

# PEC3 TFM UOC

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## PEC 3.

### 1. Fase exploratoria

#### 1.1 Lectura y preparación de los datos

El fichero de datos contiene 145 variables. Muchas de ellas se pueden omitir porque son las respuestas a cada una de las preguntas de tres cuestionarios diferentes y en este estudio se utilizarán sólo las puntuaciones estandarizadas del cuestionario DMSES completo y el de cada uno de su cuatro apartados.

También se descartarán las variables que son la categorización de otras variables del fichero. Si alguna categorización o agrupación de valores fuera necesaria se creará en su debido momento.

Por otra lado se crearán variables nuevas:

- BMI: la variable continua BMI puede estar más relacionada con la diabetes que no las variables peso y altura (estas dos variables se descartarán una vez se haya calculado el BMI).
- sobrepeso: la variable categórica sobrepeso (1:Sí, 0:No) se calculará a partir del BMI (BMI>25: sobrepeso)
- obesidad: la variable categórica obesidad (1:Sí, 0:No) se calculará a partir del BMI (BMI>30: obesidad)
- alerta: la variable categórica alerta (1:Sí, 0:No) se calculará a partir de la variable hba1c (hba1c>7%). Se considera que un valor de hba1c > 7% indica que la diabetes no está siendo bien controlado por el paciente.

```
library(MASS)
library(dplyr)
library(ggplot2)
library(mgcv)
library(gnm)
library(GGally)
library(gmodels)
library(Hmisc)
library(caret)
library(ROCR)
library(gridExtra)
library(corrplot)
library(kableExtra)
library(faraway)
library(ggpubr)
library(klaR)

setwd("C:/Users/ehm24/Documents/master/TFM")

datos.raw <- read.csv("./datos/MontiFinal.csv")

# eliminamos las preguntas de los cuestionarios, categorizaciones de variables y
# otras variables no relevantes para el estudio
datos <- datos.raw[,-c(1,2,15,22,26:84,113:131,137:142,144:145)]

# definimos los factores

# Patient identifier
datos$id.code <- as.factor(datos$id.code)
# Hospital identifier
datos$hospid <- factor(datos$hospid,levels=c(1,2,3,4),
                         labels=c("phupaman","srinakarin","weganonrat","chula"))
# Sex
datos$gender <- factor(datos$gender,levels=c(1,2),
                         labels=c("Hombre","Mujer"))
# Marital status
```

```

datos$mstatus <- factor(datos$mstatus, levels=c(1,2,3,4,5),
                         labels=c("Soltero", "Casado",
                                  "Viudo", "Divorciado", "Separado"))

# Education level
datos$edu <- factor(datos$edu,
                      levels=c(1,2,3,4,5,6),
                      labels=c("Sin estudios", "Primarios", "Secundarios",
                              "Grado", "Master", "Grado Superior"))

# Religion
datos$religion <- factor(datos$religion, levels=c(1,2,3,4),
                           labels=c("Budismo", "Islam", "Cristianismo", "Otra religión"))

# Income
datos$income <- factor(datos$income, levels=c(1,2,3,4,5,6),
                        labels=c("menos de 4,999 bath", "5,000-9,999 bath",
                                "10,000-14,999 bath", "15,000-19,999 bath",
                                "20,000-24,999 bath", "más de 25,000 bath"))

# Family history of T2DM
datos$famhx <- factor(datos$famhx, levels=c(0,1), labels=c("No", "Sí"))

# Comorbid disease
datos$comob <- factor(datos$comob, levels=c(0,1), labels=c("No", "Sí"))

# Comorbidity lipidemia
datos$comlip <- factor(datos$comlip, levels=c(0,1), labels=c("No", "Sí"))

# Comorbidity hypertension
datos$comht <- factor(datos$comht, levels=c(0,1), labels=c("No", "Sí"))

# Comorbidity coronary heart disease
datos$comchd <- factor(datos$comchd, levels=c(0,1), labels=c("No", "Sí"))

# Comorbidity kidney disease
datos$comkid <- factor(datos$comkid, levels=c(0,1), labels=c("No", "Sí"))

# Other comorbidity
datos$comoth <- factor(datos$comoth, levels=c(0,1), labels=c("No", "Sí"))

# Type of Treatment of DM
datos$dmrx <- factor(datos$dmrx,
                      levels=c(1,2,3,4),
                      labels=c("Sin medicación", "Hipoglicémico oral",
                              "Insulina", "Ambos"))

# Smoking
datos$smk <- factor(datos$smk, levels=c(1,2,3),
                      labels=c("Sí", "Exfumador", "No"))

# Alcohol
datos$alcohol <- factor(datos$alcohol, levels=c(1,2,3),
                         labels=c("Sí", "Exbebedor", "No"))

# Diabetes Complication
datos$compli <- factor(datos$compli, levels=c(0,1), labels=c("No", "Sí"))

# Cerebrovascular Accident
datos$cva <- factor(datos$cva, levels=c(0,1), labels=c("No", "Sí"))

# Cerebral Infraction
datos$cereinfrac <- factor(datos$cereinfrac, levels=c(0,1), labels=c("No", "Sí"))

# Ischemic Stroke
datos$ishemic <- factor(datos$ishemic, levels=c(0,1), labels=c("No", "Sí"))

# Stroke, Not specify
datos$stroke <- factor(datos$stroke, levels=c(0,1), labels=c("No", "Sí"))

# Cerebral Hemorrhage
datos$cerebhem <- factor(datos$cerebhem, levels=c(0,1), labels=c("No", "Sí"))

```

```

# Transient Ischemic Attack
datos$itia <- factor(datos$itia,levels=c(0,1),labels=c("No", "Sí"))
# Angina pectoris
datos$angia <- factor(datos$angia,levels=c(0,1),labels=c("No", "Sí"))
# Congestive Heart Failure
datos$chf <- factor(datos$chf,levels=c(0,1),labels=c("No", "Sí"))
# Myocardial Infraction
datos$mi <- factor(datos$mi,levels=c(0,1),labels=c("No", "Sí"))
# Coronary Revascularization
datos$cororevas <- factor(datos$cororevas,levels=c(0,1),labels=c("No", "Sí"))
# Peripheral Arterial Disease
datos$pad <- factor(datos$pad,levels=c(0,1),labels=c("No", "Sí"))
# Neuropathy
datos$neuropath <- factor(datos$neuropath,levels=c(0,1),labels=c("No", "Sí"))
# Renal Insufficiency
datos$renal <- factor(datos$renal,levels=c(0,1),labels=c("No", "Sí"))
# Diabetes Nephropathy
datos$dn <- factor(datos$dn,levels=c(0,1),labels=c("No", "Sí"))
# Diabetes Retinopathy
datos$dr <- factor(datos$dr,levels=c(0,1),labels=c("No", "Sí"))
# Other complication
datos$othcomp <- factor(datos$othcomp,levels=c(0,1),labels=c("No", "Sí"))

# creación de variables derivadas

# alerta: 1-Sí si hba1c > 7% (diabetes no controlada)
datos$alerta <- factor(ifelse(datos$hba1c > 7,1,0),
                       levels=c(0,1),
                       labels=c("No", "Sí"))

# BMI
datos$bmi <- datos$weight/(datos$height/100)**2
# sobrepeso, BMI >25
datos$sobrepeso <- factor(ifelse(datos$bmi > 25,1,0),
                           levels=c(0,1),labels=c("No", "Sí"))
# obesidad, BMI > 30
datos$obesidad <- factor(ifelse(datos$bmi > 30,1,0),
                           levels=c(0,1),labels=c("No", "Sí"))

# transformación a variable tipo date de todas las variables fecha
# estas variables son útiles para poder determinar que datos tienen
# información actualizada
datos$fecha.hba1c <- as.Date(datos$hba1cdate,"%d/%m/%y")
datos$fecha.ldl <- as.Date(datos$ldldate,"%d/%m/%y")
datos$fecha.hdl <- as.Date(datos$hdldate,"%d/%m/%y")
datos$fecha.trig <- as.Date(datos$trigdate,"%d/%m/%y")
datos$fecha.bp <- as.Date(datos$bpdate,"%d/%m/%y")

# eliminación de variables no necesarias
drop.cols <- c("weight","height","hba1cdate","ldldate","hdldate","trigdate","bpdate")
datos <- datos %>% select(-all_of(drop.cols))

```

### 1.1.1 Lectura y creación de variables derivadas

**1.1.2 Datos faltantes** Se tiene sólo datos faltantes en dos variables tipo fecha (fecha.ldl y fecha.bp) y en sólo dos pacientes.

```
# datos faltantes
datos[!complete.cases(datos),]
```

```
##      id.code      hospid gender mstatus age          edu religion
## 225      225 wegaronrat Hombre `Casado  56 Secundarios    Islam
## 352      352 wegaronrat Hombre   Viudo  70 Primarios Budismo
##           income dmdura famhx comob comclip comht comchd comkid comoth
## 225 menos de 4,999 bath     4   No    Sí    Sí    Sí   No   No   No
## 352 menos de 4,999 bath     5   No    Sí    Sí    Sí   No   No   No
##           dmrx      smk alcohol hba1c ldl hdl trig sbp dbp compli
## 225 Hipoglicémico oral     No      No  6.0  99  68 111 137  95   No
## 352        Ambos Exfumador Exbebedor  6.7  76  46  72 133  22   Sí
##           cva cereinfrac ishemic stroke cerebhem tia angia chf mi cororevas pad
## 225   No       No    No    No    No    No    No    No    No    No
## 352   No       No    Sí    No    No    No    No    No    No    No
##           neuropath renal dn dr othcomp DMSES.Diet DMSES.Monitor DMSES.Physical
## 225     No    No No No    No  0.3336945  0.1225384 -0.6551139
## 352     No    No No No    No  0.1123347  0.3966739  0.3133142
##           DMSES.Regimen DMSES.Total    DK.10 alerta      bmi sobre peso obesidad
## 225 -0.5854147 -0.7842956 4.685086    No 33.62209      Sí      Sí
## 352  0.1183689  0.9406917 4.550101    No 22.65625      No      No
##           fecha.hba1c fecha.ldl fecha.hdl fecha.trig   fecha.bp
## 225 2016-02-15 <NA> 2015-06-18 2015-06-18 2016-05-16
## 352 2016-01-15 2016-05-13 2016-05-23 2016-05-23 <NA>
```

**1.1.3 Outliers** Las variables continuas son:

```
age
dmdura
hba1c
ldl
hdl
trig
sbp
dbp
DMSES.Diet
DMSES.Monitor
DMSES.Physical
DMSES.Regimen
DMSES.Total
DK.10
```

```
flag_outliers <- function(x, na.rm = TRUE, ...) {
  qnt <- quantile(x, probs=c(.25, .75), na.rm = na.rm, ...)
  H <- 1.5 * IQR(x)
  y <- x
  y[x < (qnt[1] - H)] <- NA
  y[x > (qnt[2] + H)] <- NA
  z <- as.factor(as.integer(is.na(y)))
  return(z)
}
```

```

datos$age_out <- flag_outliers(datos$age)
datos$dmdura_out <- flag_outliers(datos$dmdura)
datos$hba1c_out <- flag_outliers(datos$hba1c)
datos$ldl_out <- flag_outliers(datos$ldl)
datos$hdl_out <- flag_outliers(datos$hdl)
datos$trig_out <- flag_outliers(datos$trig)
datos$sbp_out <- flag_outliers(datos$sbp)
datos$dbp_out <- flag_outliers(datos$dbp)
datos$DMSES.Diet_out <- flag_outliers(datos$DMSES.Diet)
datos$DMSES.Monitor_out <- flag_outliers(datos$DMSES.Monitor)
datos$DMSES.Physical_out <- flag_outliers(datos$DMSES.Physical)
datos$DMSES.Regimen_out <- flag_outliers(datos$DMSES.Regimen)
datos$DMSES.Total_out <- flag_outliers(datos$DMSES.Total)
datos$DK.10_out <- flag_outliers(datos$DK.10)
datos$bmi_out <- flag_outliers(datos$bmi)

summary(datos)

```

```

##      id.code          hospid       gender      mstatus        age
## 1      : 1    phupaman : 60   Hombre:208  Soltero : 57  Min.  :26.00
## 2      : 1    srinakarin: 77   Mujer :492   `Casado :462  1st Qu.:59.00
## 3      : 1 wegaronrat:241           :       Viudo   :165  Median :65.00
## 4      : 1      chula     :322           :       Divorciado:13  Mean   :65.16
## 5      : 1           :       :       Separado : 3   3rd Qu.:73.00
## 6      : 1           :       :       Max.   :95.00
## (Other):694
##              edu            religion          income
## Sin estudios : 47    Budismo      :543    menos de 4,999 bath:318
## Primarios    :381    Islam        :152    5,000-9,999 bath  : 95
## Secundarios   :146    Cristianismo : 5    10,000-14,999 bath : 86
## Grado         : 99    Otra religión: 0    15,000-19,999 bath : 48
## Master        : 25           :       20,000-24,999 bath : 48
## Grado Superior:  2           :       más de 25,000 bath :105
##
##      dmdura      famhx      comob      comlip      comht      comchd      comkid      comoth
## Min.    : 4.00  No:370  No: 42  No: 95  No: 97  No:662  No:512  No:699
## 1st Qu.: 7.00  Sí:330  Sí:658  Sí:605  Sí:603  Sí: 38  Sí:188  Sí:  1
## Median :10.00
## Mean   :13.53
## 3rd Qu.:20.00
## Max.   :45.00
##
##              dmrx        smk        alcohol        hba1c
## Sin medicación : 12  Sí       : 23  Sí       : 42  Min.   : 2.000
## Hipoglicémico oral:409  Exfumador: 88  Exbebedor: 89  1st Qu.: 6.400
## Insulina       : 94  No       :589   No       :569  Median : 7.100
## Ambos          :185           :       Mean   : 7.579
##                           :       3rd Qu.: 8.300
##                           :       Max.   :15.000
##
##      ldl        hdl        trig        sbp
## Min.    : 8.7  Min.    :17.00  Min.    :29.30  Min.    : 93.0
## 1st Qu.: 81.0 1st Qu.:41.88  1st Qu.:95.75  1st Qu.:123.0

```

```

## Median : 97.0 Median : 50.00 Median :127.00 Median :133.0
## Mean :100.8 Mean : 50.75 Mean :149.02 Mean :134.8
## 3rd Qu.:116.0 3rd Qu.: 58.00 3rd Qu.:175.00 3rd Qu.:145.0
## Max. :221.0 Max. :116.00 Max. :999.00 Max. :217.0
##
##      dbp      compli     cva     cereinfrac ishemic   stroke cerebhem
## Min. : 22.00 No:429  No:699  No:700  No:688  No:698  No:700
## 1st Qu.: 65.00 Sí:271  Sí: 1   Sí: 0   Sí: 12  Sí:  2   Sí:  0
## Median : 73.00
## Mean : 73.02
## 3rd Qu.: 80.00
## Max. :112.00
##
##      tia      angia     chf      mi     cororevas pad    neuropath renal
## No:699  No:700  No:692  No:675  No:699  No:696  No:695  No:582
## Sí: 1   Sí: 0   Sí: 8   Sí: 25  Sí:  1   Sí:  4   Sí:  5   Sí:118
##
##      dn      dr     othcomp DMSES.Diet      DMSES.Monitor
## No:619  No:561  No:699  Min. :-1.45946  Min. :-0.84225
## Sí: 81  Sí:139  Sí: 1   1st Qu.:-0.53693  1st Qu.:-0.23065
##                               Median :-0.06537  Median :-0.03718
##                               Mean   : 0.00000  Mean   : 0.00000
##                               3rd Qu.: 0.52029  3rd Qu.: 0.24502
##                               Max.   : 1.03434  Max.   : 0.55056
##
##      DMSES.Physical      DMSES.Regimen      DMSES.Total      DK.10
## Min. :-1.28709  Min. :-2.86027  Min. :-5.6289  Min. : 0.000
## 1st Qu.:-0.28906 1st Qu.: 0.07856  1st Qu.:-1.0268 1st Qu.: 4.224
## Median : 0.01757  Median : 0.09450  Median :-0.0258  Median : 5.486
## Mean   : 0.00000  Mean   : 0.00000  Mean   : 0.0000  Mean   : 5.535
## 3rd Qu.: 0.29446  3rd Qu.: 0.10978  3rd Qu.: 1.0416  3rd Qu.: 6.919
## Max.   : 0.79336  Max.   : 0.51344  Max.   : 2.5059  Max.   :10.000
##
##      alerta      bmi      sobrepeso obesidad fecha.hba1c
## No:333  Min. :14.31  No:301   No:518   Min. :2006-02-01
## Sí:367  1st Qu.:22.91  Sí:399   Sí:182   1st Qu.:2016-03-01
##                               Median :25.96  Median :2016-05-04
##                               Mean   :27.08  Mean   :2016-03-07
##                               3rd Qu.:30.14  3rd Qu.:2016-06-07
##                               Max.   :76.03  Max.   :2016-07-04
##
##      fecha.ldl      fecha.hdl      fecha.trig
## Min. :2012-11-08  Min. :2006-04-23  Min. :2012-11-08
## 1st Qu.:2016-02-04 1st Qu.:2016-01-13  1st Qu.:2016-02-02
## Median :2016-04-21  Median :2016-03-29  Median :2016-04-21
## Mean   :2016-02-19  Mean   :2016-01-26  Mean   :2016-02-27
## 3rd Qu.:2016-05-31  3rd Qu.:2016-05-31  3rd Qu.:2016-05-31
## Max.   :2016-09-03  Max.   :2016-12-09  Max.   :2016-12-21
## NA's   :1
##      fecha.bp      age_out dmdura_out hba1c_out ldl_out hdl_out trig_out

```

```

## Min.   :2006-04-27   0:692   0:692      0:666      0:674   0:683   0:665
## 1st Qu.:2016-04-22   1:  8    1:  8      1: 34      1: 26    1: 17    1: 35
## Median :2016-05-19
## Mean    :2016-05-14
## 3rd Qu.:2016-06-16
## Max.    :2035-03-27
## NA's     :1
## sbp_out dbp_out DMSES.Diet_out DMSES.Monitor_out DMSES.Physical_out
## 0:684   0:687   0:700      0:700      0:696
## 1: 16   1: 13          1:  4
##
##
##
##
##
## DMSES.Regimen_out DMSES.Total_out DK.10_out bmi_out
## 0:578       0:698       0:694       0:686
## 1:122       1:  2       1:  6       1: 14
##
##
##
##
##
## flags para outliers
vars_out <- c("age_out", "dmdura_out", "hba1c_out", "ldl_out", "hdl_out", "trig_out", "sbp_out", "dbp_out",
             "DMSES.Diet_out", "DMSES.Monitor_out", "DMSES.Physical_out", "DMSES.Regimen_out",
             "DMSES.Total_out", "DK.10_out")

# la variable datos$out valdrá uno si alguna de las variables continuas es outlier, 0 en caso contrario
datos$out <- apply(datos[, vars_out], 1, max)

# variables continuas
vars_cont <- c("age", "dmdura", "hba1c", "ldl", "hdl", "trig", "sbp", "dbp",
               "DMSES.Diet", "DMSES.Monitor", "DMSES.Physical", "DMSES.Regimen",
               "DMSES.Total", "DK.10")

# variables categóricas
vars_cat <- c("id.code", "hospid", "gender", "mstatus", "edu", "religion", "income",
              "famhx", "comob", "comlip", "comht", "comchd", "comkid", "comoth", "dmrx",
              "smk", "alcohol", "compli", "cva", "cereinfrac", "ishemic", "stroke", "cerebhem",
              "tia", "angia", "chf", "mi", "cororevas", "pad", "neuropath", "renal", "dn",
              "dr", "othcomp", "alerta", "sobrepeso", "obesidad", vars_out, "out")

# otras variables
vars_otras <- c("fecha.hba1c", "fecha.ldl", "fecha.hdl", "fecha.trig", "fecha.bp")

# todas las variables
vars <- c(vars_cat, vars_cont, vars_otras)

# pacientes con alguna variable continua outlier
pat_out <- datos %>% filter(out==1)

```

```

dim(pat_out)

## [1] 234 73

dim(datos)

## [1] 700 73

attach(datos)

```

La estructura del fichero inicial, ya con todas las variables derivadas creadas es la que sigue:

```

# descripción del fichero con el que se trabajará
str(datos)

## 'data.frame':    700 obs. of  73 variables:
##   $ id.code      : Factor w/ 700 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
##   $ hospid       : Factor w/ 4 levels "phupaman","srinakarin",...: 1 1 1 1 1 1 1 1 1 1 ...
##   $ gender       : Factor w/ 2 levels "Hombre","Mujer": 1 2 1 2 1 2 1 2 2 2 ...
##   $ mstatus      : Factor w/ 5 levels "Soltero","Casado",...: 2 2 2 3 3 2 2 2 2 2 ...
##   $ age          : int  51 55 47 54 71 55 59 64 58 69 ...
##   $ edu          : Factor w/ 6 levels "Sin estudios",...: 4 2 2 2 2 2 ...
##   $ religion     : Factor w/ 4 levels "Budismo","Islam",...: 1 1 1 1 1 1 1 1 1 1 ...
##   $ income        : Factor w/ 6 levels "menos de 4,999 bath",...: 5 2 1 1 1 1 6 1 1 1 ...
##   $ dmdura       : int  4 4 5 20 10 4 4 22 4 14 ...
##   $ famhx        : Factor w/ 2 levels "No","Sí": 2 2 1 1 1 1 1 2 1 ...
##   $ comob         : Factor w/ 2 levels "No","Sí": 2 2 2 2 2 2 2 2 1 2 ...
##   $ comlip        : Factor w/ 2 levels "No","Sí": 2 2 2 2 1 2 2 2 1 2 ...
##   $ comht         : Factor w/ 2 levels "No","Sí": 2 1 2 2 2 1 2 2 1 2 ...
##   $ comchd        : Factor w/ 2 levels "No","Sí": 1 1 1 1 2 1 1 1 1 1 ...
##   $ comkid        : Factor w/ 2 levels "No","Sí": 1 1 2 1 2 1 1 1 1 1 ...
##   $ comoth        : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ dmrx          : Factor w/ 4 levels "Sin medicación",...: 2 2 2 4 3 2 2 2 2 4 ...
##   $ smk           : Factor w/ 3 levels "Sí","Exfumador",...: 2 3 2 3 2 3 3 3 3 3 ...
##   $ alcohol        : Factor w/ 3 levels "Sí","Exbebedor",...: 2 3 2 3 1 3 2 3 3 3 ...
##   $ hba1c          : num  9.7 7.1 8 7.2 8.8 8 9.8 6.3 6.7 7.7 ...
##   $ ldl           : num  123.7 89.8 119 202.1 58.6 ...
##   $ hdl           : num  45.2 49.5 50.7 47 35.7 35.3 42 44.9 46 35.6 ...
##   $ trig          : num  248.9 276.9 165.6 84.7 149.5 ...
##   $ sbp           : int  130 120 168 121 118 119 119 150 124 169 ...
##   $ dbp           : int  80 70 94 56 65 63 83 76 76 93 ...
##   $ compli        : Factor w/ 2 levels "No","Sí": 1 1 2 1 2 1 1 1 1 1 ...
##   $ cva            : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ cereinfrac    : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ ischemic       : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ stroke         : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ cerebhem       : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ tia            : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ angia          : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ chf             : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
##   $ mi              : Factor w/ 2 levels "No","Sí": 1 1 1 1 2 1 1 1 1 1 ...

```

```

## $ cororevas      : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
## $ pad            : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
## $ neuropath      : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
## $ renal           : Factor w/ 2 levels "No","Sí": 1 1 2 1 2 1 1 1 1 1 ...
## $ dn              : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
## $ dr              : Factor w/ 2 levels "No","Sí": 1 1 2 1 1 1 1 1 1 1 ...
## $ othcomp          : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
## $ DMSES.Diet       : num -0.132233 -0.000414 1.031174 -1.102578 -1.064826 ...
## $ DMSES.Monitor    : num -0.133 0.158 0.527 -0.168 -0.37 ...
## $ DMSES.Physical   : num -0.1775 0.09218 0.79015 -0.00571 0.02158 ...
## $ DMSES.Regimen     : num 0.0909 0.106 -0.0232 0.0916 0.0824 ...
## $ DMSES.Total        : num -0.352 0.355 2.325 -1.184 -1.331 ...
## $ DK.10             : num 5.77 6.66 4.27 5.19 5.65 ...
## $ alerta            : Factor w/ 2 levels "No","Sí": 2 2 2 2 2 2 2 1 1 2 ...
## $ bmi               : num 23 25.6 22.6 25.7 21.1 ...
## $ sobrepeso          : Factor w/ 2 levels "No","Sí": 1 2 1 2 1 1 2 1 2 1 ...
## $ obesidad           : Factor w/ 2 levels "No","Sí": 1 1 1 1 1 1 1 1 1 1 ...
## $ fecha.hba1c        : Date, format: "2014-07-10" "2014-07-26" ...
## $ fecha.ldl            : Date, format: "2015-11-06" "2015-02-16" ...
## $ fecha.hdl            : Date, format: "2015-11-06" "2015-02-16" ...
## $ fecha.trig           : Date, format: "2015-11-06" "2015-02-16" ...
## $ fecha.bp              : Date, format: "2016-02-19" "2016-02-24" ...
## $ age_out              : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ dmdura_out           : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ hba1c_out             : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ ldl_out                : Factor w/ 2 levels "0","1": 1 1 1 2 1 1 1 1 1 1 ...
## $ hdl_out                : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ trig_out               : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ sbp_out                : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ dbp_out                : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ DMSES.Diet_out         : Factor w/ 1 level "0": 1 1 1 1 1 1 1 1 1 1 ...
## $ DMSES.Monitor_out      : Factor w/ 1 level "0": 1 1 1 1 1 1 1 1 1 1 ...
## $ DMSES.Physical_out     : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ DMSES.Regimen_out       : Factor w/ 2 levels "0","1": 1 1 2 1 1 1 2 1 1 1 ...
## $ DMSES.Total_out         : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ DK.10_out               : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ bmi_out                 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ out                     : chr "0" "0" "1" "1" ...

