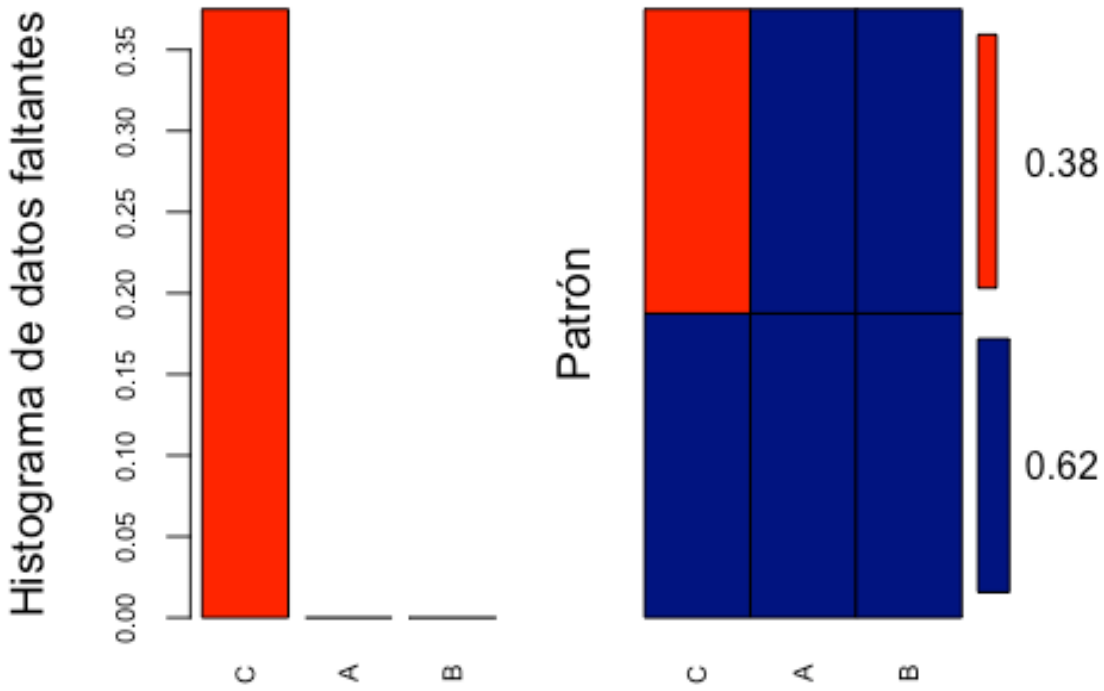
```
## 'data.frame':    8 obs. of  3 variables:
##  $ A: int  26 42 86 9 20 89 NA NA
##  $ B: int  88 66 54 92 83 NA NA NA
##  $ C: int  32 21 NA NA NA 41 35 33
```

```
# Guardo el dataset PATT para generar el fichero PATT.rds
# (a efectos de reproducibilidad posterior)
saveRDS(pattern4, "PATT.rds")

# Apertura del dataset PATT
# (Descomentar la línea siguiente si fuera necesario abrirlo para
reproducibilidad posterior)
# pattern4 <- readRDS("PATT.rds")

# Ilustración 28: Visualización de patrón de datos faltantes del dataset
PATT
aggr_plot <- aggr(pattern4, col=c('navyblue','red'), numbers=TRUE,
sortVars=TRUE, labels=names(pattern4), cex.axis=.7, gap=3,
ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##  Variable Count
##         B 0.375
##         C 0.375
##         A 0.250
```

```r
# Imputación múltiple del dataframe PATT
imp <- mice(pattern4, seed=4, print=FALSE)

# Imputación efectiva del dataset PATT
pattern4_completed = complete(imp)

# Ilustración XX: Visualización de patrón de datos en dataset PATT
después de la imputación efectiva
aggr_plot <- aggr(pattern4_completed, col=c('navyblue','red'),
numbers=TRUE, sortVars=TRUE, labels=names(pattern4_completed),
cex.axis=.7, gap=3, ylab=c("Histograma de datos faltantes","Patrón"))
```




```
##
##  Variables sorted by number of missings:
##  Variable Count
##         C 0.375
##         A 0.000
##         B 0.000
```

```
# Verificación del modelo de imputación empleado en cada variable
imp$meth
```

```
##     A     B     C
## "pmm" "pmm" "pmm"
```