```

## 1.2 Exploración unidimensional

Una primera vista a las variables de nuestro fichero:

```
summary(datos[,-c(1)])
```

```

##      hospid      gender      mstatus      age
## phupaman : 60  Hombre:208  Soltero : 57  Min.   :26.00
## srinakarin: 77 Mujer :492   'Casado' :462  1st Qu.:59.00
## wegaronrat:241                      Viudo   :165  Median :65.00
## chula     :322                      Divorciado:13  Mean   :65.16
##                               Separado : 3   3rd Qu.:73.00
##                               Max.   :95.00
##
```

```

##          edu             religion           income
## Sin estudios : 47   Budismo      :543   menos de 4,999 bath:318
## Primarios    :381   Islam        :152   5,000-9,999 bath  : 95
## Secundarios   :146   Cristianismo : 5   10,000-14,999 bath : 86
## Grado         : 99   Otra religión: 0   15,000-19,999 bath : 48
## Master        : 25                           20,000-24,999 bath : 48
## Grado Superior:  2                           más de 25,000 bath :105
##
##          dmdura      famhx     comob     comlip     comht     comchd     comkid     comoth
## Min.    : 4.00  No:370  No: 42  No: 95  No: 97  No:662  No:512  No:699
## 1st Qu.: 7.00  Sí:330  Sí:658  Sí:605  Sí:603  Sí: 38  Sí:188  Sí:  1
## Median  :10.00
## Mean    :13.53
## 3rd Qu.:20.00
## Max.   :45.00
##
##          dmrx       smk       alcohol      hba1c
## Sin medicación : 12  Sí      : 23  Sí      : 42  Min.   : 2.000
## Hipoglicémico oral:409  Exfumador: 88  Exbebedor: 89  1st Qu.: 6.400
## Insulina       : 94  No      :589  No      :569  Median  : 7.100
## Ambos          :185
##
##          ldl       hdl       trig       sbp
## Min.    : 8.7  Min.    :17.00  Min.    :29.30  Min.   : 93.0
## 1st Qu.: 81.0 1st Qu.: 41.88 1st Qu.: 95.75 1st Qu.:123.0
## Median  : 97.0 Median  : 50.00 Median  :127.00 Median  :133.0
## Mean    :100.8 Mean    : 50.75 Mean    :149.02 Mean   :134.8
## 3rd Qu.:116.0 3rd Qu.: 58.00 3rd Qu.:175.00 3rd Qu.:145.0
## Max.   :221.0  Max.   :116.00 Max.   :999.00 Max.   :217.0
##
##          dbp      compli     cva      cereinfrac  ischemic   stroke   cerebhem
## Min.    :22.00  No:429  No:699  No:700  No:688  No:698  No:700
## 1st Qu.: 65.00  Sí:271  Sí:  1  Sí:  0  Sí: 12  Sí:  2  Sí:  0
## Median  : 73.00
## Mean    : 73.02
## 3rd Qu.: 80.00
## Max.   :112.00
##
##          tia      angia     chf      mi      cororevas  pad      neuropath  renal
## No:699  No:700  No:692  No:675  No:699  No:696  No:695  No:582
## Sí:  1  Sí:  0  Sí:  8  Sí: 25  Sí:  1  Sí:  4  Sí:  5  Sí:118
##
##          dn       dr      othcomp   DMSES.Diet      DMSES.Monitor
## No:619  No:561  No:699  Min.   :-1.45946  Min.   :-0.84225
## Sí: 81  Sí:139  Sí:  1  1st Qu.:-0.53693  1st Qu.:-0.23065
##                               Median :-0.06537  Median :-0.03718
##                               Mean   : 0.00000  Mean   : 0.00000
##                               3rd Qu.: 0.52029  3rd Qu.: 0.24502

```

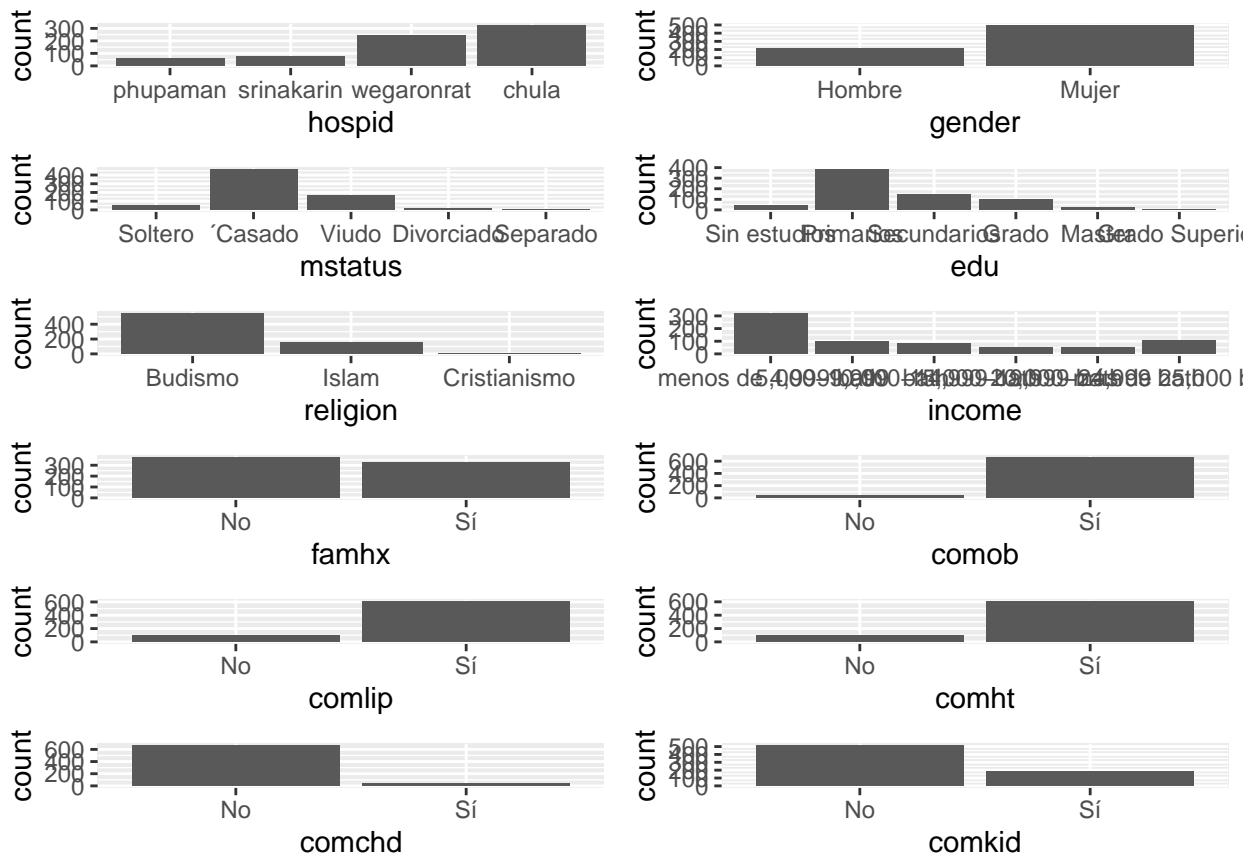
```

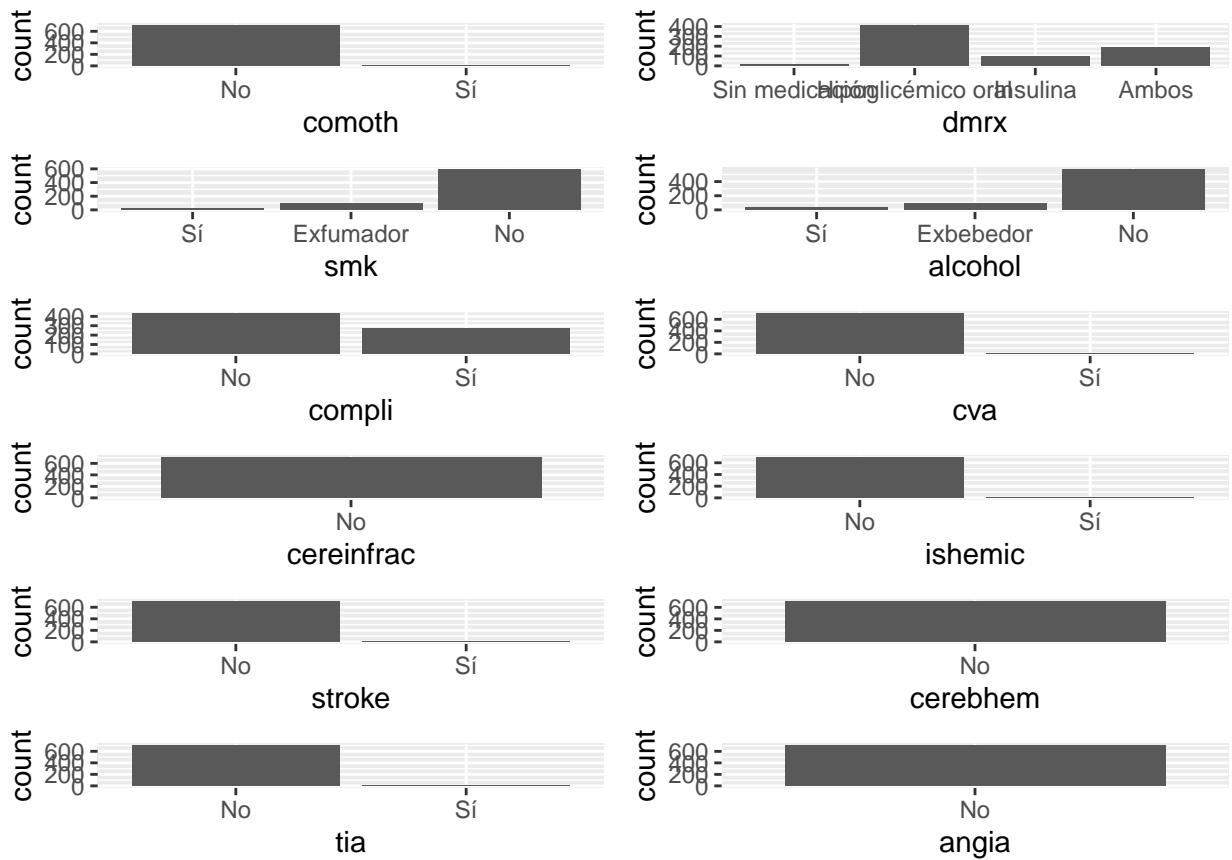
##                               Max.    : 1.03434   Max.    : 0.55056
##
## DMSES.Physical      DMSES.Regimen      DMSES.Total      DK.10
## Min.    :-1.28709   Min.    :-2.86027   Min.    :-5.62899  Min.    : 0.000
## 1st Qu.:-0.28906   1st Qu.: 0.07856   1st Qu.:-1.02681 1st Qu.: 4.224
## Median  : 0.01757   Median  : 0.09450   Median :-0.02581  Median : 5.486
## Mean    : 0.00000   Mean    : 0.00000   Mean    : 0.00000  Mean    : 5.535
## 3rd Qu.: 0.29446   3rd Qu.: 0.10978   3rd Qu.: 1.04161  3rd Qu.: 6.919
## Max.    : 0.79336   Max.    : 0.51344   Max.    : 2.50591  Max.    :10.000
##
## alerta      bmi      sobrepeso obesidad fecha.hba1c
## No:333     Min.    :14.31    No:301     No:518     Min.    :2006-02-01
## Sí:367     1st Qu.:22.91    Sí:399     Sí:182     1st Qu.:2016-03-01
##                           Median  :25.96    Median  :2016-05-04
##                           Mean    :27.08    Mean    :2016-03-07
##                           3rd Qu.:30.14    3rd Qu.:2016-06-07
##                           Max.    :76.03    Max.    :2016-07-04
##
## fecha.ldl      fecha.hdl      fecha.trig
## Min.    :2012-11-08  Min.    :2006-04-23  Min.    :2012-11-08
## 1st Qu.:2016-02-04  1st Qu.:2016-01-13  1st Qu.:2016-02-02
## Median  :2016-04-21  Median  :2016-03-29  Median  :2016-04-21
## Mean    :2016-02-19  Mean    :2016-01-26  Mean    :2016-02-27
## 3rd Qu.:2016-05-31  3rd Qu.:2016-05-31  3rd Qu.:2016-05-31
## Max.    :2016-09-03  Max.    :2016-12-09  Max.    :2016-12-21
## NA's    :1
##
## fecha.bp      age_out dmdura_out hba1c_out ldl_out hdl_out trig_out
## Min.    :2006-04-27 0:692   0:692     0:666    0:674   0:683   0:665
## 1st Qu.:2016-04-22 1:  8    1:  8     1: 34    1: 26    1: 17    1: 35
## Median  :2016-05-19
## Mean    :2016-05-14
## 3rd Qu.:2016-06-16
## Max.    :2035-03-27
## NA's    :1
##
## sbp_out dbp_out DMSES.Diet_out DMSES.Monitor_out DMSES.Physical_out
## 0:684   0:687   0:700        0:700        0:696
## 1: 16   1: 13           1: 4
##
## DMSES.Regimen_out DMSES.Total_out DK.10_out bmi_out      out
## 0:578       0:698       0:694       0:686   Length:700
## 1:122       1:  2       1:  6       1: 14   Class  :character
##                           Mode   :character
##
## DMSES.Physical_out DMSES.Regimen_out DMSES.Total_out DK.10_out bmi_out      out
## 0:698       0:694       0:694       0:686   Length:700
## 1:  2       1:  6       1: 14   Class  :character
##                           Mode   :character

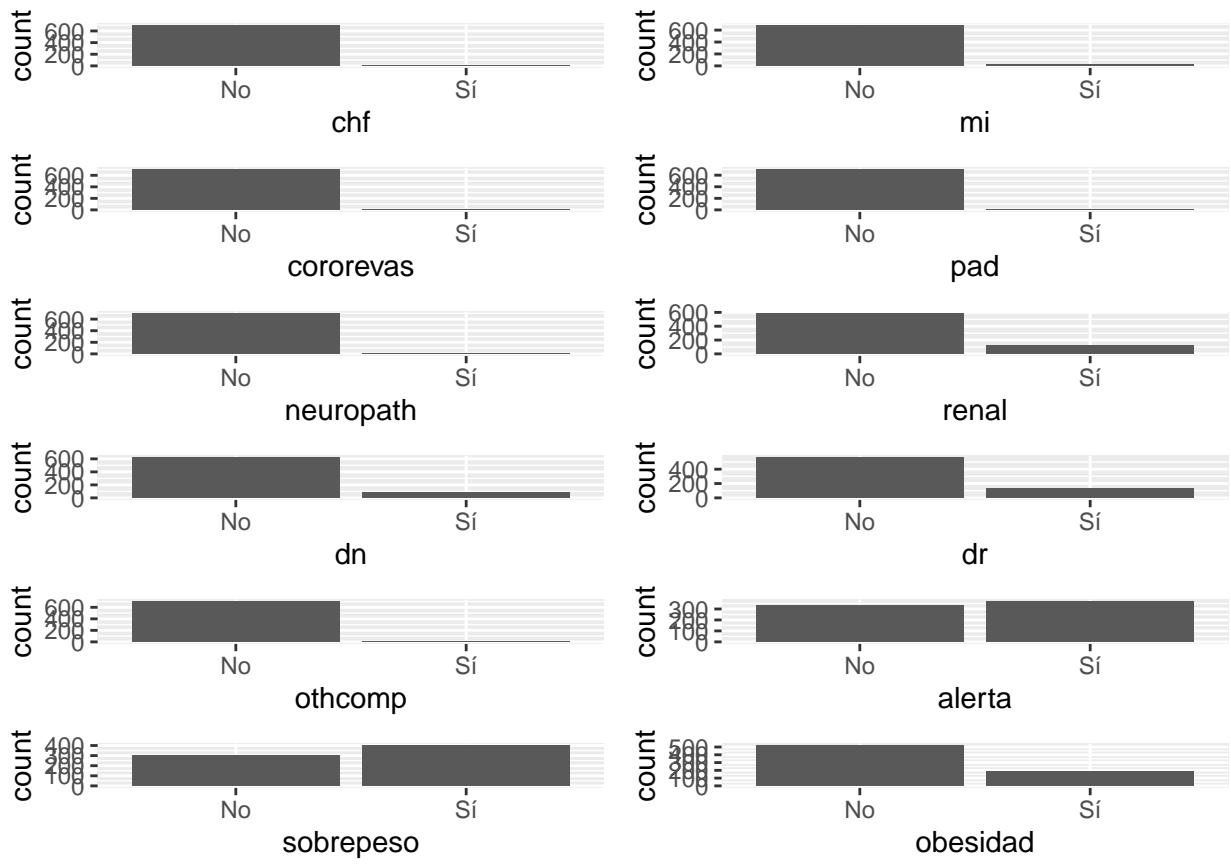
```

Los únicos valores faltantes se dan en las variables fecha.ldl y fecha.bp, un único caso para cada variable. De momento se decide no eliminar los registros.

Analizamos con un poco más de detalle las variables categóricas







Analizamos con un poco más de detalle las variables continuas.

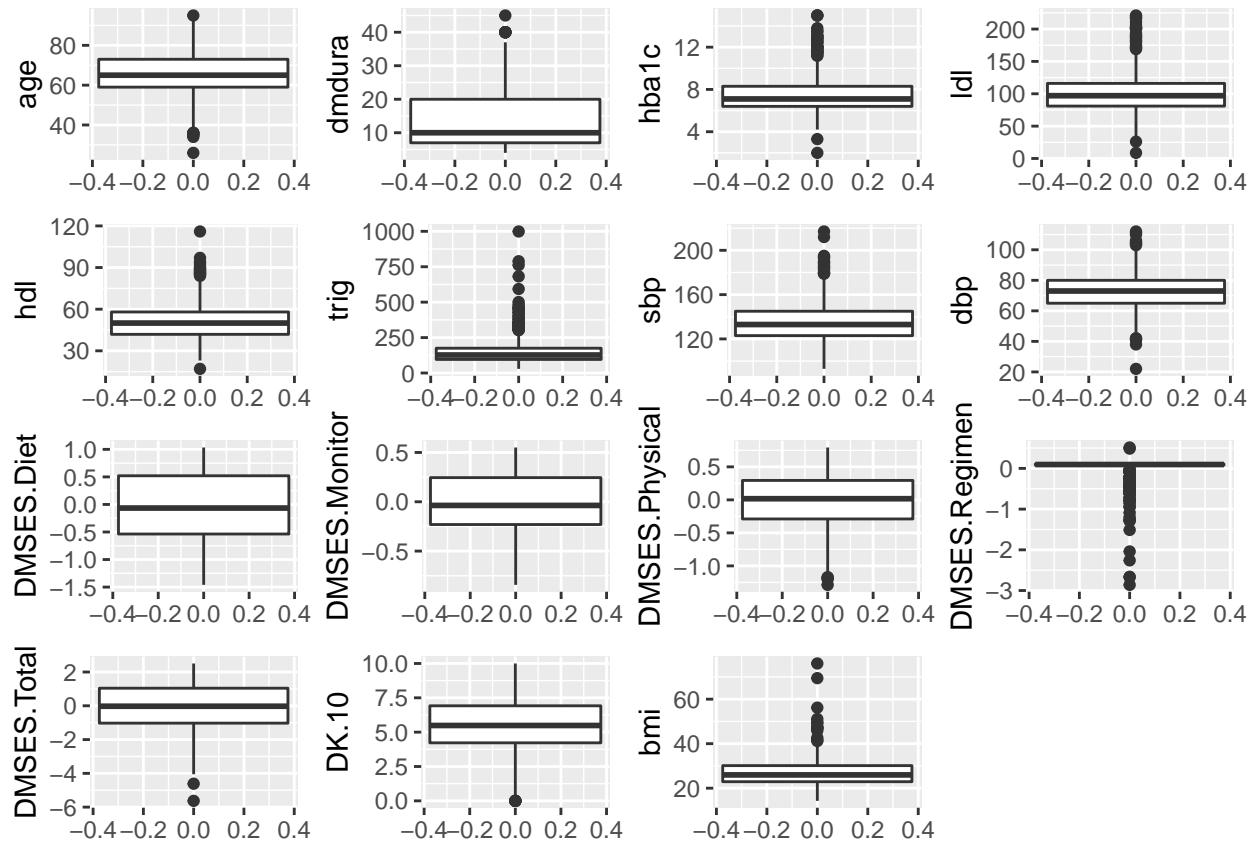
- Boxplot (con outliers)

```

bx_age          <- ggplot(datos,aes(y=age)) + geom_boxplot()
bx_dmdura       <- ggplot(datos,aes(y=dmdura)) + geom_boxplot()
bx_hba1c        <- ggplot(datos,aes(y=hba1c)) + geom_boxplot()
bx_ldl          <- ggplot(datos,aes(y=ldl)) + geom_boxplot()
bx_hdl          <- ggplot(datos,aes(y=hdl)) + geom_boxplot()
bx_trig         <- ggplot(datos,aes(y=trig)) + geom_boxplot()
bx_sbp          <- ggplot(datos,aes(y=sbp)) + geom_boxplot()
bx_dbp          <- ggplot(datos,aes(y=dbp)) + geom_boxplot()
bx_DMSES.Diet   <- ggplot(datos,aes(y=DMSES.Diet)) + geom_boxplot()
bx_DMSES.Monitor <- ggplot(datos,aes(y=DMSES.Monitor)) + geom_boxplot()
bx_DMSES.Physical <- ggplot(datos,aes(y=DMSES.Physical)) + geom_boxplot()
bx_DMSES.Regimen <- ggplot(datos,aes(y=DMSES.Regimen)) + geom_boxplot()
bx_DMSES.Total   <- ggplot(datos,aes(y=DMSES.Total)) + geom_boxplot()
bx_DK.10         <- ggplot(datos,aes(y=DK.10)) + geom_boxplot()
bx_bmi          <- ggplot(datos,aes(y=bmi)) + geom_boxplot()

grid.arrange(bx_age,bx_dmdura,bx_hba1c,bx_ldl,bx_hdl,bx_trig,bx_sbp,bx_dbp,
             bx_DMSES.Diet, bx_DMSES.Monitor, bx_DMSES.Physical, bx_DMSES.Regimen,
             bx_DMSES.Total, bx_DK.10, bx_bmi,ncol=4)

```



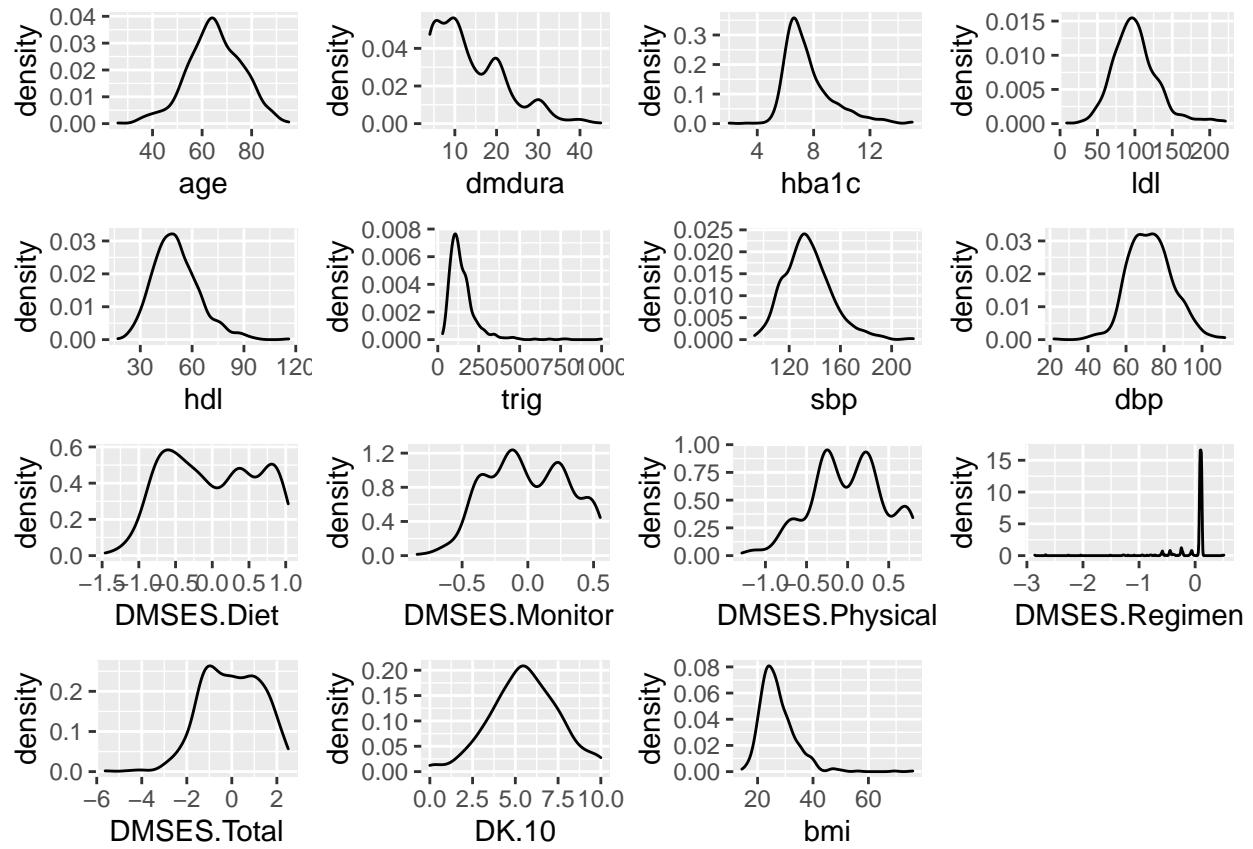
- Densidades

```

den_age           <- ggplot(datos,aes(x=age)) + geom_density()
den_dmdura        <- ggplot(datos,aes(x=dmdura)) + geom_density()
den_hba1c         <- ggplot(datos,aes(x=hba1c)) + geom_density()
den_ldl           <- ggplot(datos,aes(x=ldl)) + geom_density()
den_hdl           <- ggplot(datos,aes(x=hdl)) + geom_density()
den_trig          <- ggplot(datos,aes(x=trig)) + geom_density()
den_sbp           <- ggplot(datos,aes(x=sbp)) + geom_density()
den_dbp           <- ggplot(datos,aes(x=dbp)) + geom_density()
den_DMSES.Diet    <- ggplot(datos,aes(x=DMSES.Diet)) + geom_density()
den_DMSES.Monitor <- ggplot(datos,aes(x=DMSES.Monitor)) + geom_density()
den_DMSES.Physical <- ggplot(datos,aes(x=DMSES.Physical)) + geom_density()
den_DMSES.Regimen <- ggplot(datos,aes(x=DMSES.Regimen)) + geom_density()
den_DMSES.Total   <- ggplot(datos,aes(x=DMSES.Total)) + geom_density()
den_DK.10          <- ggplot(datos,aes(x=DK.10)) + geom_density()
den_bmi            <- ggplot(datos,aes(x=bmi)) + geom_density()

grid.arrange(den_age,den_dmdura,den_hba1c,den_ldl,den_hdl,den_trig,den_sbp,den_dbp,
             den_DMSES.Diet, den_DMSES.Monitor, den_DMSES.Physical, den_DMSES.Regimen,
             den_DMSES.Total, den_DK.10, den_bmi,ncol=4)

```



- Normalidad

Ningun predictor sigue una distribución normal según el test de normalidad de Shapiro y según el QQ plot tenemos normalidad en edad, hdl, sbp, dbp, DMSES.Total y DK.10.

```
shapiro.test(datos$age)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  datos$age
## W = 0.99459, p-value = 0.01385
```

```
shapiro.test(datos$dmdura)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  datos$dmdura
## W = 0.90381, p-value < 2.2e-16
```

```
shapiro.test(datos$hba1c)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$hba1c  
## W = 0.88872, p-value < 2.2e-16
```

```
shapiro.test(datos$ldl)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$ldl  
## W = 0.95629, p-value = 1.435e-13
```

```
shapiro.test(datos$hdl)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$hdl  
## W = 0.97306, p-value = 4.687e-10
```

```
shapiro.test(datos$trig)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$trig  
## W = 0.73709, p-value < 2.2e-16
```

```
shapiro.test(datos$sbp)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$sbp  
## W = 0.97534, p-value = 1.774e-09
```

```
shapiro.test(datos$dbp)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$dbp  
## W = 0.99086, p-value = 0.0002488
```

```
shapiro.test(datos$DMSES.Diet)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$DMSES.Diet  
## W = 0.94977, p-value = 1.089e-14
```

```
shapiro.test(datos$DMSES.Monitor)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$DMSES.Monitor  
## W = 0.97283, p-value = 4.121e-10
```

```
shapiro.test(datos$DMSES.Physical)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$DMSES.Physical  
## W = 0.9796, p-value = 2.638e-08
```

```
shapiro.test(datos$DMSES.Regimen)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$DMSES.Regimen  
## W = 0.41931, p-value < 2.2e-16
```

```
shapiro.test(datos$DMSES.Total)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$DMSES.Total  
## W = 0.98158, p-value = 1.038e-07
```

```
shapiro.test(datos$DK.10)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: datos$DK.10  
## W = 0.99402, p-value = 0.007196
```

```
shapiro.test(datos$bmi)
```

```

##  

## Shapiro-Wilk normality test  

##  

## data: datos$bmi  

## W = 0.88978, p-value < 2.2e-16

#ggqqplot(datos[,vars_cont],combine = TRUE,facet.by=c(5,3))

qq_age          <- ggqqplot(datos$age)
qq_dmdura       <- ggqqplot(datos$dmdura)
qq_hba1c        <- ggqqplot(datos$hba1c)
qq_ldl          <- ggqqplot(datos$ldl)
qq_hdl          <- ggqqplot(datos$hdl)
qq_trig         <- ggqqplot(datos$trig)
qq_sbp          <- ggqqplot(datos$sbp)
qq_dbp          <- ggqqplot(datos$dbp)
qq_DMSES.Diet   <- ggqqplot(datos$DMSES.Diet)
qq_DMSES.Monitor <- ggqqplot(datos$DMSES.Monitor)
qq_DMSES.Physical <- ggqqplot(datos$DMSES.Physical)
qq_DMSES.Regimen <- ggqqplot(datos$DMSES.Regimen)
qq_DMSES.Total   <- ggqqplot(datos$DMSES.Total)
qq_DK.10        <- ggqqplot(datos$DK.10)
qq_bmi          <- ggqqplot(datos$bmi)

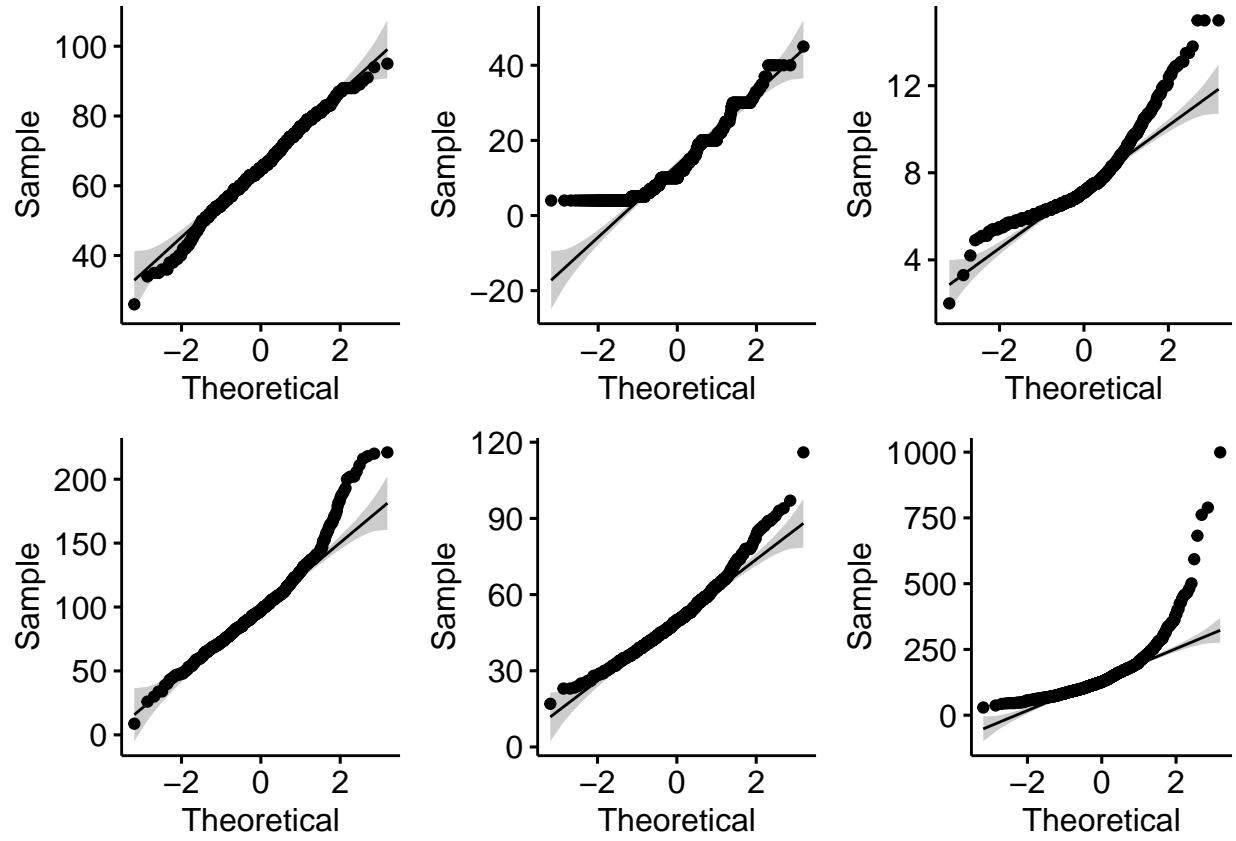
#Arrange all the plots onto one page

#plot_grid(qq_age, qq_dmdura, qq_hba1c, qq_ldl, qq_hdl, qq_trig,
#           qq_sbp, qq_dbp, qq_DMSES.Diet, qq_DMSES.Monitor,
#           qq_DMSES.Physical, qq_DMSES.Regimen, qq_DMSES.Total,
#           qq_DK.10, qq_bmi, nrow=5,ncol=3)

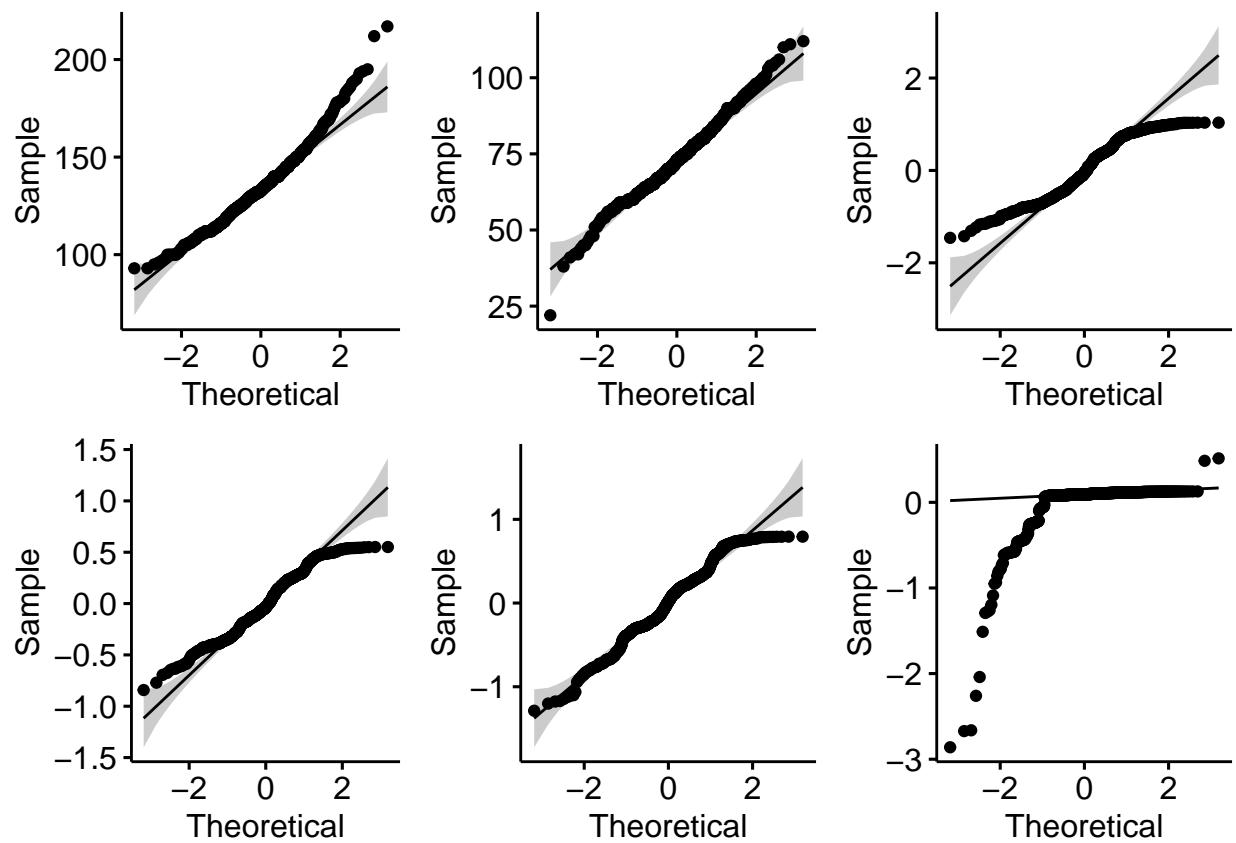
#grid.arrange(qq_age, qq_dmdura, qq_hba1c, qq_ldl, qq_hdl, qq_trig,
#              qq_sbp, qq_dbp, qq_DMSES.Diet, qq_DMSES.Monitor,
#              qq_DMSES.Physical, qq_DMSES.Regimen, qq_DMSES.Total,
#              qq_DK.10, qq_bmi, ncol=2)

grid.arrange(qq_age, qq_dmdura, qq_hba1c, qq_ldl, qq_hdl, qq_trig, ncol=3)

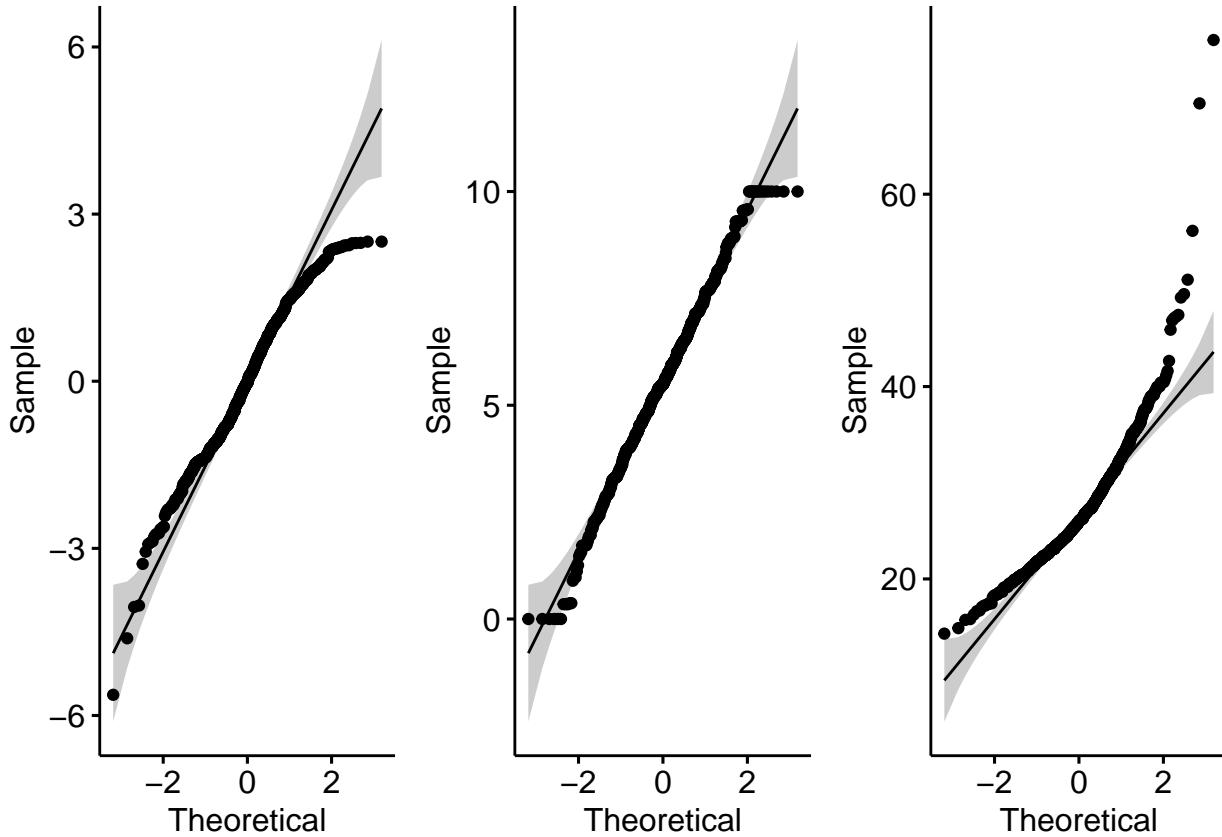
```



```
grid.arrange(qq_sbp, qq_dbp, qq_DMSES.Diet,
qq_DMSES.Monitor,
qq_DMSES.Physical, qq_DMSES.Regimen, ncol = 3)
```



```
grid.arrange(qq_DMSES.Total,qq_DK.10, qq_bmi, ncol=3)
```



### 1.3 Exploración multidimensional

Los niveles de correlación entre las puntuaciones DMSES y el resto de variables continuas son bajos a excepción de la variable hba1c. La mayor correlación entre hba1c y las puntuaciones DMSES se da con el factor dieta. Se detecta que las diferentes puntuaciones del cuestionario DMSES están fuertemente relacionadas, por lo que se puede considerar tomar sólo una para el análisis. La puntuación total y la de la parte de la dieta son las mejoras candidatas debido a que tienen una correlación más alta con hba1c.

```
dim(datos[,vars_cont])
## [1] 700 14

str(datos[,vars_cont])
## 'data.frame':    700 obs. of  14 variables:
## $ age          : int  51 55 47 54 71 55 59 64 58 69 ...
## $ dmdura       : int  4 4 5 20 10 4 4 22 4 14 ...
## $ hba1c        : num  9.7 7.1 8 7.2 8.8 8 9.8 6.3 6.7 7.7 ...
## $ ldl          : num  123.7 89.8 119 202.1 58.6 ...
## $ hdl          : num  45.2 49.5 50.7 47 35.7 35.3 42 44.9 46 35.6 ...
## $ trig         : num  248.9 276.9 165.6 84.7 149.5 ...
## $ sbp          : int  130 120 168 121 118 119 119 150 124 169 ...
## $ dbp          : int  80 70 94 56 65 63 83 76 76 93 ...
## $ DMSES.Diet   : num  -0.132233 -0.000414 1.031174 -1.102578 -1.064826 ...
```

```

## $ DMSES.Monitor : num -0.133 0.158 0.527 -0.168 -0.37 ...
## $ DMSES.Physical: num -0.1775 0.09218 0.79015 -0.00571 0.02158 ...
## $ DMSES.Regimen : num 0.0909 0.106 -0.0232 0.0916 0.0824 ...
## $ DMSES.Total    : num -0.352 0.355 2.325 -1.184 -1.331 ...
## $ DK.10          : num 5.77 6.66 4.27 5.19 5.65 ...

```

```

M <- cor(datos[,c(vars_cont)])
knitr::kable(round(M,2))

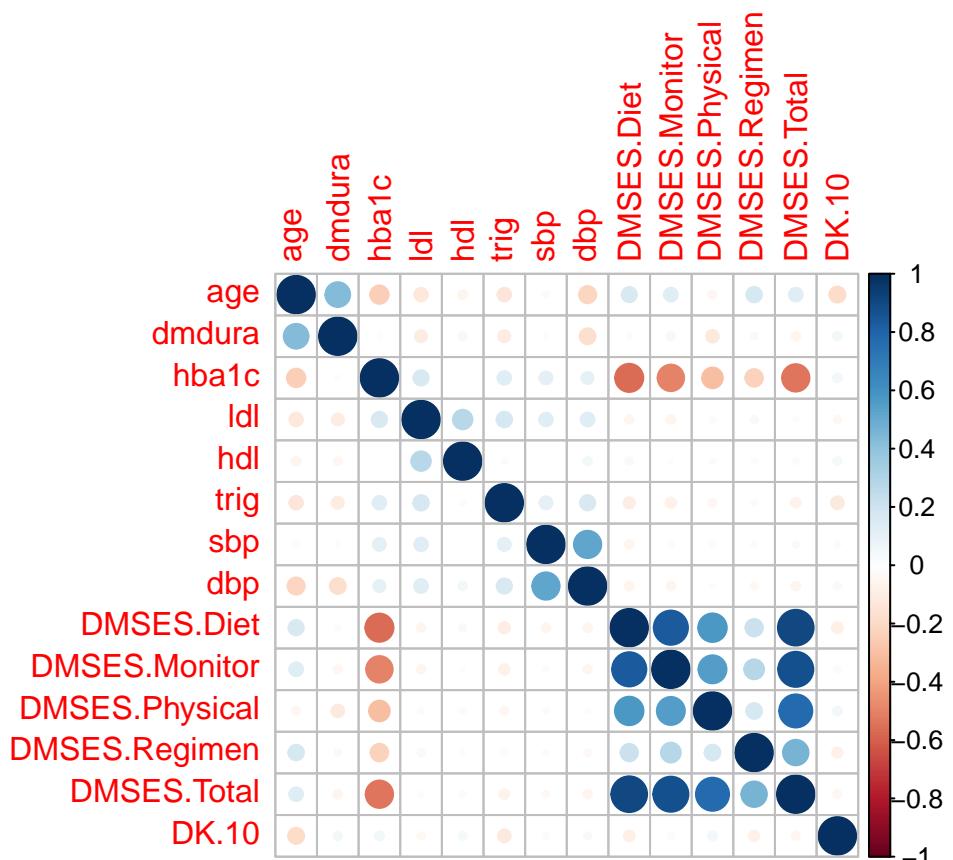
```

	age	dmdura	hb1c	ldl	hdl	trig	sbp	dbp	DMSES.Diet	DMSES.Monitor	DMSES.Physical	DMSES.Regimen	DMSES.Total	DK.10
age	1.00	0.44	-0.24	-0.13	-0.06	-0.13	0.03	-0.21		0.16				0.14
dmdura	0.44	1.00	-0.02	-0.10	-0.05	-0.11	-0.01	-0.18		-0.02				-0.05
hb1c	-0.24	-0.02	1.00	0.17	0.00	0.13	0.12	0.11		-0.56				-0.50
ldl	-0.13	-0.10	0.17	1.00	0.27	0.17	0.13	0.14		-0.05				-0.05
hdl	-0.06	-0.05	0.00	0.27	1.00	-0.02	0.00	0.05		0.04				-0.01
trig	-0.13	-0.11	0.13	0.17	-0.02	1.00	0.12	0.17		-0.09				-0.08
sbp	0.03	-0.01	0.12	0.13	0.00	0.12	1.00	0.53		-0.05				-0.02
dbp	-0.21	-0.18	0.11	0.14	0.05	0.17	0.53	1.00		-0.05				-0.05
DMSES.Diet	0.16	-0.02	-0.56	-0.05	0.04	-0.09	-0.05	-0.05		1.00				0.83
DMSES.Monitor	0.14	-0.05	-0.50	-0.05	-0.01	-0.08	-0.02	-0.05		0.83				1.00
DMSES.Physical	-0.04	-0.11	-0.30	0.02	0.02	-0.04	-0.02	-0.02		0.58				0.56
DMSES.Regimen	0.17	0.03	-0.22	0.04	0.02	0.02	0.02	-0.04		0.22				0.28
DMSES.Total	0.13	-0.05	-0.53	-0.02	0.03	-0.07	-0.03	-0.05		0.91				0.88
DK.10	-0.18	0.05	0.06	-0.04	0.05	-0.12	0.03	0.04		-0.08				-0.03

```

corrplot(M,method="circle")

```



```

# vamos a ordenar las correlaciones
flattenCorrMatrix <- function(cormat) {
  ut <- upper.tri(cormat)
  dd <- data.frame(
    row = rownames(cormat)[row(cormat)[ut]],
    column = rownames(cormat)[col(cormat)[ut]],
    cor  =(cormat)[ut]
  )
  dd <- dd[order(abs(dd$cor), decreasing = T),]
  dd$cor <- round(dd$cor, 3)
  dd
}

flattenCorrMatrix(M)

```

	row	column	cor
## 75	DMSES.Diet	DMSES.Total	0.908
## 76	DMSES.Monitor	DMSES.Total	0.876
## 45	DMSES.Diet	DMSES.Monitor	0.832
## 77	DMSES.Physical	DMSES.Total	0.779
## 54	DMSES.Diet	DMSES.Physical	0.578
## 31	hba1c	DMSES.Diet	-0.563
## 55	DMSES.Monitor	DMSES.Physical	0.558
## 69	hba1c	DMSES.Total	-0.534
## 28	sbp	dbp	0.530
## 39	hba1c	DMSES.Monitor	-0.499
## 78	DMSES.Regimen	DMSES.Total	0.461
## 1	age	dmdura	0.436
## 48	hba1c	DMSES.Physical	-0.303
## 65	DMSES.Monitor	DMSES.Regimen	0.281
## 10	ldl	hdl	0.271
## 2	age	hba1c	-0.241
## 58	hba1c	DMSES.Regimen	-0.221
## 64	DMSES.Diet	DMSES.Regimen	0.215
## 22	age	dbp	-0.211
## 79	age	DK.10	-0.183
## 23	dmdura	dbp	-0.179
## 66	DMSES.Physical	DMSES.Regimen	0.178
## 56	age	DMSES.Regimen	0.172
## 14	ldl	trig	0.170
## 6	hba1c	ldl	0.167
## 27	trig	dbp	0.165
## 29	age	DMSES.Diet	0.165
## 25	ldl	dbp	0.137
## 37	age	DMSES.Monitor	0.136
## 67	age	DMSES.Total	0.135
## 13	hba1c	trig	0.131
## 11	age	trig	-0.131
## 19	ldl	sbp	0.131
## 4	age	ldl	-0.129
## 21	trig	sbp	0.119
## 18	hba1c	sbp	0.118
## 84	trig	DK.10	-0.117

```

## 47      dmdura DMSES.Physical -0.113
## 24      hba1c      dbp  0.105
## 12      dmdura      trig -0.105
## 5       dmdura      ldl  -0.102
## 34      trig      DMSES.Diet -0.090
## 87      DMSES.Diet      DK.10 -0.084
## 42      trig      DMSES.Monitor -0.078
## 90  DMSES.Regimen      DK.10 -0.076
## 72      trig      DMSES.Total -0.069
## 7       age       hdl  -0.059
## 81      hba1c      DK.10  0.056
## 89  DMSES.Physical      DK.10  0.055
## 36      dbp      DMSES.Diet -0.054
## 40      ldl      DMSES.Monitor -0.053
## 74      dbp      DMSES.Total -0.053
## 35      sbp      DMSES.Diet -0.053
## 44      dbp      DMSES.Monitor -0.052
## 68      dmdura     DMSES.Total -0.052
## 26      hdl      dbp   0.051
## 32      ldl      DMSES.Diet -0.051
## 80      dmdura     DK.10  0.051
## 38      dmdura     DMSES.Monitor -0.049
## 8       dmdura     hdl  -0.048
## 91  DMSES.Total      DK.10 -0.046
## 83      hdl      DK.10  0.046
## 46      age      DMSES.Physical -0.043
## 51      trig     DMSES.Physical -0.043
## 82      ldl      DK.10 -0.040
## 59      ldl      DMSES.Regimen  0.038
## 86      dbp      DK.10  0.038
## 33      hdl      DMSES.Diet  0.037
## 63      dbp      DMSES.Regimen -0.036
## 73      sbp      DMSES.Total -0.032
## 57      dmdura     DMSES.Regimen  0.031
## 88  DMSES.Monitor      DK.10 -0.030
## 16      age       sbp  0.028
## 71      hdl      DMSES.Total  0.027
## 85      sbp      DK.10  0.026
## 50      hdl     DMSES.Physical 0.025
## 61      trig     DMSES.Regimen  0.024
## 15      hdl      trig  -0.023
## 49      ldl     DMSES.Physical 0.023
## 62      sbp     DMSES.Regimen  0.022
## 43      sbp     DMSES.Monitor -0.022
## 52      sbp     DMSES.Physical -0.021
## 30      dmdura     DMSES.Diet -0.021
## 53      dbp     DMSES.Physical -0.020
## 70      ldl     DMSES.Total -0.020
## 60      hdl     DMSES.Regimen  0.017
## 3       dmdura     hba1c -0.016
## 17      dmdura     sbp  -0.012
## 41      hdl     DMSES.Monitor -0.012
## 20      hdl      sbp  -0.005
## 9       hba1c     hdl   0.003

```

```

cor(hba1c,DMSES.Diet)

## [1] -0.5630537

cor(hba1c,DMSES.Physical)

## [1] -0.3027804

cor(hba1c,DMSES.Monitor)

## [1] -0.4987917

cor(hba1c,DMSES.Regimen)

## [1] -0.2206762

cor(hba1c,DMSES.Total)

## [1] -0.5339001

```

Podemos ver que las diferentes puntuaciones del cuestionario DMSES (total o de alguna de sus partes) están muy relacionadas. De entre todas las puntuaciones, la del factor dieta es la que mayor correlación tienen con la hba1c, por lo que parece razonable centrarse en el uso de sólo esa puntuación para buscar una relación con la hba1c y descartar el resto de puntuaciones del cuestionario DMSES del análisis.

Vemos en qué medida están relacionadas las puntuaciones del cuestionario DMSES entre sí.

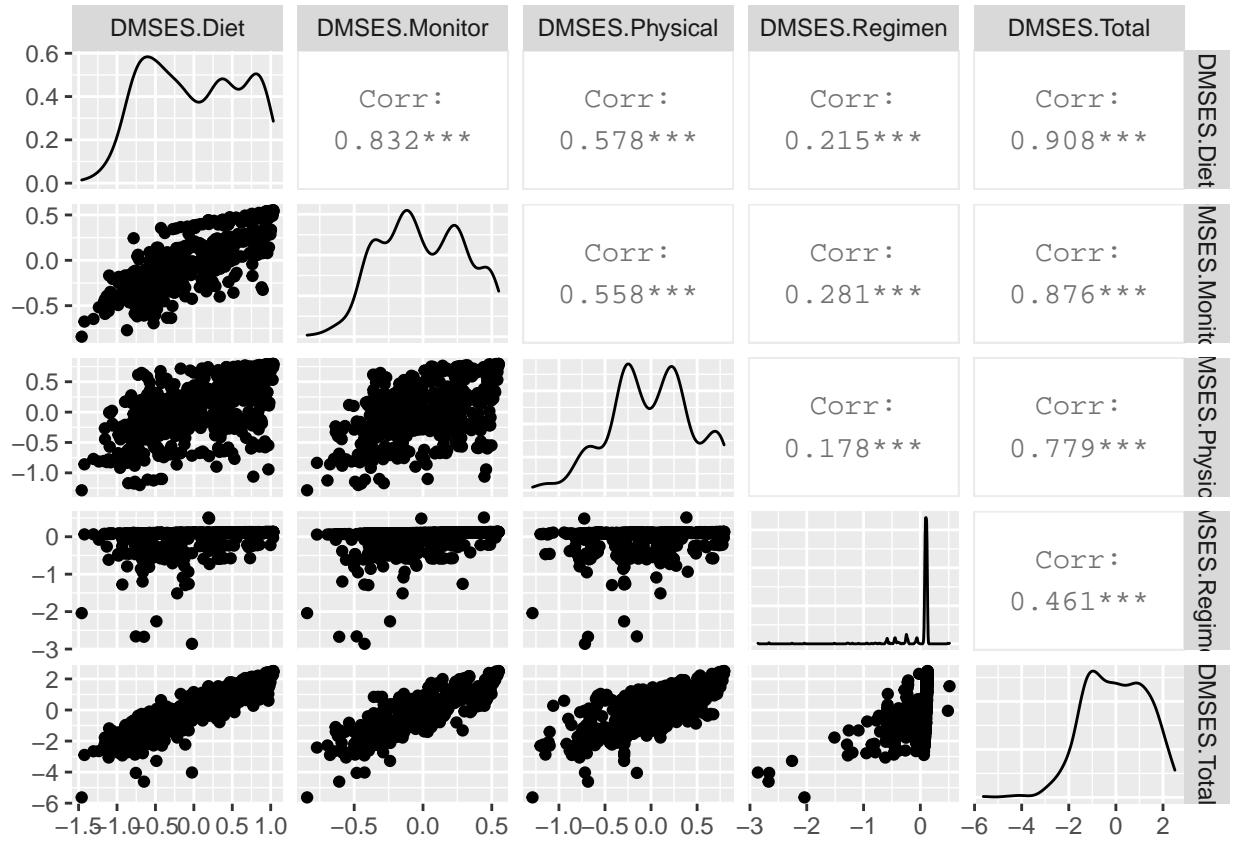
```

# demostración DMSES total es la suma de los 4 subscores
max(DMSES.Total - (DMSES.Diet + DMSES.Monitor + DMSES.Physical + DMSES.Regimen))

## [1] 7.105427e-15

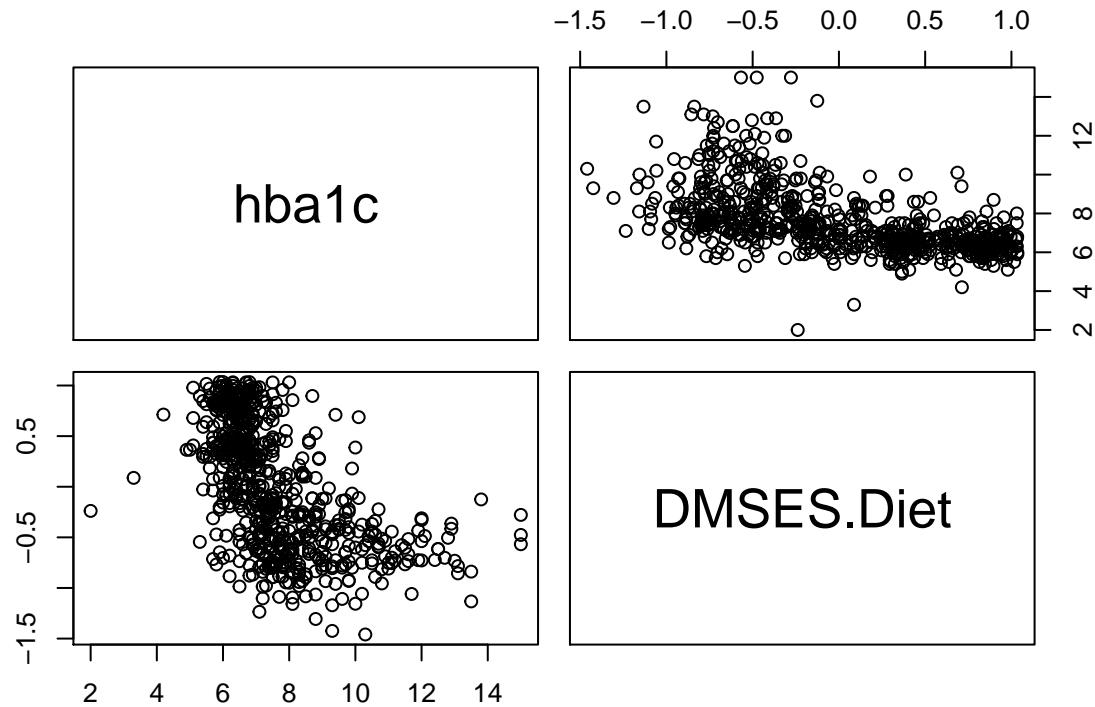
# relación entre los diferentes subscores
ggpairs(datos[,c("DMSES.Diet","DMSES.Monitor","DMSES.Physical","DMSES.Regimen","DMSES.Total")])

```

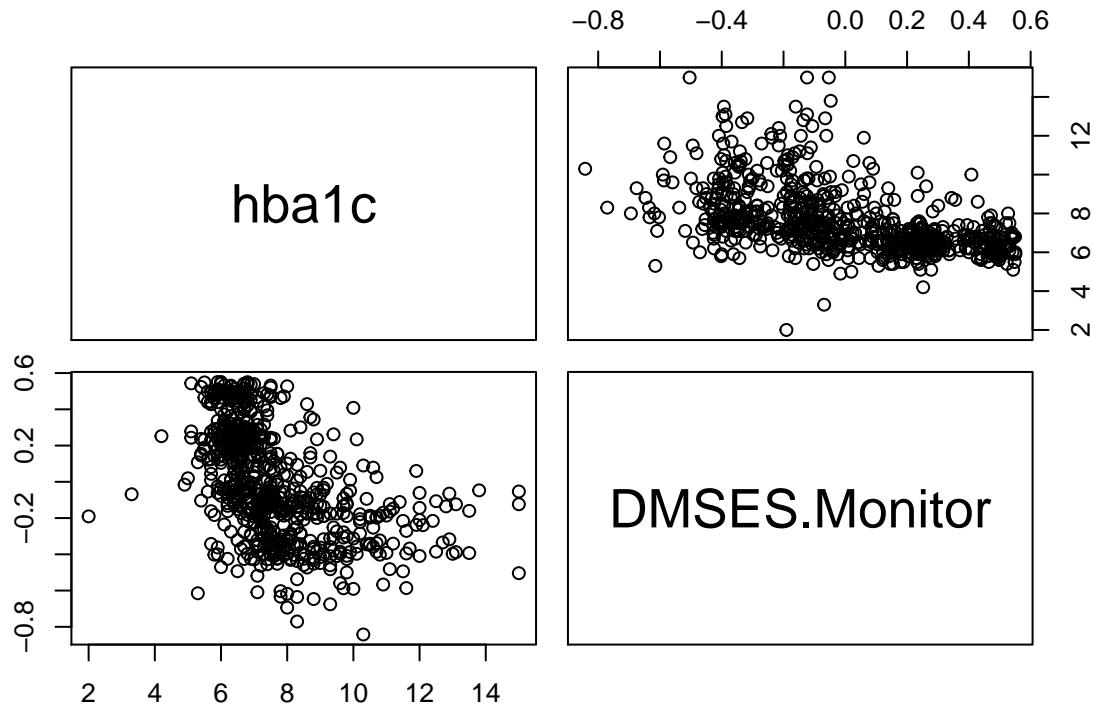


Al querer buscar las relaciones entre las puntuaciones del cuestionario DMSES (la puntuación total y la de las partes ‘dieta’, ‘monitor’, ‘régimen’ y ‘estado físico’) y el nivel de hba1c se observa que no hay una relación lineal a priori. Se valorará hacer transformaciones adecuadas para comprobar si se puede hallar una relación.

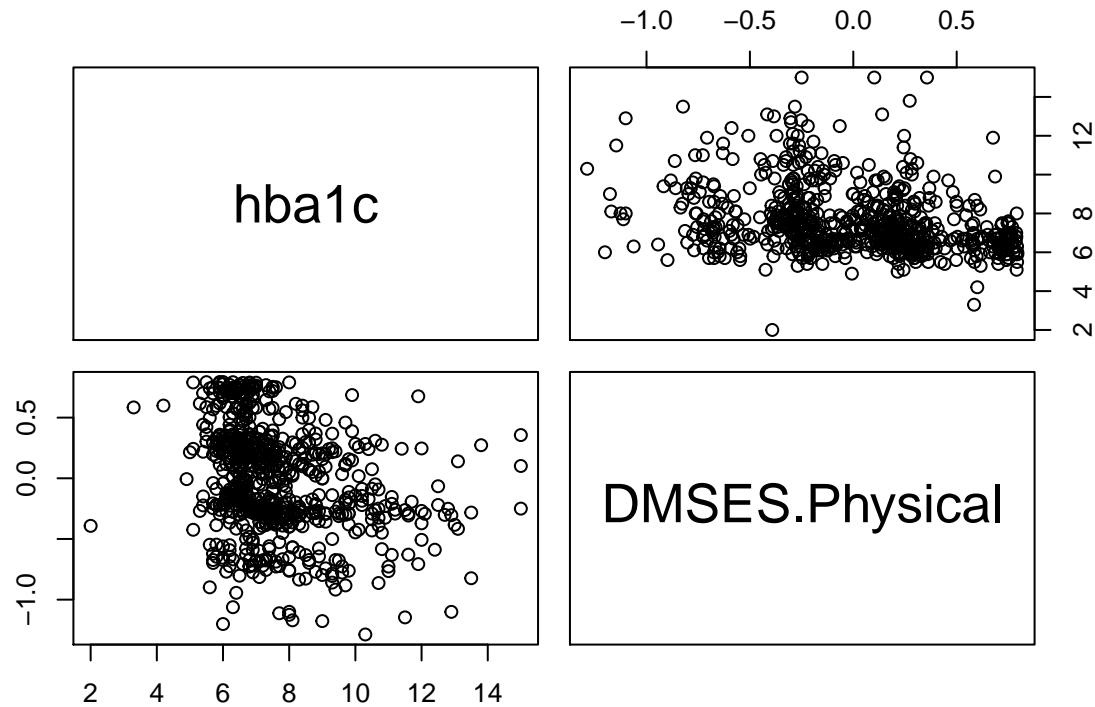
```
par(mfrow=c(2,3))
pairs(~ hba1c + DMSES.Diet ,data=datos)
```



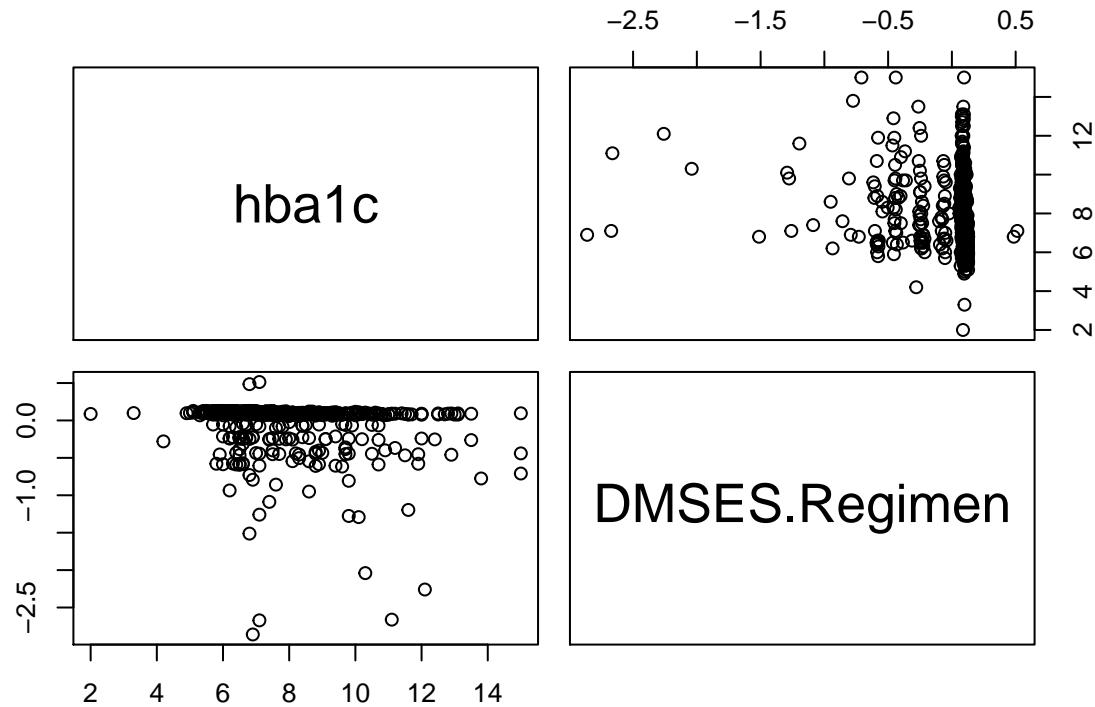
```
pairs(~ hba1c + DMSES.Monitor, data=datos)
```



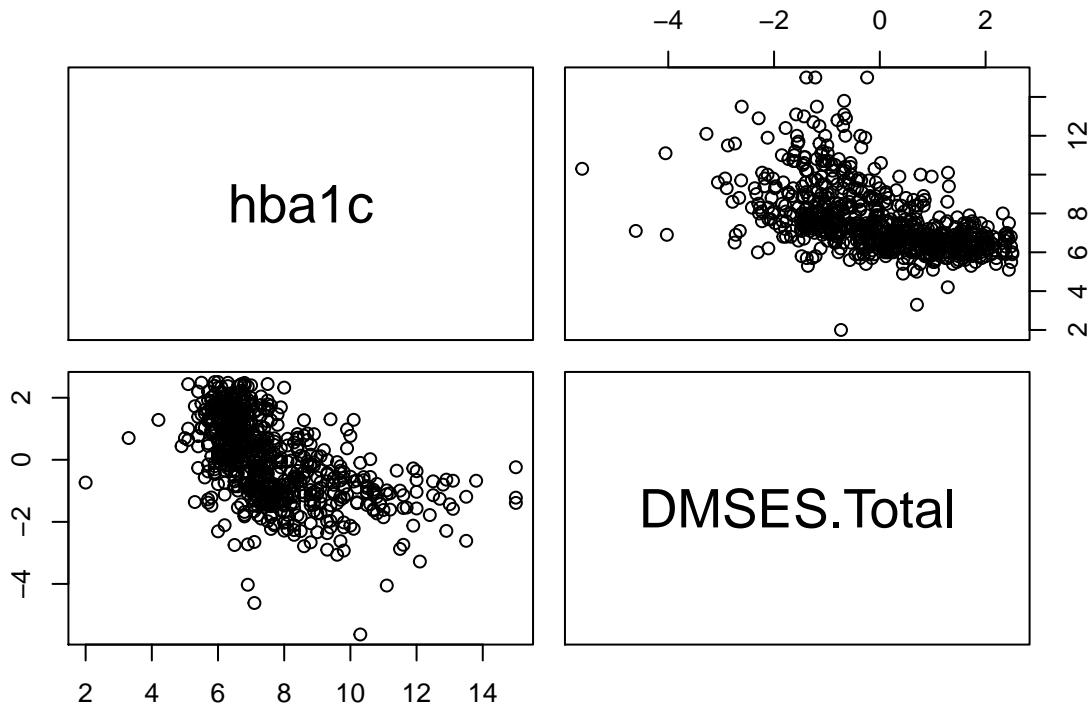
```
pairs(~ hba1c + DMSES.Physical, data=datos)
```



```
pairs(~ hba1c + DMSES.Regimen, data=datos)
```



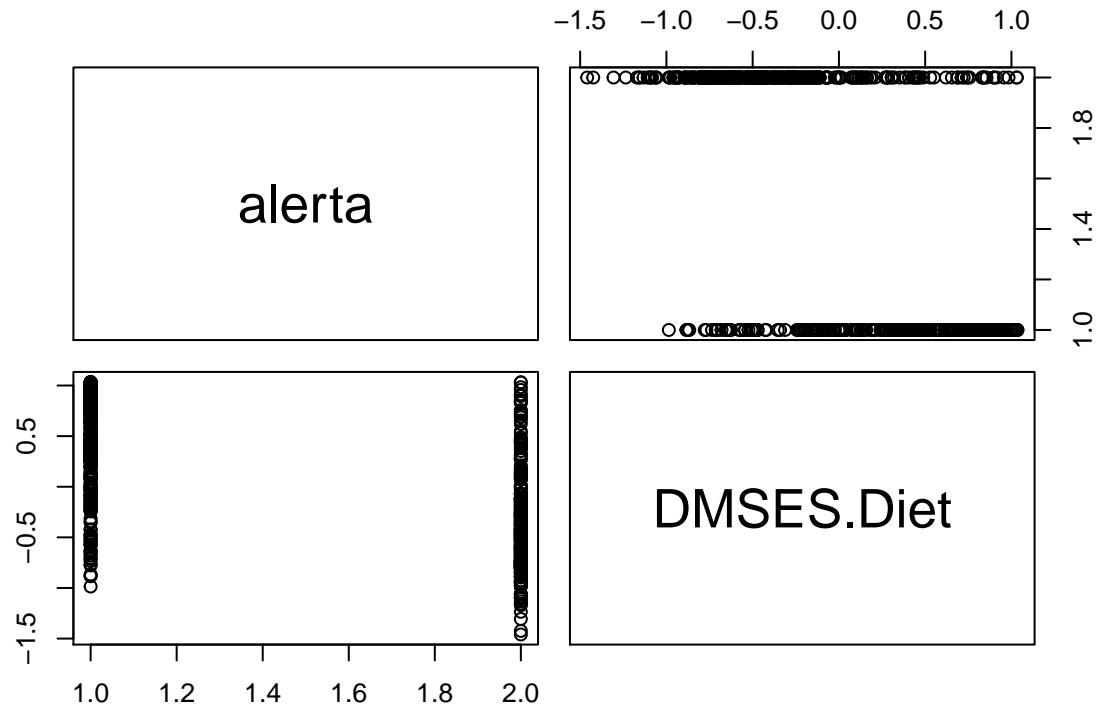
```
pairs(~ hba1c + DMSES.Total, data=datos)
```



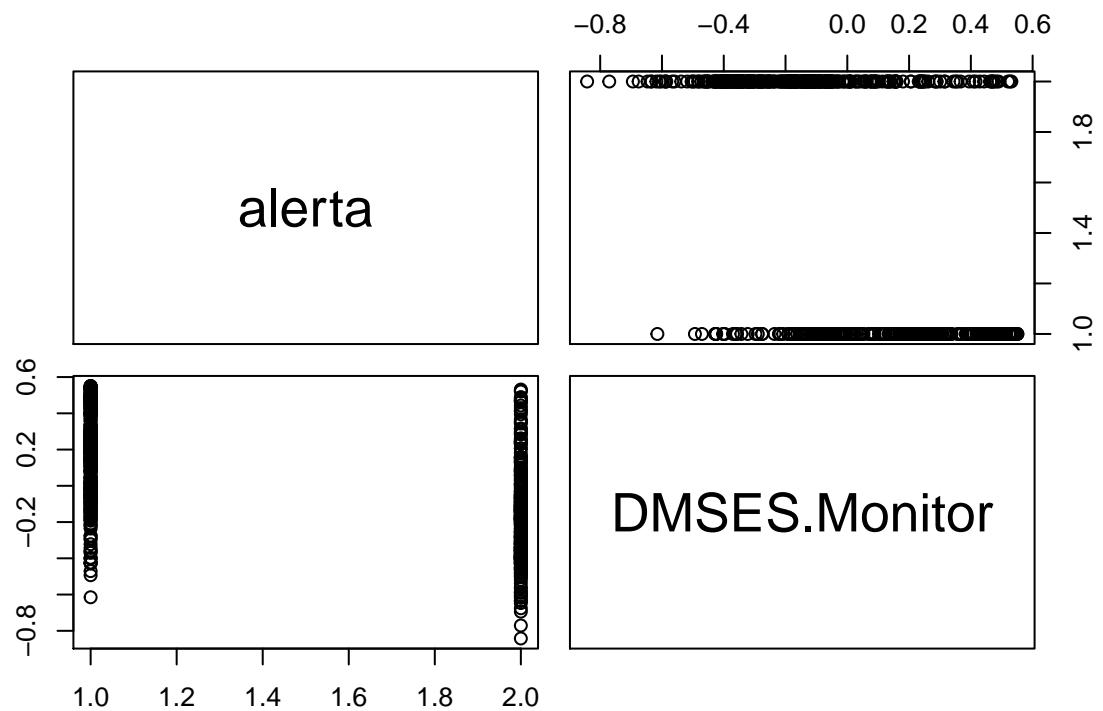
```
par(mfrow=c(1,1))
```

Tampoco se detecta una relación clara entre las puntuaciones del cuestionario DMSES y la variable categórica 'alerta'.

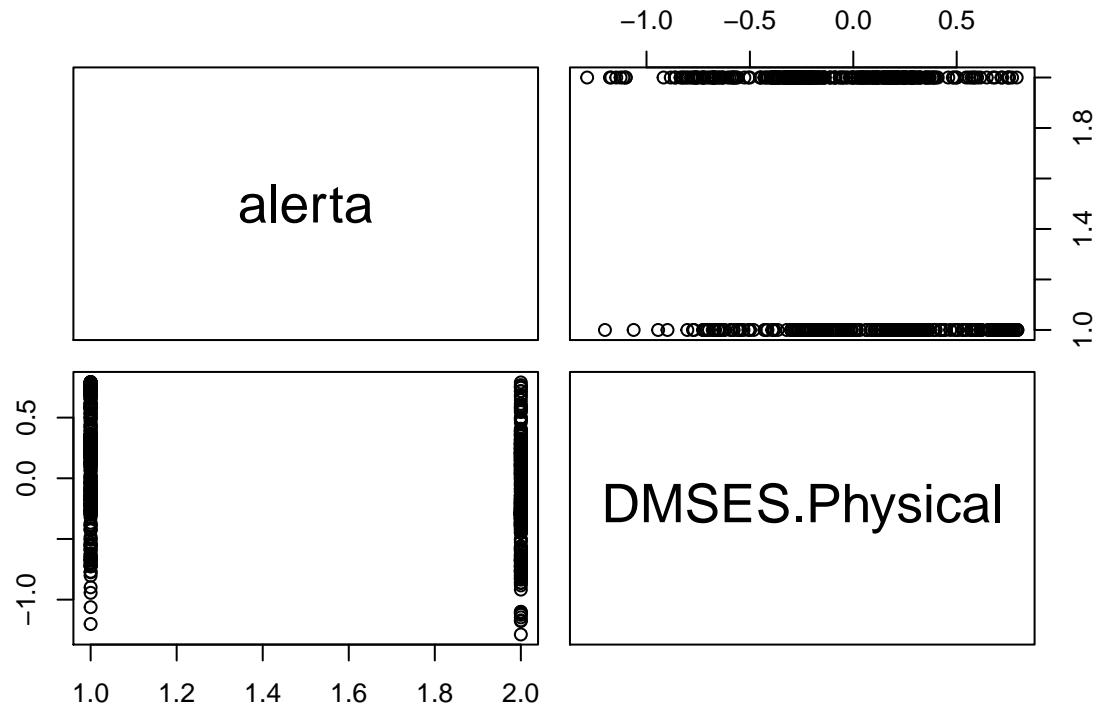
```
pairs(~ alerta + DMSES.Diet ,data=datos)
```



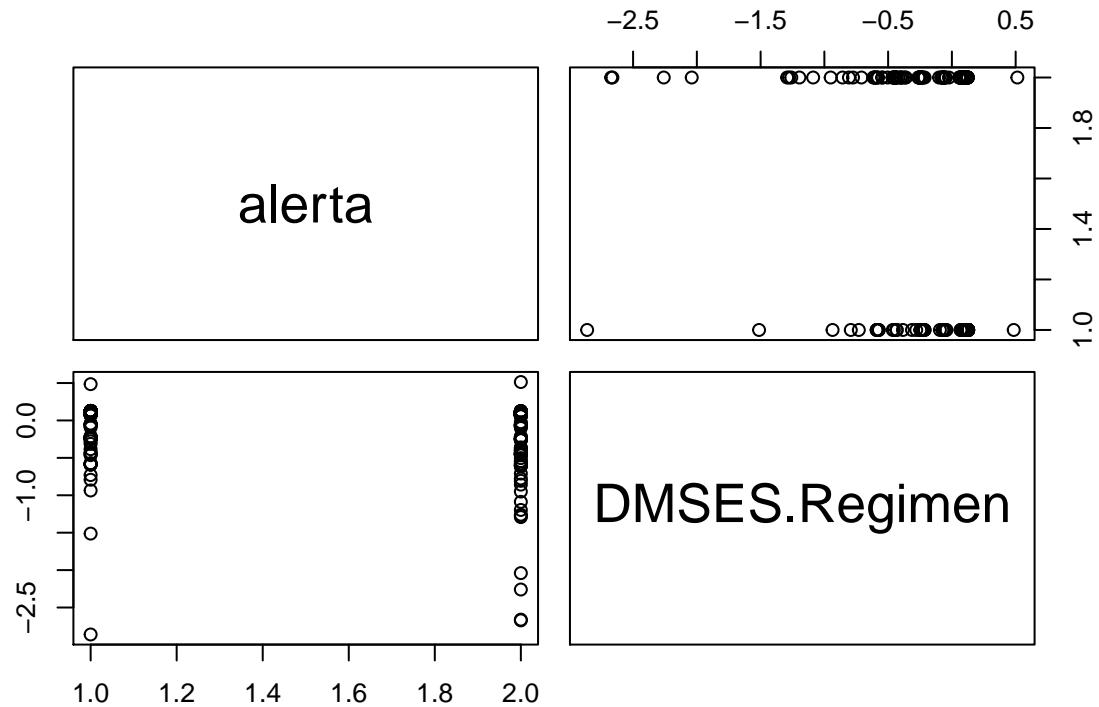
```
pairs(~ alerta + DMSES.Monitor, data=datos)
```



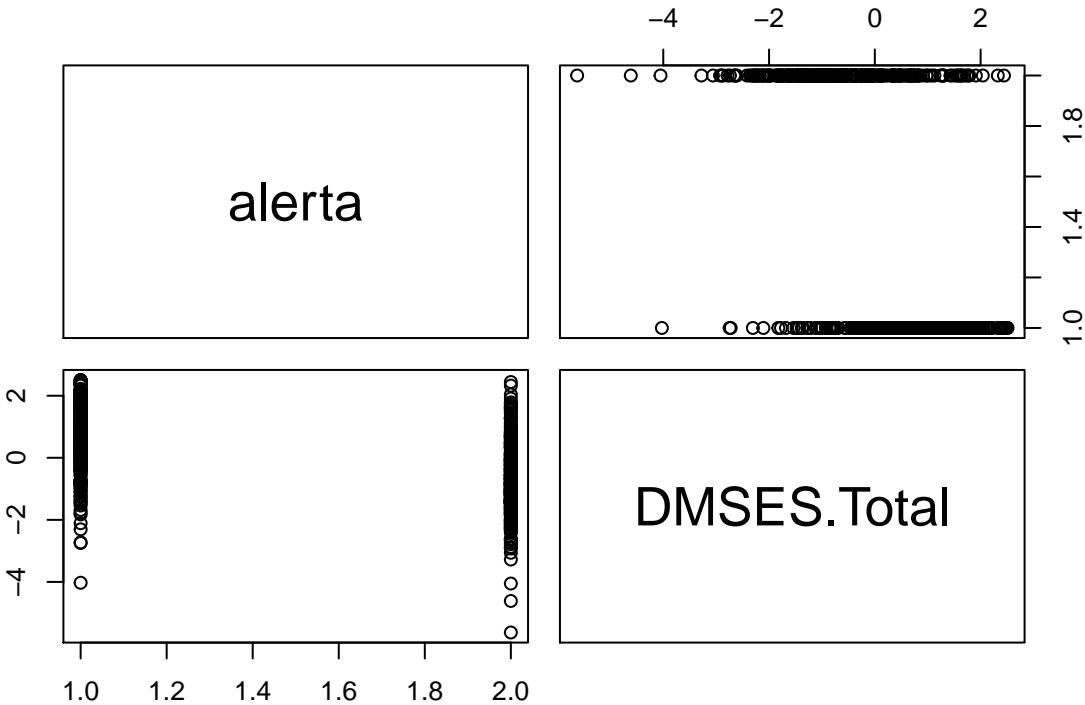
```
pairs(~ alerta + DMSES.Physical, data=datos)
```



```
pairs(~ alerta + DMSES.Regimen, data=datos)
```



```
pairs(~ alerta + DMSES.Total, data=datos)
```



Análisis multivariante de las variables discretas

Las variables discretas con poca variabilidad no se toman en cuenta (cva, cereinfrac, ischemic, stroke, cereb-hem,tia, angia, chf, cororevas, pad, neuropath )

```
chisq.test(datos$alerta,datos$hospid)
```

```
##  
## Pearson's Chi-squared test  
##  
## data: datos$alerta and datos$hospid  
## X-squared = 21.203, df = 3, p-value = 9.551e-05
```

```
chisq.test(datos$alerta,datos$gender)
```

```
##  
## Pearson's Chi-squared test with Yates' continuity correction  
##  
## data: datos$alerta and datos$gender  
## X-squared = 0.32616, df = 1, p-value = 0.5679
```

```
chisq.test(datos$alerta,datos$mstatus)
```

```
## Warning in chisq.test(datos$alerta, datos$mstatus): Chi-squared approximation  
## may be incorrect
```

```

##  

## Pearson's Chi-squared test  

##  

## data: datos$alerta and datos$mstatus  

## X-squared = 12.419, df = 4, p-value = 0.01449

chisq.test(datos$alerta,datos$edu)

## Warning in chisq.test(datos$alerta, datos$edu): Chi-squared approximation may be
## incorrect

##  

## Pearson's Chi-squared test  

##  

## data: datos$alerta and datos$edu  

## X-squared = 8.9276, df = 5, p-value = 0.112

chisq.test(datos$alerta,datos$religion)

## Warning in chisq.test(datos$alerta, datos$religion): Chi-squared approximation
## may be incorrect

##  

## Pearson's Chi-squared test  

##  

## data: datos$alerta and datos$religion  

## X-squared = 2.6512, df = 2, p-value = 0.2656

chisq.test(datos$alerta,datos$income)

##  

## Pearson's Chi-squared test  

##  

## data: datos$alerta and datos$income  

## X-squared = 11.121, df = 5, p-value = 0.04904

chisq.test(datos$alerta,datos$famhx)

##  

## Pearson's Chi-squared test with Yates' continuity correction
##  

## data: datos$alerta and datos$famhx  

## X-squared = 0.9669, df = 1, p-value = 0.3255

chisq.test(datos$alerta,datos$comob)

##  

## Pearson's Chi-squared test with Yates' continuity correction
##  

## data: datos$alerta and datos$comob  

## X-squared = 1.2299, df = 1, p-value = 0.2674

```

```

chisq.test(datos$alerta,datos$comlip)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$comlip
## X-squared = 1.0754, df = 1, p-value = 0.2997

chisq.test(datos$alerta,datos$comht)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$comht
## X-squared = 0.63726, df = 1, p-value = 0.4247

chisq.test(datos$alerta,datos$comchd)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$comchd
## X-squared = 4.8263, df = 1, p-value = 0.02803

chisq.test(datos$alerta,datos$comkid)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$comkid
## X-squared = 39.775, df = 1, p-value = 2.849e-10

chisq.test(datos$alerta,datos$comoth)

## Warning in chisq.test(datos$alerta, datos$comoth): Chi-squared approximation may
## be incorrect

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$comoth
## X-squared = 4.3425e-28, df = 1, p-value = 1

chisq.test(datos$alerta,datos$dmrx)

##
## Pearson's Chi-squared test
##
## data: datos$alerta and datos$dmrx
## X-squared = 75.467, df = 3, p-value = 2.878e-16

```

```

chisq.test(datos$alerta,datos$smk)

##
##  Pearson's Chi-squared test
##
## data:  datos$alerta and datos$smk
## X-squared = 0.77241, df = 2, p-value = 0.6796

chisq.test(datos$alerta,datos$alcohol)

##
##  Pearson's Chi-squared test
##
## data:  datos$alerta and datos$alcohol
## X-squared = 0.75205, df = 2, p-value = 0.6866

chisq.test(datos$alerta,datos$compli)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  datos$alerta and datos$compli
## X-squared = 97.093, df = 1, p-value < 2.2e-16

chisq.test(datos$alerta,datos$mi)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  datos$alerta and datos$mi
## X-squared = 6.7972, df = 1, p-value = 0.00913

chisq.test(datos$alerta,datos$renal)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  datos$alerta and datos$renal
## X-squared = 22.828, df = 1, p-value = 1.772e-06

chisq.test(datos$alerta,datos$dn)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  datos$alerta and datos$dn
## X-squared = 14.389, df = 1, p-value = 0.0001487

```

```

chisq.test(datos$alerta,datos$dr)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$dr
## X-squared = 65.391, df = 1, p-value = 6.141e-16

chisq.test(datos$alerta,datos$sobrepeso)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$sobrepeso
## X-squared = 2.4841, df = 1, p-value = 0.115

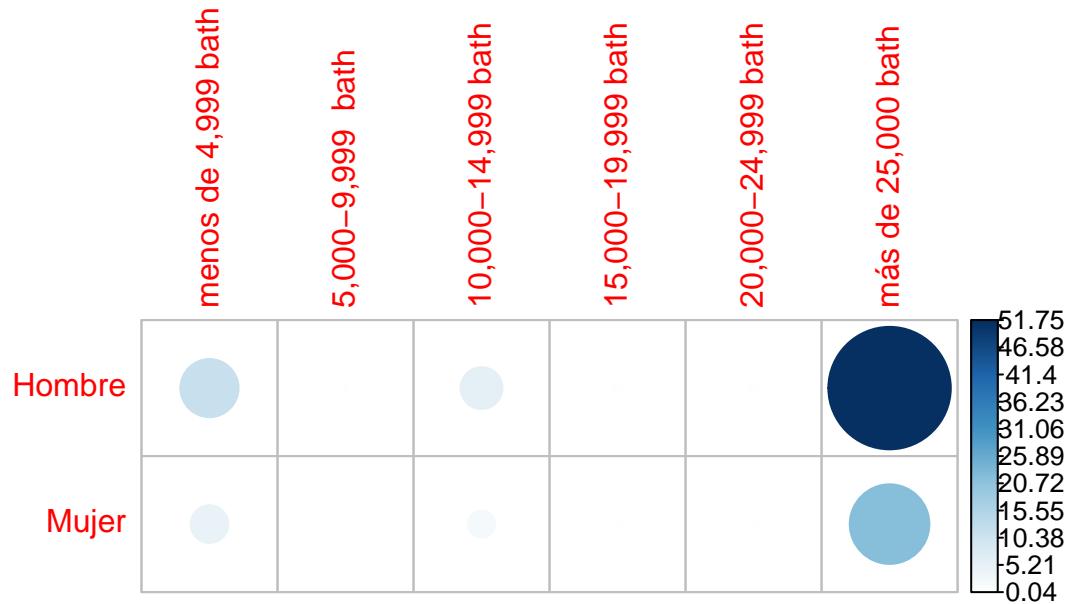
chisq.test(datos$alerta,datos$obesidad)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: datos$alerta and datos$obesidad
## X-squared = 0.1288, df = 1, p-value = 0.7197

# caso gráfico

chisq <- chisq.test(datos$gender,datos$income)
# Contibution in percentage (%)
contrib <- 100*chisq$residuals^2/chisq$statistic
# Visualize the contribution
corrplot(contrib, is.cor = FALSE)

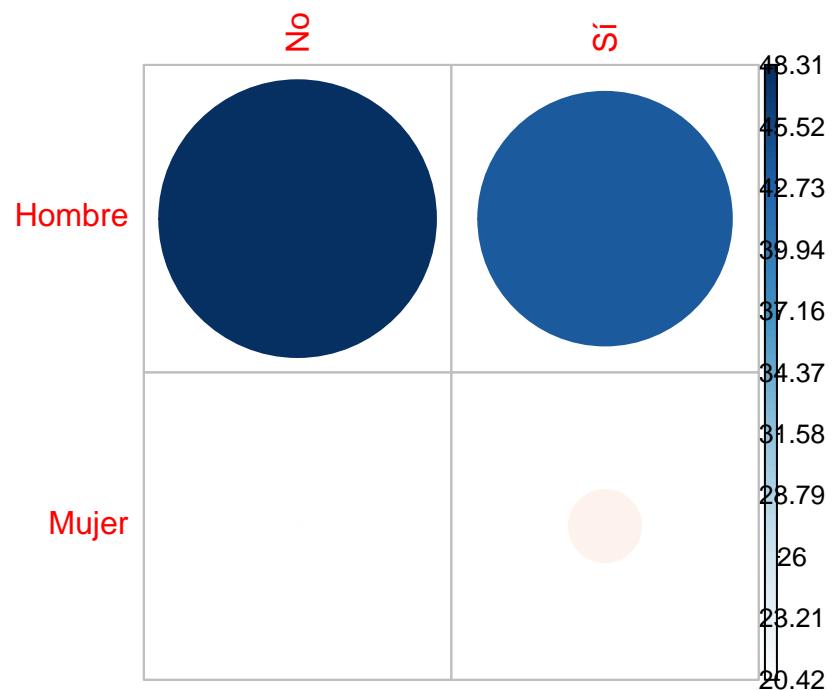
```



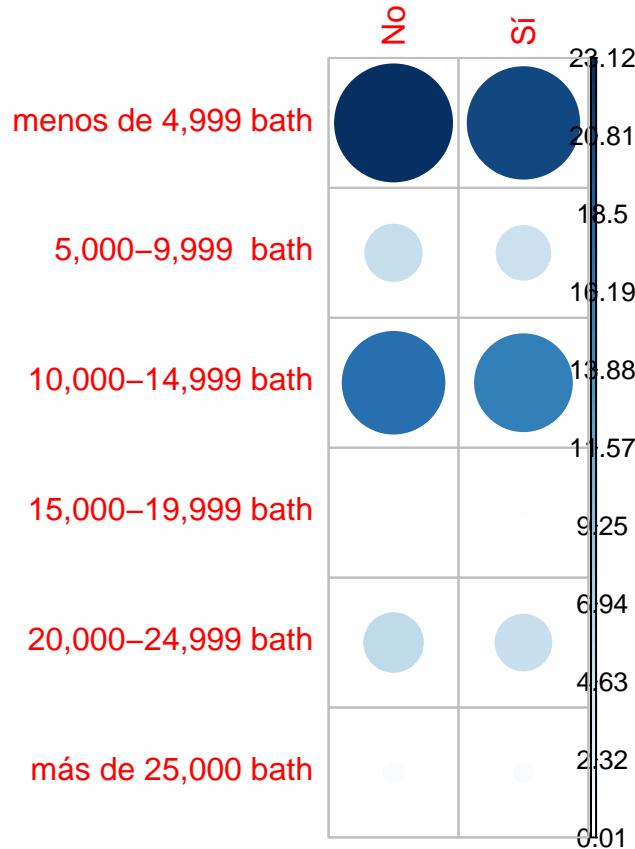
```

chisq <- chisq.test(datos$gender,datos$alerta)
# Contibution in percentage (%)
contrib <- 100*chisq$residuals^2/chisq$statistic
# Visualize the contribution
corrplot(contrib, is.cor = FALSE)

```



```
chisq <- chisq.test(datos$income,datos$alerta)
# Contribution in percentage (%)
contrib <- 100*chisq$residuals^2/chisq$statistic
# Visualize the contribution
corrplot(contrib, is.cor = FALSE)
```



## 2 Regresión lineal

El objetivo de este apartado será comprobar si la puntuación del test DMSES (total o de alguno de sus apartados) puede predecir el valor de la variable 'hba1c'.

```
par(mfrow=c(2,2))
mod <- lm(hba1c ~ DMSES.Total + DK.10 + age + renal + ldl + bmi,data=datos)
(smod <- summary(mod))
```

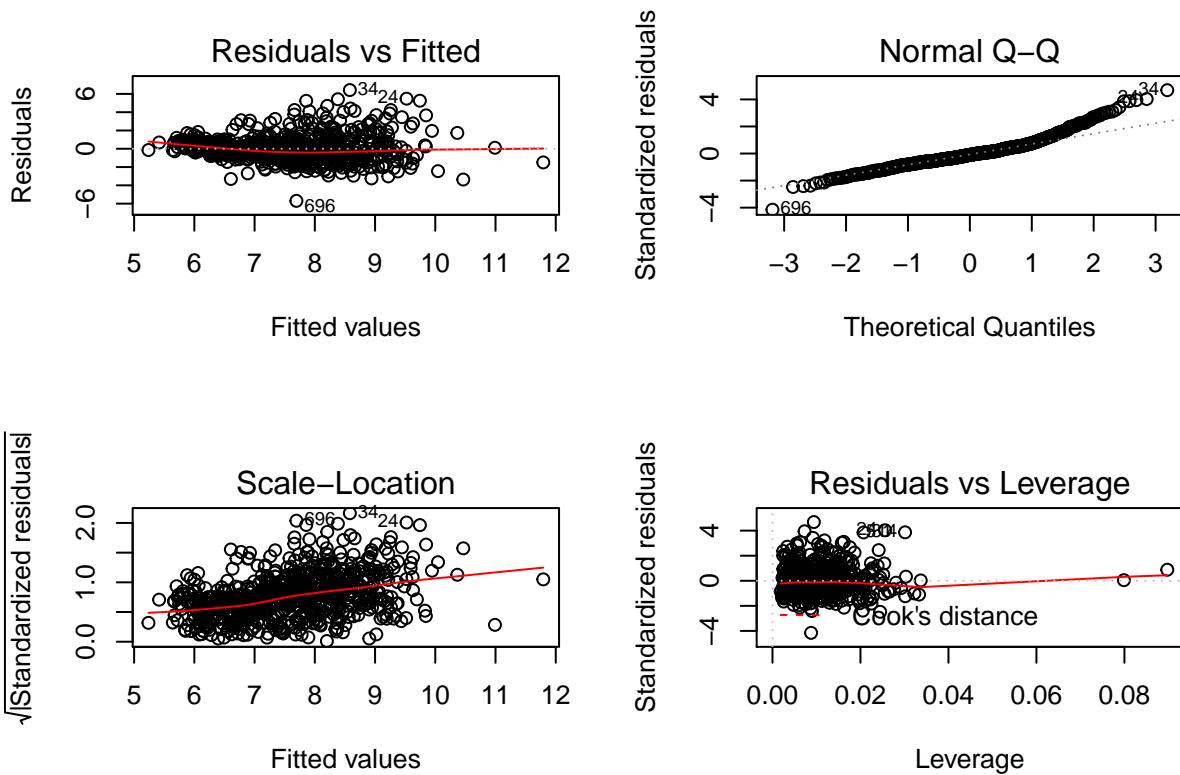
```
##
## Call:
## lm(formula = hba1c ~ DMSES.Total + DK.10 + age + renal + ldl +
##     bmi, data = datos)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -5.6945 -0.8032 -0.1390  0.6161  6.4182 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 8.902466  0.543628 16.376 < 2e-16 ***
## DMSES.Total -0.631903  0.041203 -15.336 < 2e-16 ***
## DK.10        0.019167  0.026675  0.719  0.4727    
## age         -0.028289  0.005113 -5.533 4.46e-08 ***
```

```

## renalSi      0.629150   0.143612   4.381 1.36e-05 ***
## ldl         0.007478   0.001714   4.363 1.48e-05 ***
## bmi        -0.016461   0.008569  -1.921  0.0551 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.377 on 693 degrees of freedom
## Multiple R-squared:  0.3538, Adjusted R-squared:  0.3482
## F-statistic: 63.24 on 6 and 693 DF,  p-value: < 2.2e-16

```

```
plot(mod)
```



```
vif(mod)
```

```

## DMSES.Total          DK.10           age       renalSi      ldl       bmi
##     1.076190     1.051559    1.153334    1.067002    1.021586    1.083572

```

```

# eliminamos DK.10
mod <- lm(hba1c ~ DMSES.Total +           age + renal + ldl + bmi, data=datos)
(smod <- summary(mod))

```

```

##
## Call:
## lm(formula = hba1c ~ DMSES.Total + age + renal + ldl + bmi, data = datos)

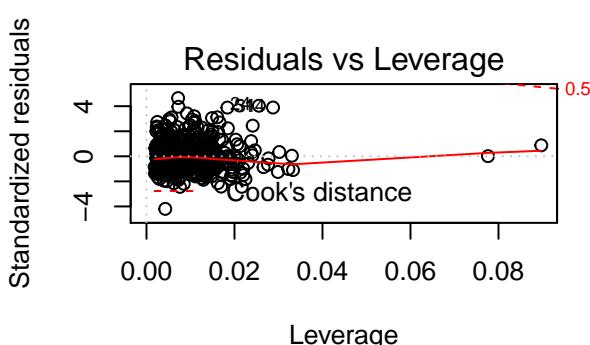
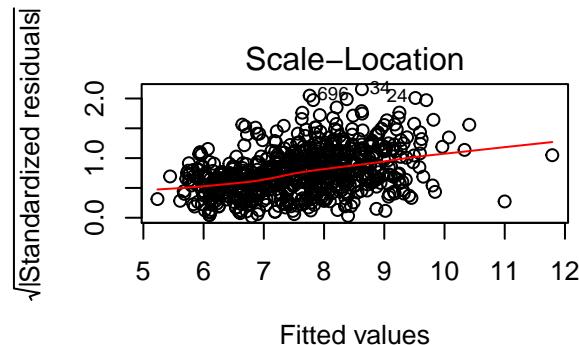
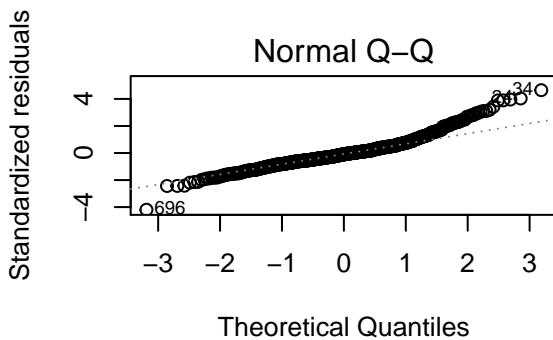
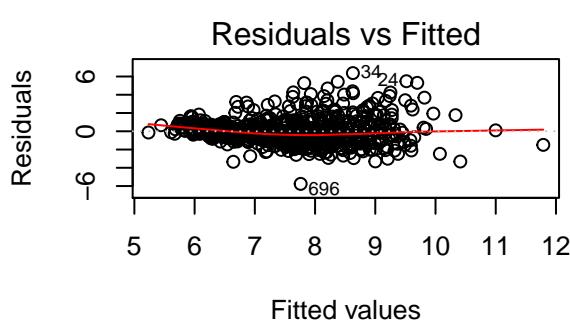
```

```

## 
## Residuals:
##   Min     1Q Median     3Q    Max
## -5.7610 -0.7966 -0.1314  0.5947  6.3716
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 9.064169  0.494685 18.323 < 2e-16 ***
## DMSES.Total -0.633259  0.041145 -15.391 < 2e-16 ***
## age         -0.028930  0.005032 -5.749 1.35e-08 ***
## renalSi      0.618438  0.142786  4.331 1.70e-05 ***
## ldl          0.007401  0.001710  4.328 1.72e-05 ***
## bmi         -0.016621  0.008564 -1.941  0.0527 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.377 on 694 degrees of freedom
## Multiple R-squared:  0.3533, Adjusted R-squared:  0.3487
## F-statistic: 75.84 on 5 and 694 DF,  p-value: < 2.2e-16

```

```
plot(mod)
```



```
vif(mod)
```

```

## DMSES.Total       age      renalSi      ldl      bmi
## 1.073931 1.118247 1.055502 1.017605 1.082847

```

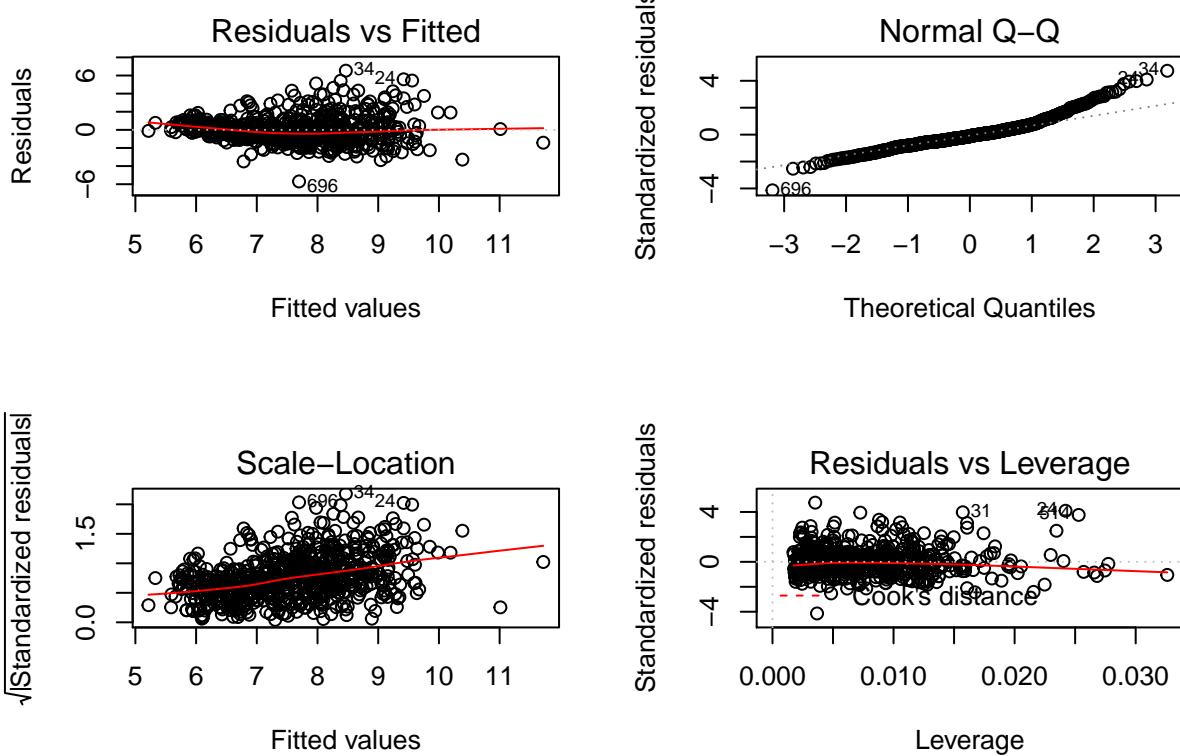
```

# eliminamos BMI
mod <- lm(hba1c ~ DMSES.Total + age + renal + ldl , data=datos)
(smod <- summary(mod))

## 
## Call:
## lm(formula = hba1c ~ DMSES.Total + age + renal + ldl, data = datos)
## 
## Residuals:
##      Min    1Q Median    3Q   Max 
## -5.6961 -0.7706 -0.1625  0.5901  6.5332 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 8.454447  0.382888 22.081 < 2e-16 ***
## DMSES.Total -0.626578  0.041082 -15.252 < 2e-16 ***
## age         -0.026500  0.004884 -5.426 7.97e-08 ***
## renalSi     0.611629  0.143027  4.276 2.17e-05 ***
## ldl          0.007424  0.001713  4.334 1.68e-05 *** 
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 
## 
## Residual standard error: 1.379 on 695 degrees of freedom
## Multiple R-squared:  0.3498, Adjusted R-squared:  0.3461 
## F-statistic: 93.48 on 4 and 695 DF,  p-value: < 2.2e-16

plot(mod)

```



```
vif(mod)
```

```
## DMSES.Total      age      renalSí      ldl
##   1.066413     1.049026    1.054865    1.017554
```

```
par(mfrow=c(1,1))
```

No se consigue tener un R<sup>2</sup> elevado ni corregir la no normalidad de los residuos. Aplicamos logaritmos a 'hba1c' (variable estrictamente positiva) y se mejora un poco la situación en cuanto a normalidad pero el R<sup>2</sup> sigue sin subir. Búsqueda de outliers pendiente.

```
par(mfrow=c(2,2))
mod <- lm(log(hba1c) ~ DMSES.Total + age + renal + ldl , data=datos)
(smod <- summary(mod))
```

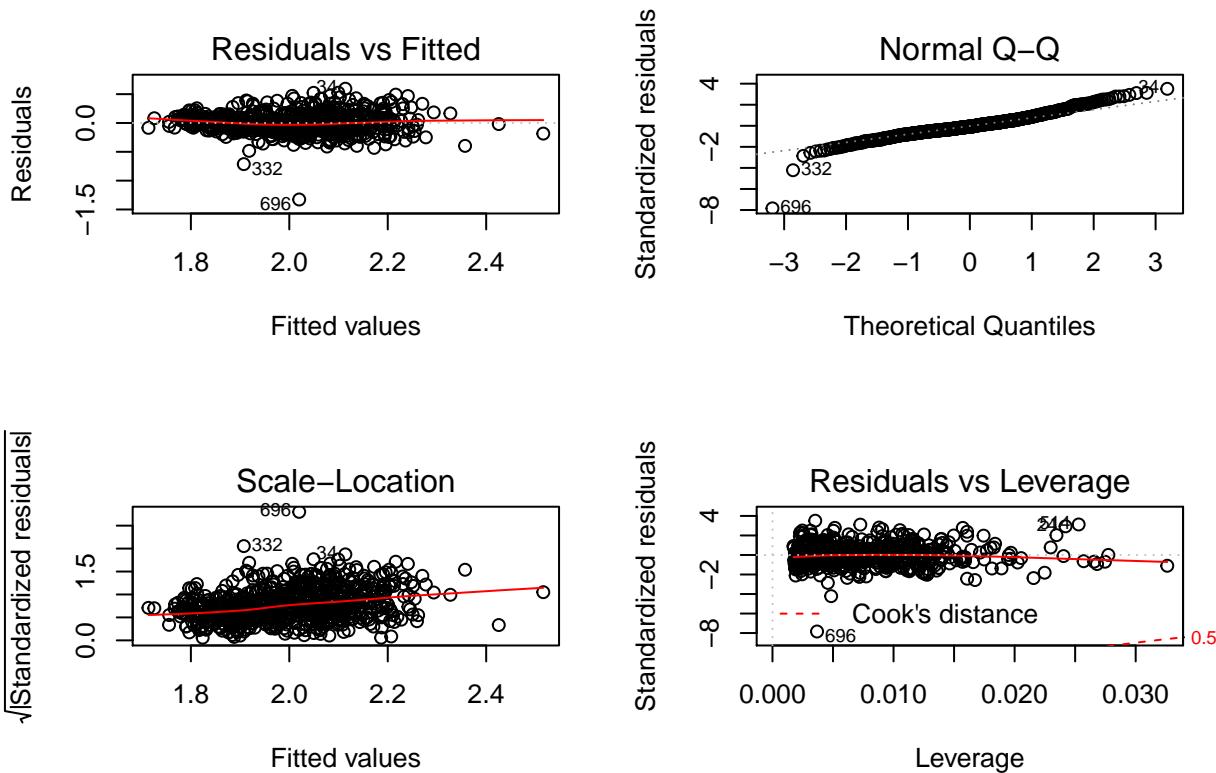
```
##
## Call:
## lm(formula = log(hba1c) ~ DMSES.Total + age + renal + ldl, data = datos)
##
## Residuals:
##       Min     1Q Median     3Q    Max
## -1.32692 -0.09223 -0.01355  0.08516  0.59417
##
## Coefficients:
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.1135308  0.0470599 44.911 < 2e-16 ***
## DMSES.Total -0.0786385  0.0050494 -15.574 < 2e-16 ***
## age         -0.0031851  0.0006003 -5.306 1.51e-07 ***
## renalSí      0.0684713  0.0175791  3.895 0.000108 ***
## ldl          0.0008448  0.0002106  4.012 6.67e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1695 on 695 degrees of freedom
## Multiple R-squared:  0.3504, Adjusted R-squared:  0.3466
## F-statistic:  93.7 on 4 and 695 DF,  p-value: < 2.2e-16

```

```
plot(mod)
```



```
vif(mod)
```

```

## DMSES.Total           age        renalSí        ldl
##     1.066413     1.049026    1.054865    1.017554

```

```
par(mfrow=c(1,1))
```

```

datos$dmrx1 <- as.factor(ifelse(datos$dmrx=="Sin medicación",1,0))
datos$dmrx2 <- as.factor(ifelse(datos$dmrx=="Hipoglicémico oral",1,0))

```

```

datos$dmrx3 <- as.factor(ifelse(datos$dmrx=="Insulina",1,0))

table(datos$obesidad)

## 
##   No   Sí
## 518 182

datos[1:10,c("dmrx","dmrx1","dmrx2","dmrx3")]

##          dmrx dmrx1 dmrx2 dmrx3
## 1 Hipoglicémico oral    0     1     0
## 2 Hipoglicémico oral    0     1     0
## 3 Hipoglicémico oral    0     1     0
## 4           Ambos    0     0     0
## 5       Insulina    0     0     1
## 6 Hipoglicémico oral    0     1     0
## 7 Hipoglicémico oral    0     1     0
## 8 Hipoglicémico oral    0     1     0
## 9 Hipoglicémico oral    0     1     0
## 10          Ambos   0     0     0

var.cat.inf   <- c("alerta","obesidad","sobrepeso","gender","renal","dmrx1","dmrx2","dmrx3","dn","dr")
var.cont.norm <- c("age", "hdl", "sbp", "dbp", "DMSES.Total", "DK.10")
var.interes   <- c(var.cat.inf,var.cont.norm)
var.interes

## [1] "alerta"      "obesidad"     "sobrepeso"    "gender"       "renal"
## [6] "dmrx1"       "dmrx2"       "dmrx3"       "dn"          "dr"
## [11] "age"         "hdl"         "sbp"         "dbp"         "DMSES.Total"
## [16] "DK.10"

datos1 <- datos[,var.interes]
dim(datos1)

## [1] 700 16

# Fit the full model
#full.model <- lm(alerta ~., data = datos1)
#summary(full.model)
# Stepwise regression model
#step.model <- stepAIC(full.model, direction = "both", trace = FALSE)
#summary(step.model)

require(leaps)

## Loading required package: leaps

```

```

b <- regsubsets(alerta~, data=datos1, nvmax = 15)
rs <- summary(b)
rs$which

##      (Intercept) obesidadSí sobrepesoSí genderMujer renalSí dmrx11 dmrx21 dmrx31
## 1        TRUE    FALSE     FALSE    FALSE    FALSE    FALSE    FALSE    FALSE
## 2        TRUE    FALSE     FALSE    FALSE    FALSE    FALSE    FALSE    FALSE
## 3        TRUE    FALSE     FALSE    FALSE    FALSE    FALSE    FALSE    FALSE
## 4        TRUE    FALSE     FALSE    FALSE    FALSE    FALSE    FALSE    TRUE
## 5        TRUE    TRUE     FALSE    FALSE    FALSE    FALSE    FALSE    TRUE
## 6        TRUE    TRUE     FALSE    FALSE    FALSE    FALSE    TRUE    FALSE
## 7        TRUE    TRUE     FALSE    FALSE    FALSE    FALSE    TRUE    FALSE
## 8        TRUE    TRUE     FALSE    FALSE    FALSE    TRUE    FALSE    TRUE
## 9        TRUE    TRUE     FALSE    FALSE    FALSE    TRUE    TRUE    TRUE
## 10       TRUE    TRUE     FALSE    FALSE    FALSE    TRUE    TRUE    TRUE
## 11       TRUE    TRUE     FALSE    FALSE    FALSE    TRUE    TRUE    TRUE
## 12       TRUE    TRUE     TRUE    FALSE    FALSE    TRUE    TRUE    TRUE
## 13       TRUE    TRUE     TRUE    TRUE    TRUE    TRUE    TRUE    TRUE
## 14       TRUE    TRUE     TRUE    TRUE    TRUE    TRUE    TRUE    FALSE
## 15       TRUE    TRUE     TRUE    TRUE    TRUE    TRUE    TRUE    TRUE
##      dnSí drSí age   hdl   sbp   dbp DMSES.Total DK.10
## 1  FALSE FALSE FALSE FALSE FALSE FALSE        TRUE FALSE
## 2  FALSE TRUE  FALSE FALSE FALSE FALSE        TRUE FALSE
## 3  FALSE TRUE  TRUE  FALSE FALSE FALSE        TRUE FALSE
## 4  FALSE TRUE  TRUE  FALSE FALSE FALSE        TRUE FALSE
## 5  FALSE TRUE  TRUE  FALSE FALSE FALSE        TRUE FALSE
## 6  FALSE TRUE  TRUE  FALSE  TRUE FALSE        TRUE FALSE
## 7  TRUE  TRUE  TRUE  FALSE  TRUE FALSE        TRUE FALSE
## 8  TRUE  TRUE  TRUE  FALSE  TRUE FALSE        TRUE FALSE
## 9  TRUE  TRUE  TRUE  FALSE  TRUE FALSE        TRUE FALSE
## 10  TRUE  TRUE  TRUE  TRUE  TRUE FALSE        TRUE FALSE
## 11  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE        TRUE FALSE
## 12  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE        TRUE FALSE
## 13  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE        TRUE FALSE
## 14  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE        TRUE TRUE
## 15  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE        TRUE TRUE

length(rs$rss)

## [1] 15

length(2:16)

## [1] 15

rs$rss

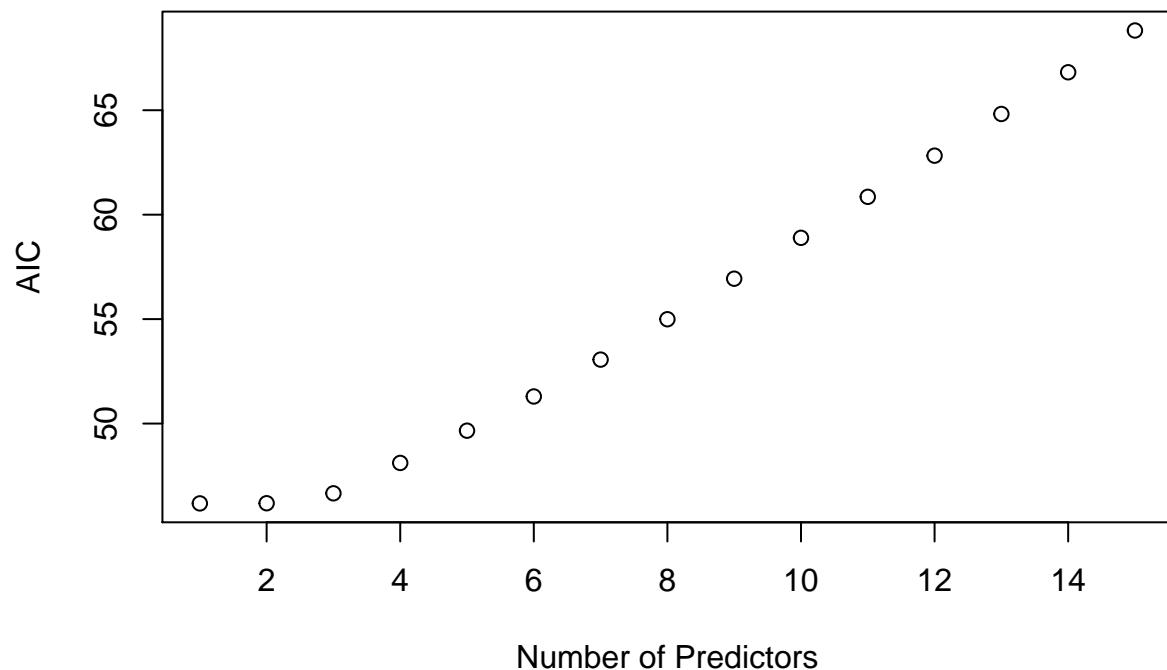
## [1] 116.2302 111.6889 108.3334 107.1566 106.1857 105.4197 104.9246 104.7829
## [9] 104.6601 104.5693 104.4905 104.4297 104.4209 104.4149 104.4148

```

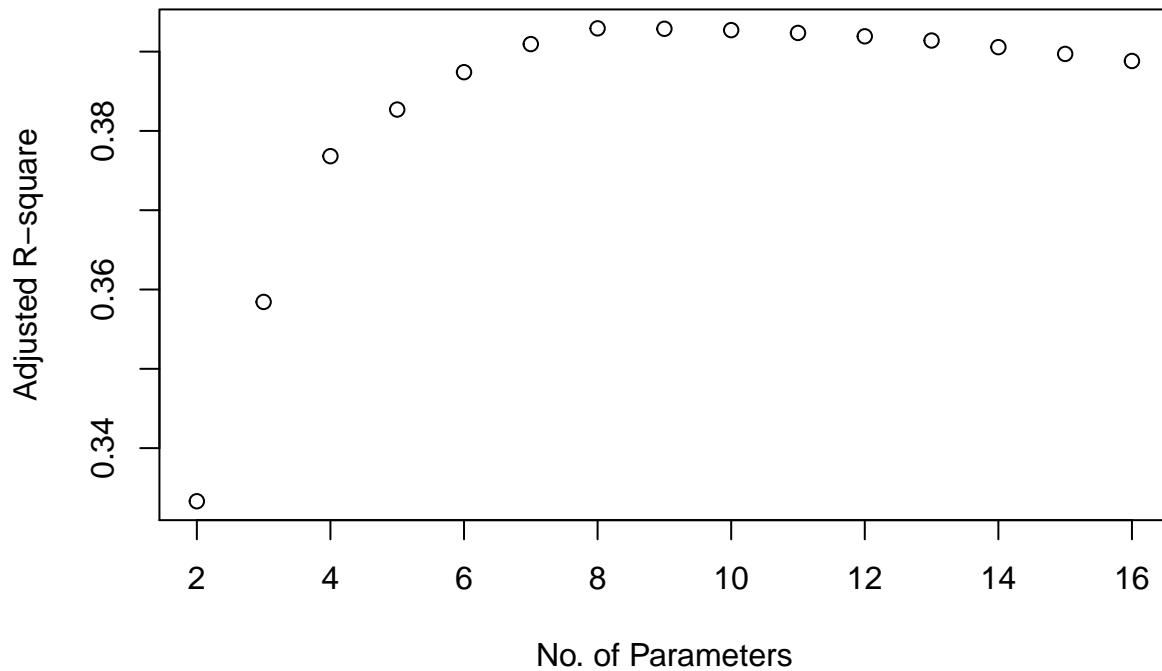
```
AIC <- 50*log(rs$rss/50) + (2:16)*2  
dim(AIC)
```

```
## NULL
```

```
plot(AIC ~ I(1:15), ylab="AIC", xlab="Number of Predictors")
```



```
plot(2:16,rs$adjr2,xlab="No. of Parameters",ylab="Adjusted R-square")
```



```
which.max(rs$adjsr2)
```

```
## [1] 7
```

### 3 Regresión logística

El objetivo de este apartado será comprobar si la puntuación del test DMSES (total o de alguno de sus apartados) puede ayudar a discriminar entre pacientes que controlan la diabetes y los que no.

#### 3.1 Preparación de los ficheros para ‘train’ y ‘test’

```
# cálculo del numero de registros para el training
# según la proporción de registros dedicado al training
pct.train <- 0.90

n <- nrow(datos)
n.train <- floor(n*pct.train)

set.seed(123)
ind.training <- sample(1:n,n.train)
length(ind.training)
```

```
## [1] 630
```

```

datos.train <- datos[ind.training,]
datos.test <- datos[-ind.training,]

dim(datos.train)

## [1] 630 73

dim(datos.test)

## [1] 70 73

```

### 3.2 Modelo DMSES subscore Diet

```

logdiet <- glm(alerta ~ DMSES.Diet, data = datos.train, family = "binomial")
summary(logdiet)

##
## Call:
## glm(formula = alerta ~ DMSES.Diet, family = "binomial", data = datos.train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.4594   -0.6957    0.3187    0.6533    2.3759
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.1710    0.1046   1.636   0.102
## DMSES.Diet   -2.8435    0.2103 -13.524  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 871.53 on 629 degrees of freedom
## Residual deviance: 574.09 on 628 degrees of freedom
## AIC: 578.09
##
## Number of Fisher Scoring iterations: 4

predicciones <- predict(logdiet,newdata=datos.test[, -c(1)],type='response')
predicciones.categ <- ifelse(predicciones > 0.5,1,0)
predicciones.categ <- factor(predicciones.categ,levels=c(0,1),labels=c("No","Sí"))

# Confusion matrix
confusionMatrix(data=predicciones.categ, reference=datos.test$alerta)

```

```

## Confusion Matrix and Statistics
##
## Reference

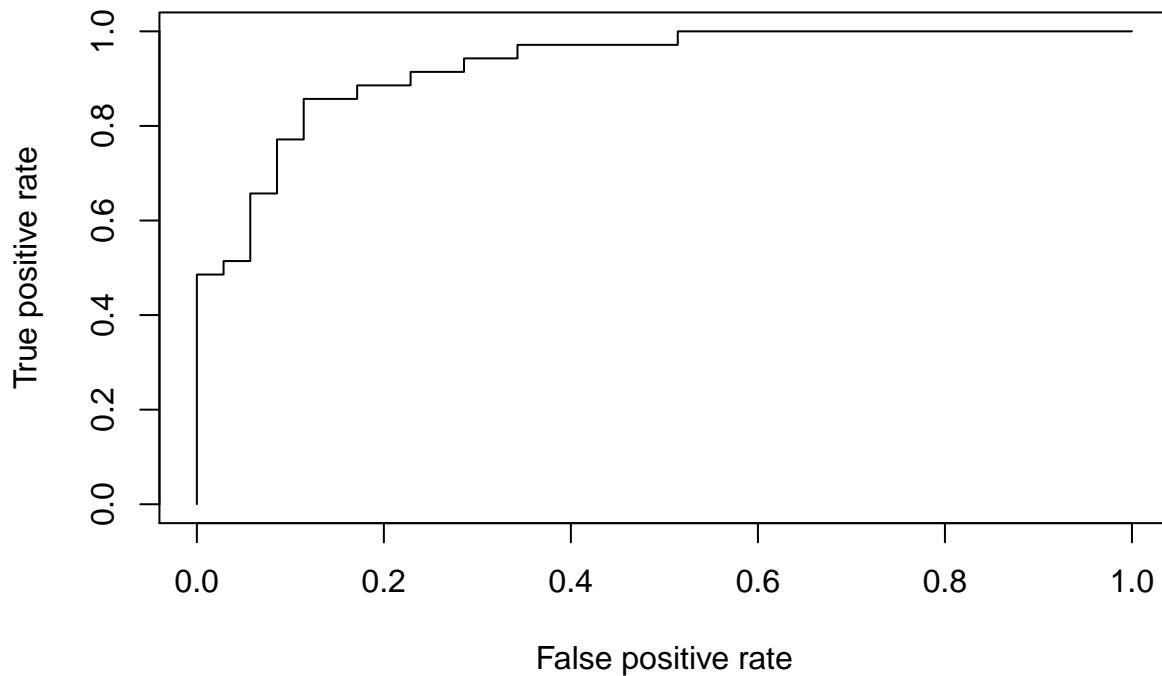
```

```

## Prediction No Si
##           No 27  4
##           Sí  8 31
##
##           Accuracy : 0.8286
##           95% CI : (0.7197, 0.9082)
##   No Information Rate : 0.5
##   P-Value [Acc > NIR] : 1.124e-08
##
##           Kappa : 0.6571
##
##   Mcnemar's Test P-Value : 0.3865
##
##           Sensitivity : 0.7714
##           Specificity : 0.8857
##           Pos Pred Value : 0.8710
##           Neg Pred Value : 0.7949
##           Prevalence : 0.5000
##           Detection Rate : 0.3857
##   Detection Prevalence : 0.4429
##           Balanced Accuracy : 0.8286
##
##           'Positive' Class : No
##

# ROC and AUC
pr <- prediction(predicciones, datos.test$alerta)
# TPR = sensitivity, FPR=specificity
prf <- performance(pr, measure = "tpr", x.measure = "fpr")
plot(prf)

```



```
auc <- performance(pr, measure = "auc")
(auc <- auc@y.values[[1]])
```

```
## [1] 0.9273469
```

```
#
#
# hay mejora si añadimos algunos predictores?
```

```
logdiet <- glm(alerta ~ DMSES.Diet + bmi + dmdura + age, data = datos.train, family = "binomial")
summary(logdiet)
```

```
##
## Call:
## glm(formula = alerta ~ DMSES.Diet + bmi + dmdura + age, family = "binomial",
##      data = datos.train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.4339   -0.6488    0.2882    0.6549    2.3968
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 3.36401   0.93008  3.617 0.000298 ***
## DMSES.Diet -2.84441   0.21587 -13.177 < 2e-16 ***
```

```

## bmi      -0.03893   0.01756  -2.217 0.026638 *
## dmdura   0.02090   0.01450   1.441 0.149525
## age     -0.03727   0.01145  -3.256 0.001129 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 871.53  on 629  degrees of freedom
## Residual deviance: 560.64  on 625  degrees of freedom
## AIC: 570.64
##
## Number of Fisher Scoring iterations: 5

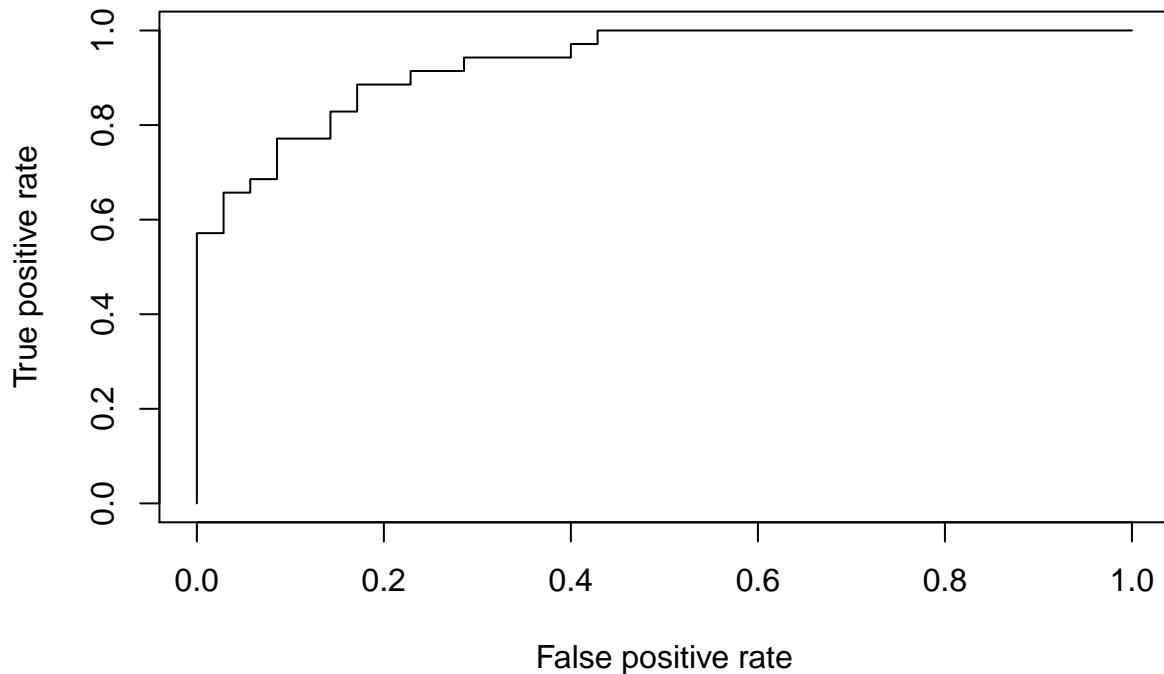
predicciones <- predict(logdiet,newdata=datos.test[,-c(1)],type='response')
predicciones.categ <- ifelse(predicciones > 0.5,1,0)
predicciones.categ <- factor(predicciones.categ,levels=c(0,1),labels=c("No","Sí"))

# Confusion matrix
confusionMatrix(data=predicciones.categ, reference=datos.test$alerta)

## Confusion Matrix and Statistics
##
##             Reference
## Prediction No Si
##       No 28  4
##       Si  7 31
##
##                 Accuracy : 0.8429
##                 95% CI : (0.7362, 0.9189)
##       No Information Rate : 0.5
##       P-Value [Acc > NIR] : 2.233e-09
##
##                 Kappa : 0.6857
##
##       Mcnemar's Test P-Value : 0.5465
##
##                 Sensitivity : 0.8000
##                 Specificity  : 0.8857
##       Pos Pred Value : 0.8750
##       Neg Pred Value : 0.8158
##                 Prevalence : 0.5000
##                 Detection Rate : 0.4000
##       Detection Prevalence : 0.4571
##       Balanced Accuracy : 0.8429
##
##       'Positive' Class : No
##

# ROC and AUC
pr <- prediction(predicciones, datos.test$alerta)
# TPR = sensitivity, FPR=specificity
prf <- performance(pr, measure = "tpr", x.measure = "fpr")
plot(prf)

```



```
auc <- performance(pr, measure = "auc")
(auc <- auc@y.values[[1]])
```

```
## [1] 0.9322449
```

### 3.3 Modelo DMSES subscore Monitor

```
logmonitor <- glm(alerta ~ DMSES.Monitor, data = datos.train, family = "binomial")
summary(logmonitor)
```

```
##
## Call:
## glm(formula = alerta ~ DMSES.Monitor, family = "binomial", data = datos.train)
##
## Deviance Residuals:
##      Min        1Q     Median        3Q       Max
## -2.3135  -0.7761   0.3617   0.7996   2.2797
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.1367    0.0977   1.399   0.162
```

```

## DMSES.Monitor -5.0037      0.4026 -12.430   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 871.53  on 629  degrees of freedom
## Residual deviance: 637.30  on 628  degrees of freedom
## AIC: 641.3
##
## Number of Fisher Scoring iterations: 4

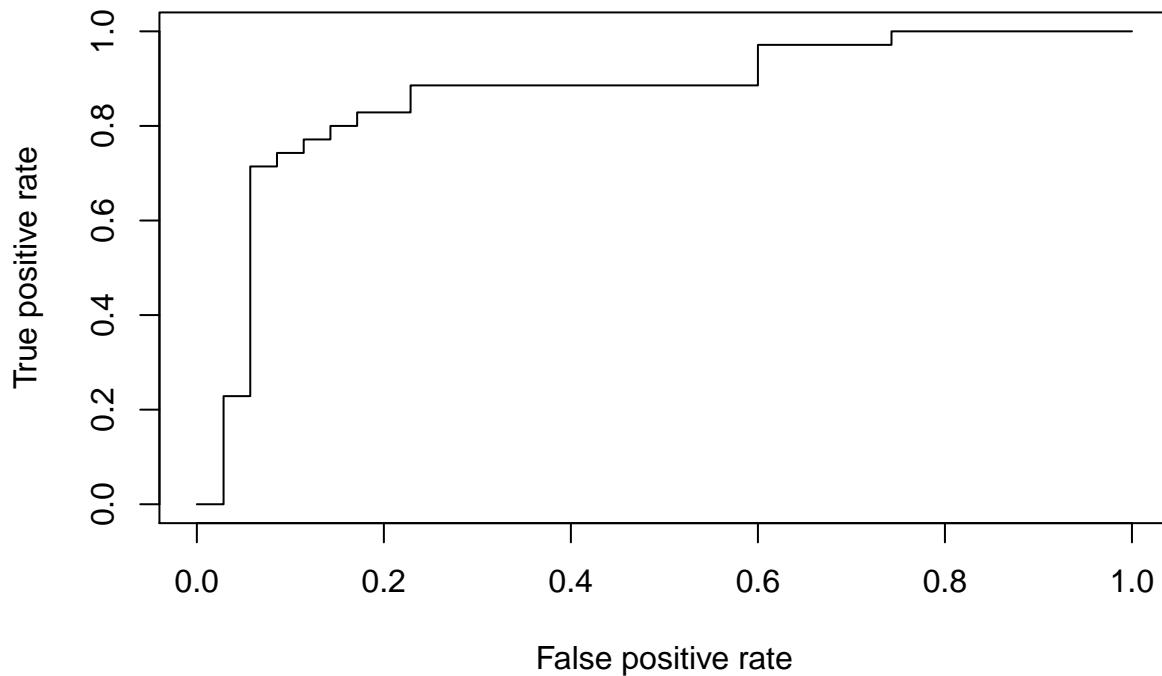
predicciones <- predict(logmonitor,newdata=datos.test[,-c(1)],type='response')
predicciones.categ <- ifelse(predicciones > 0.5,1,0)
predicciones.categ <- factor(predicciones.categ,levels=c(0,1),labels=c("No","Si"))

# Confusion matrix
confusionMatrix(data=predicciones.categ, reference=datos.test$alerta)

## Confusion Matrix and Statistics
##
##             Reference
## Prediction No Si
##       No 29  6
##       Si  6 29
##
##               Accuracy : 0.8286
##                   95% CI : (0.7197, 0.9082)
##       No Information Rate : 0.5
##       P-Value [Acc > NIR] : 1.124e-08
##
##               Kappa : 0.6571
##
##   Mcnemar's Test P-Value : 1
##
##               Sensitivity : 0.8286
##               Specificity : 0.8286
##       Pos Pred Value : 0.8286
##       Neg Pred Value : 0.8286
##           Prevalence : 0.5000
##       Detection Rate : 0.4143
##   Detection Prevalence : 0.5000
##       Balanced Accuracy : 0.8286
##
##       'Positive' Class : No
##

# ROC and AUC
pr <- prediction(predicciones, datos.test$alerta)
# TPR = sensitivity, FPR=specificity
prf <- performance(pr, measure = "tpr", x.measure = "fpr")
plot(prf)

```



```
auc <- performance(pr, measure = "auc")
(auc <- auc@y.values[[1]])
```

```
## [1] 0.8653061
```

### 3.4 Modelo DMSES subscore Regimen

```
logregimen <- glm(alerta ~ DMSES.Regimen, data = datos.train, family = "binomial")
summary(logregimen)
```

```
##
## Call:
## glm(formula = alerta ~ DMSES.Regimen, family = "binomial", data = datos.train)
##
## Deviance Residuals:
##      Min        1Q     Median        3Q       Max
## -2.4598   -1.1805    0.8935    1.1648    1.3501
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.11596   0.08078  1.436  0.15111
## DMSES.Regimen -0.99971   0.34427 -2.904  0.00369 **
## ---
```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 871.53  on 629  degrees of freedom
## Residual deviance: 860.52  on 628  degrees of freedom
## AIC: 864.52
##
## Number of Fisher Scoring iterations: 3

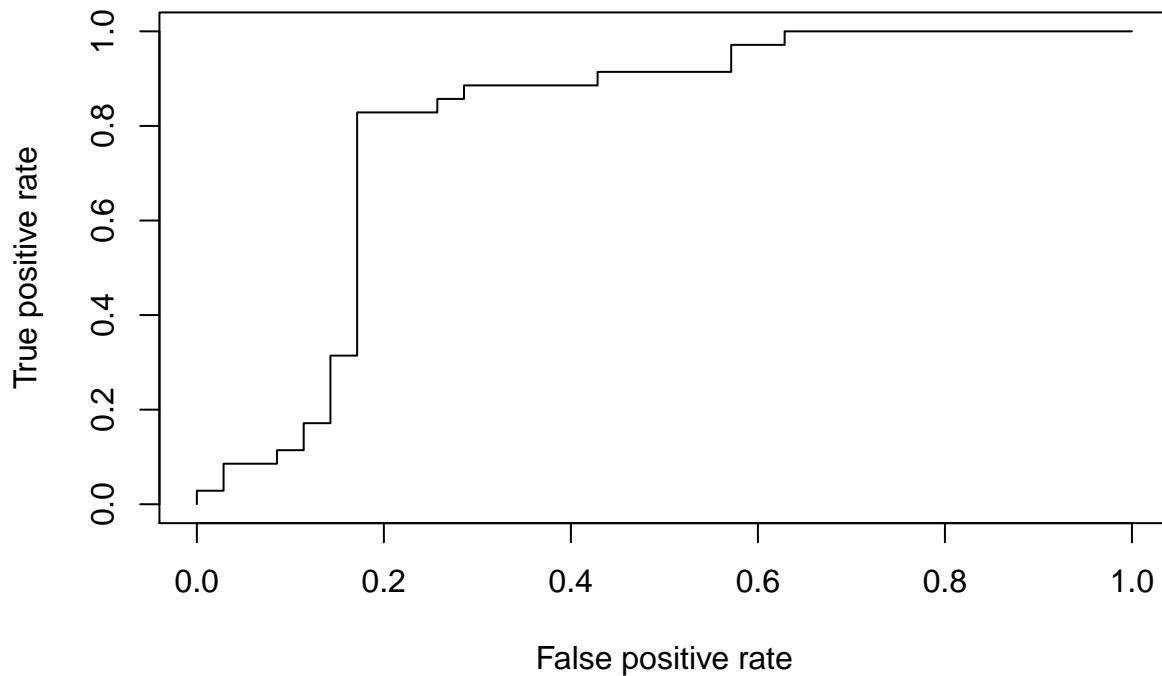
predicciones <- predict(logregimen,newdata=datos.test[,-c(1)],type='response')
predicciones.categ <- ifelse(predicciones > 0.5,1,0)
predicciones.categ <- factor(predicciones.categ,levels=c(0,1),labels=c("No","Sí"))

# Confusion matrix
confusionMatrix(data=predicciones.categ, reference=datos.test$alerta)

## Confusion Matrix and Statistics
##
##             Reference
## Prediction No Sí
##       No 10  0
##       Sí 25 35
##
##             Accuracy : 0.6429
##                 95% CI : (0.5193, 0.7539)
##     No Information Rate : 0.5
##     P-Value [Acc > NIR] : 0.01123
##
##             Kappa : 0.2857
##
## Mcnemar's Test P-Value : 1.587e-06
##
##             Sensitivity : 0.2857
##             Specificity : 1.0000
##     Pos Pred Value : 1.0000
##     Neg Pred Value : 0.5833
##             Prevalence : 0.5000
##     Detection Rate : 0.1429
## Detection Prevalence : 0.1429
##     Balanced Accuracy : 0.6429
##
##     'Positive' Class : No
##

# ROC and AUC
pr <- prediction(predicciones, datos.test$alerta)
# TPR = sensitivity, FPR=specificity
prf <- performance(pr, measure = "tpr", x.measure = "fpr")
plot(prf)

```



```
auc <- performance(pr, measure = "auc")
(auc <- auc@y.values[[1]])
```

```
## [1] 0.802449
```

### 3.5 Modelo DMSES subscore Physical

```
logphysical <- glm(alerta ~ DMSES.Physical, data = datos.train, family = "binomial")
summary(logphysical)
```

```
##
## Call:
## glm(formula = alerta ~ DMSES.Physical, family = "binomial", data = datos.train)
##
## Deviance Residuals:
##      Min        1Q     Median        3Q       Max
## -2.047   -1.086    0.688    1.023    1.660
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.12349   0.08406   1.469    0.142
## DMSES.Physical -1.53195   0.20506  -7.471 7.98e-14 ***
## ---
```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 871.53  on 629  degrees of freedom
## Residual deviance: 808.17  on 628  degrees of freedom
## AIC: 812.17
##
## Number of Fisher Scoring iterations: 4

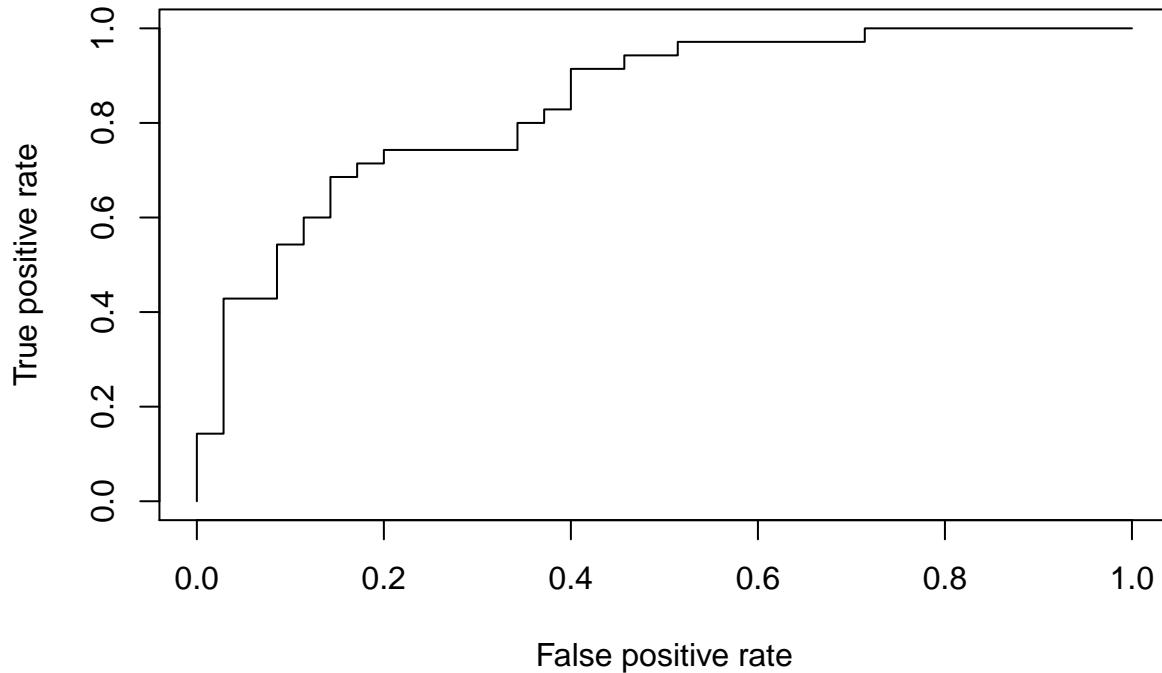
predicciones <- predict(logphysical,newdata=datos.test[,-c(1)],type='response')
predicciones.categ <- ifelse(predicciones > 0.5,1,0)
predicciones.categ <- factor(predicciones.categ,levels=c(0,1),labels=c("No","Sí"))

# Confusion matrix
confusionMatrix(data=predicciones.categ, reference=datos.test$alerta)

## Confusion Matrix and Statistics
##
##             Reference
## Prediction No Sí
##       No 23   9
##       Sí 12  26
##
##             Accuracy : 0.7
##                 95% CI : (0.5787, 0.8038)
##       No Information Rate : 0.5
##       P-Value [Acc > NIR] : 0.0005466
##
##             Kappa : 0.4
##
## Mcnemar's Test P-Value : 0.6625206
##
##             Sensitivity : 0.6571
##             Specificity : 0.7429
##       Pos Pred Value : 0.7188
##       Neg Pred Value : 0.6842
##             Prevalence : 0.5000
##       Detection Rate : 0.3286
## Detection Prevalence : 0.4571
##       Balanced Accuracy : 0.7000
##
##       'Positive' Class : No
##

# ROC and AUC
pr <- prediction(predicciones, datos.test$alerta)
# TPR = sensitivity, FPR=specificity
prf <- performance(pr, measure = "tpr", x.measure = "fpr")
plot(prf)

```



```
auc <- performance(pr, measure = "auc")
(auc <- auc@y.values[[1]])
```

```
## [1] 0.84
```

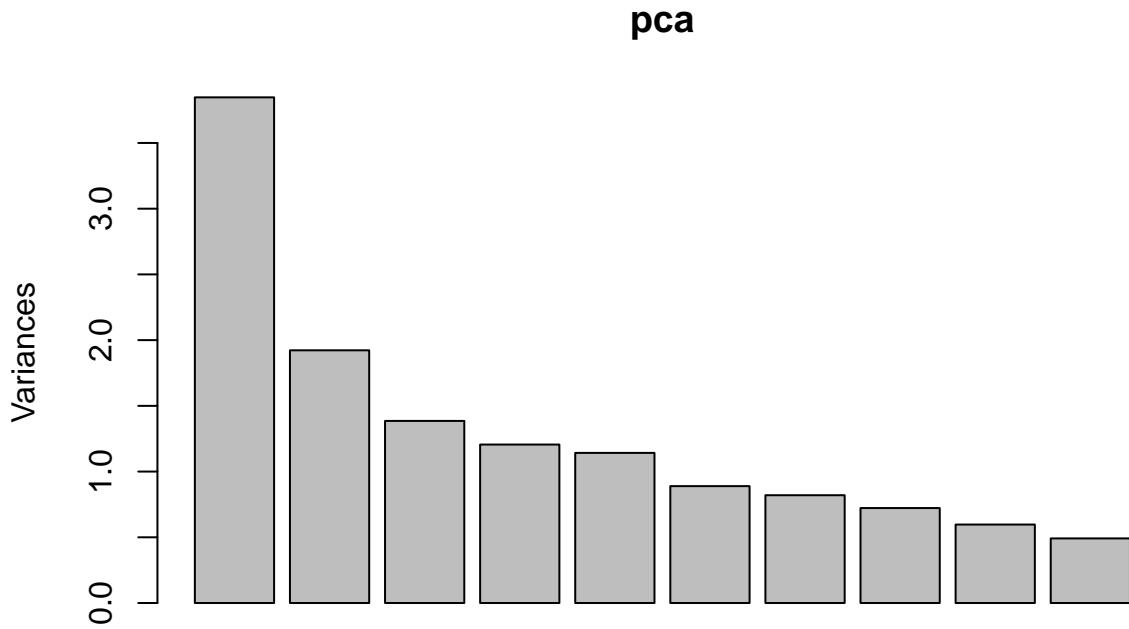
## 4. Análisis multivariante de datos

### 4.1 Análisis de componentes principales

```
pca <- prcomp(datos[,vars_cont],scale. = TRUE)
summary(pca)
```

```
## Importance of components:
##                 PC1      PC2      PC3      PC4      PC5      PC6      PC7
## Standard deviation   1.9614  1.3865  1.17696  1.0979  1.06861  0.94293  0.90553
## Proportion of Variance 0.2748  0.1373  0.09895  0.0861  0.08157  0.06351  0.05857
## Cumulative Proportion  0.2748  0.4121  0.51104  0.5971  0.67871  0.74221  0.80078
##                  PC8      PC9      PC10     PC11     PC12     PC13     PC14
## Standard deviation   0.8499  0.77263  0.7010  0.65595  0.62517  0.39650  1.46e-15
## Proportion of Variance 0.0516  0.04264  0.0351  0.03073  0.02792  0.01123  0.00e+00
## Cumulative Proportion  0.8524  0.89502  0.9301  0.96085  0.98877  1.00000  1.00e+00
```

```
plot(pca)
```

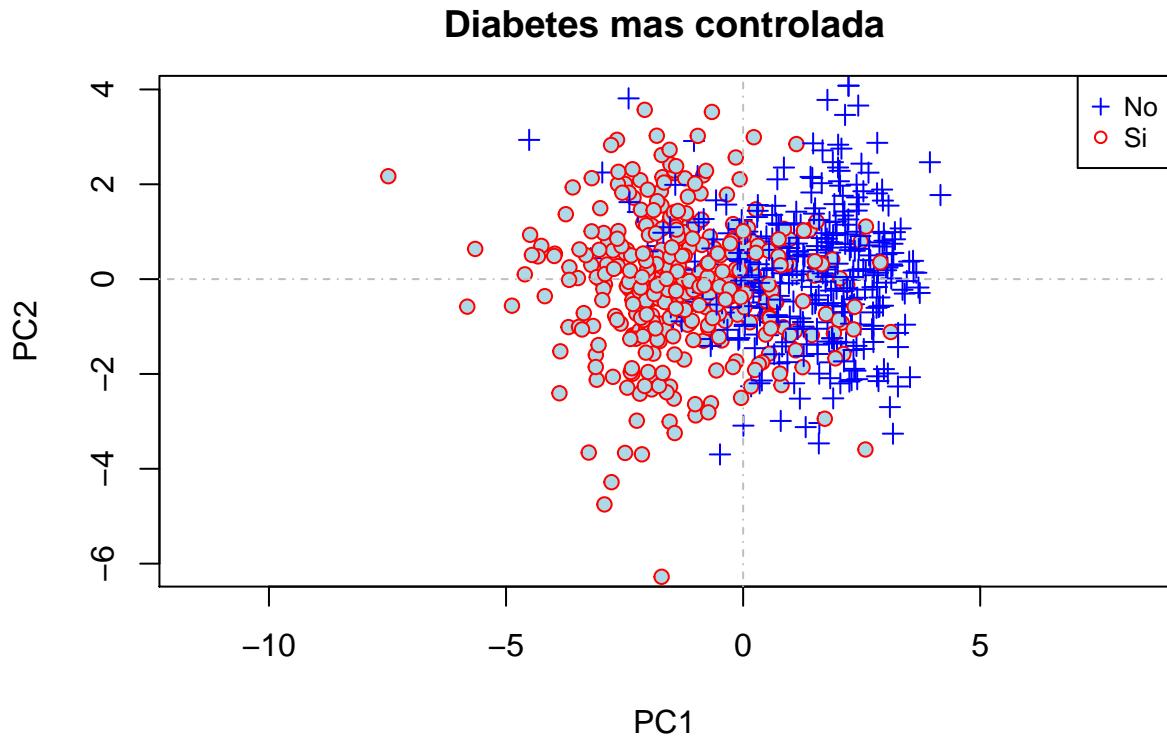


```
pca$rotation[,1:2]
```

```
##          PC1        PC2
## age      0.120473735  0.40392741
## dmdura   -0.003866627  0.40279170
## hba1c    -0.342354967 -0.12541985
## ldl      -0.048651944 -0.34591508
## hdl      0.004776580 -0.17933358
## trig     -0.071672193 -0.28174001
## sbp      -0.050084242 -0.36415949
## dbp      -0.069185880 -0.48999049
## DMSES.Diet 0.463976598 -0.05343762
## DMSES.Monitor 0.453296921 -0.07260538
## DMSES.Physical 0.368541298 -0.18103332
## DMSES.Regimen 0.217607148 -0.01393538
## DMSES.Total 0.498118566 -0.10601664
## DK.10     -0.037313670 -0.05137537
```

```
al <- as.numeric(datos$alerta)
MASS::eqscplot(pca$x[,1], pca$x[,2], pch=c(3,21)[al], col=c("blue","red")[al],
               bg="lightblue", xlab="PC1", ylab="PC2")
abline(h=0, v=0, lty=4, col="gray")
```

```
legend("topright",pch=c(3,21),col=c("blue","red"), cex=0.8,legend=c("No", "Si"))
title(main="Diabetes mas controlada",line=1)
```



```
summary(pca)$importance[,1:14]
```

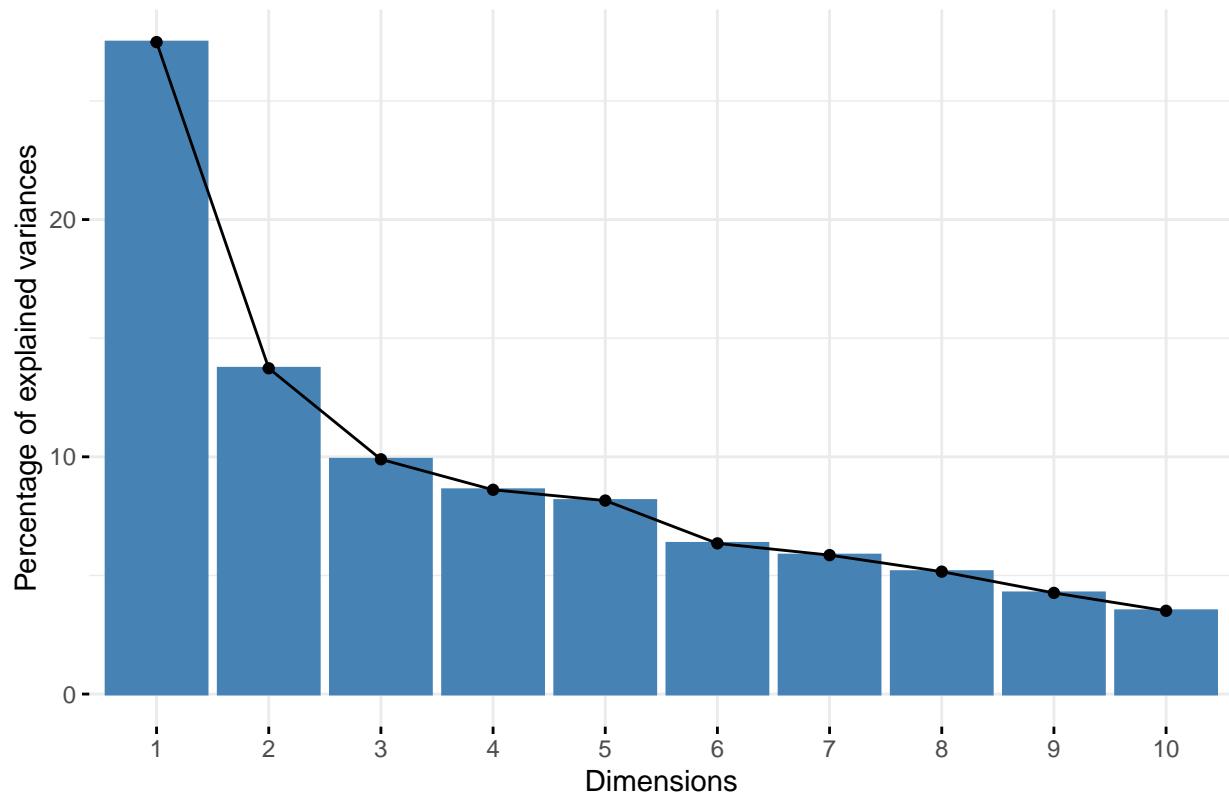
```
##          PC1       PC2       PC3       PC4       PC5       PC6
## Standard deviation 1.961366 1.386494 1.176962 1.097902 1.06861 0.9429273
## Proportion of Variance 0.274780 0.137310 0.098950 0.086100 0.08157 0.0635100
## Cumulative Proportion 0.274780 0.412090 0.511040 0.597140 0.67871 0.7422100
##          PC7       PC8       PC9       PC10      PC11
## Standard deviation 0.9055297 0.8499058 0.7726264 0.7010122 0.655951
## Proportion of Variance 0.0585700 0.0516000 0.0426400 0.0351000 0.030730
## Cumulative Proportion 0.8007800 0.8523800 0.8950200 0.9301200 0.960850
##          PC12      PC13      PC14
## Standard deviation 0.6251666 0.3964954 1.459512e-15
## Proportion of Variance 0.0279200 0.0112300 0.000000e+00
## Cumulative Proportion 0.9887700 1.0000000 1.000000e+00
```

```
library(factoextra)
```

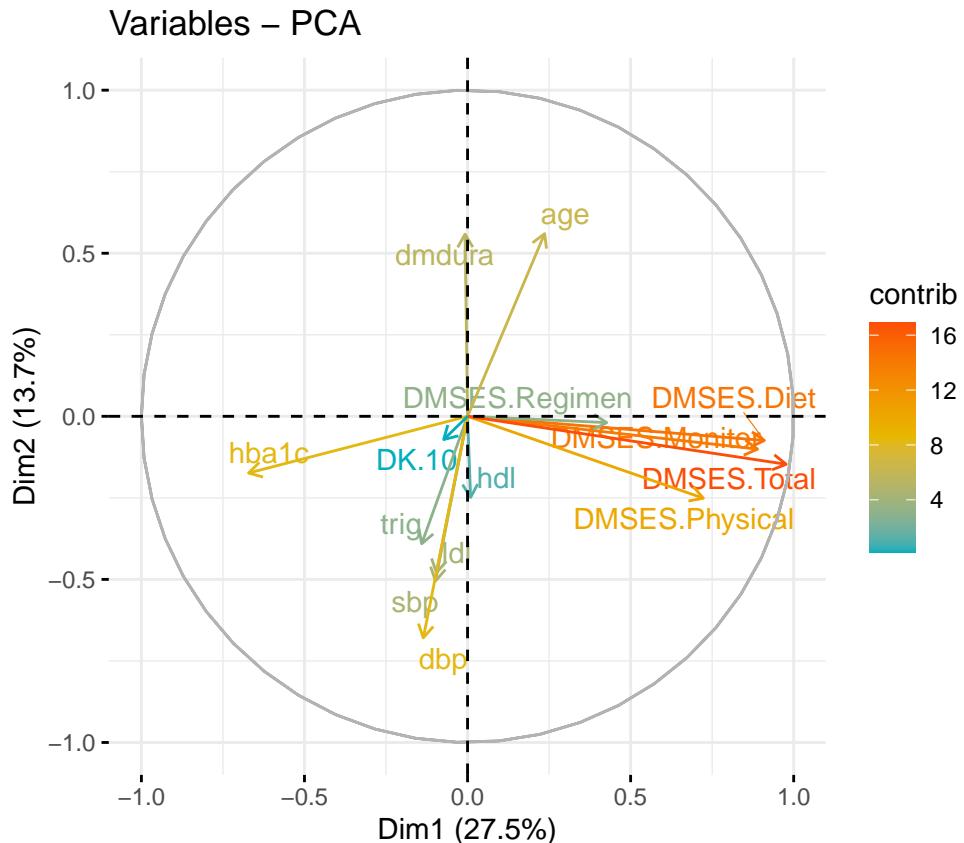
```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
fviz_eig(pca)
```

Scree plot



```
fviz_pca_var(pca,col.var = "contrib",
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
             repel = TRUE )
```



El análisis gráfico de componentes principales muestra la contribución de las variables en las dos primeras componentes principales.

## 4.2 Análisis de conglomerados

```
library(cluster)

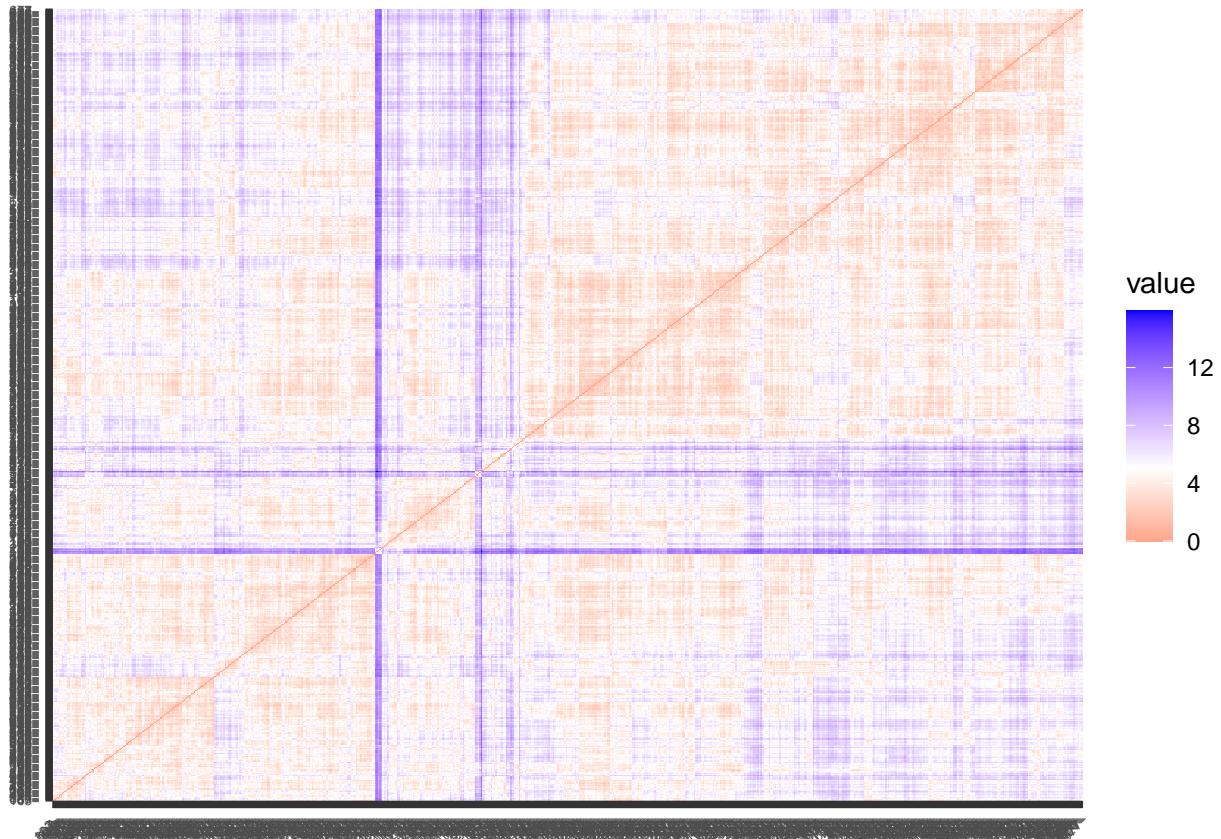
# Fijamos la semilla aleatoria
set.seed(123)

df <- scale(datos[,vars_cont])

res.dist <- get_dist(df, method = "euclidean")
head(round(as.matrix(res.dist), 2))[, 1:5]
```

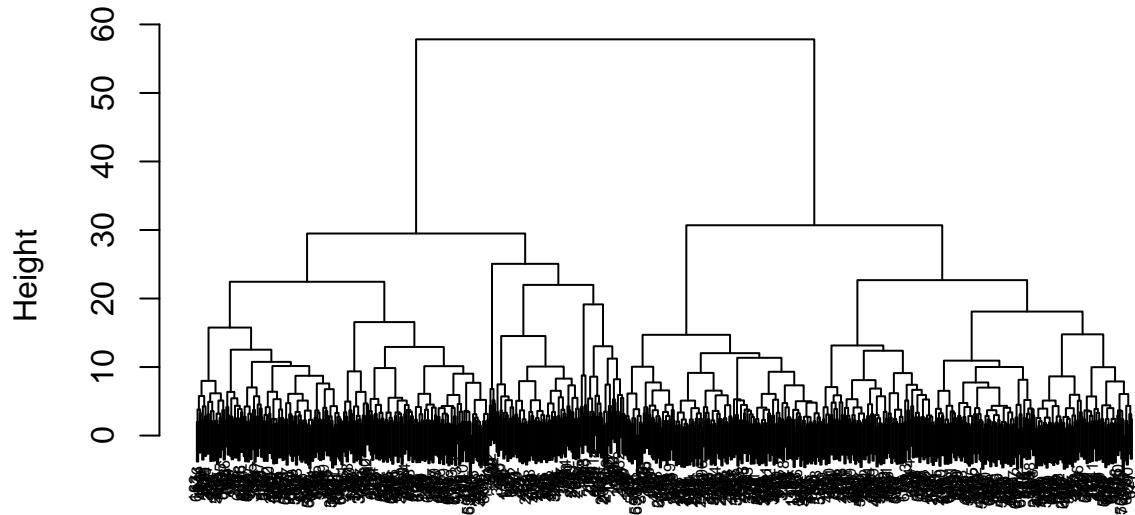
```
##      1   2   3   4   5
## 1 0.00 2.59 5.08 4.82 4.01
## 2 2.59 0.00 4.99 5.42 3.99
## 3 5.08 4.99 0.00 7.55 7.46
## 4 4.82 5.42 7.55 0.00 5.38
## 5 4.01 3.99 7.46 5.38 0.00
## 6 2.46 2.78 6.44 4.40 3.12
```

```
# Visualize the dissimilarity matrix  
fviz_dist(res.dist, lab_size = 5)
```



```
# Compute hierarchical clustering  
res.hc <- hclust(res.dist, method = "ward.D2")  
  
# Visualize  
plot(res.hc, cex = 0.5)
```

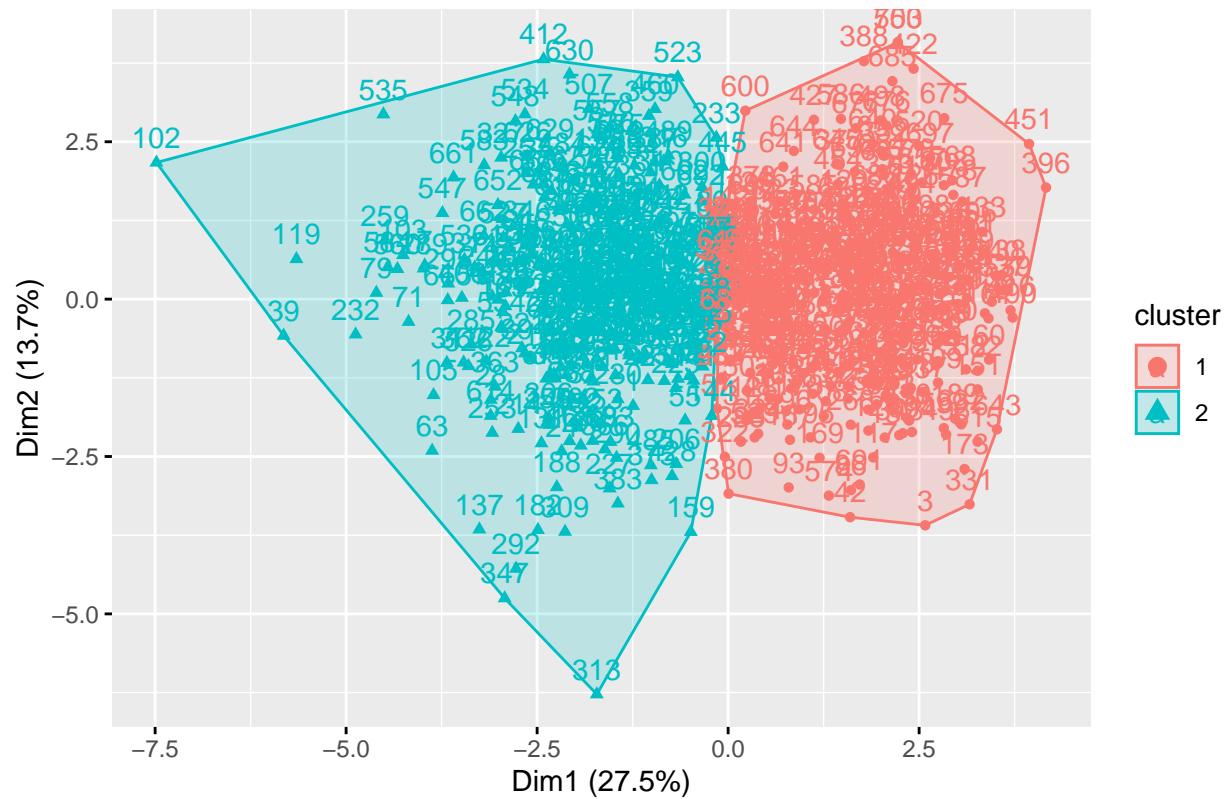
## Cluster Dendrogram



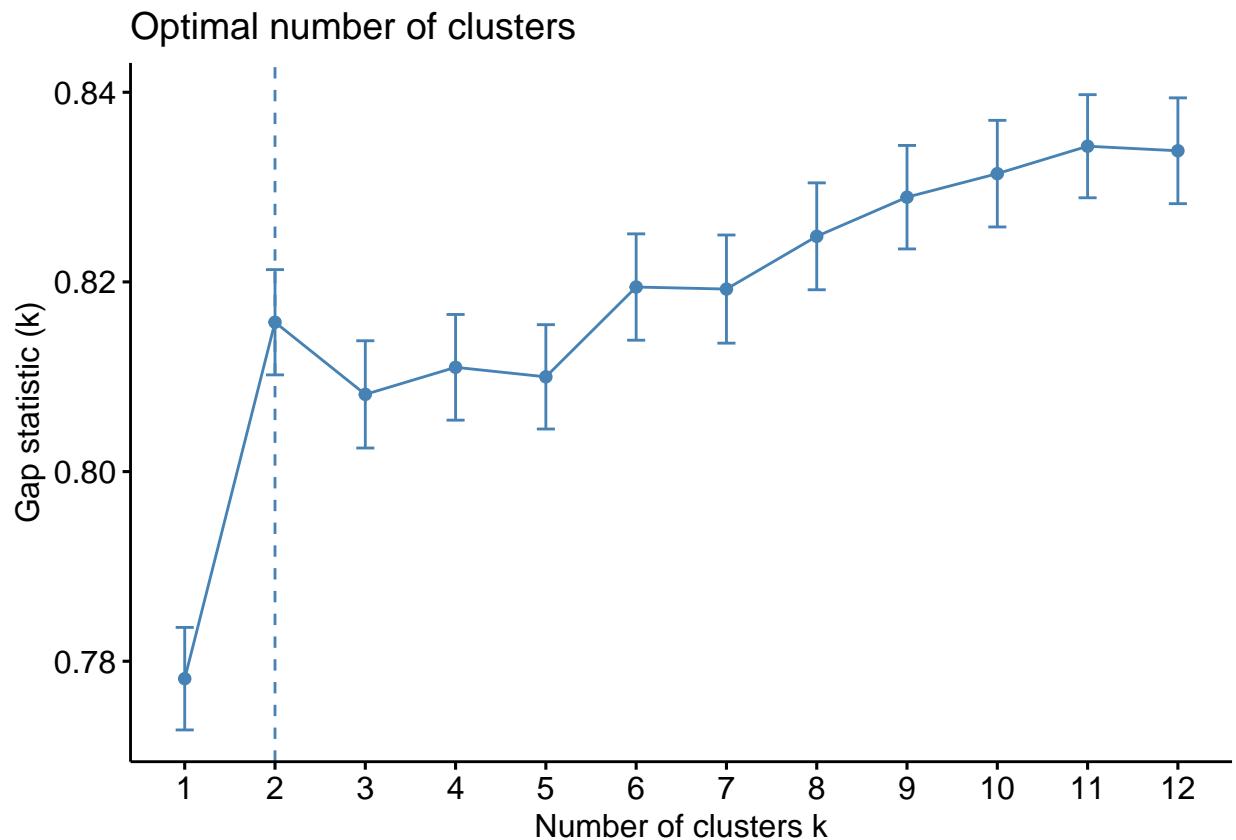
```
res.dist  
hclust (*, "ward.D2")
```

```
# Enhanced k-means clustering  
res.km <- eclust(df, "kmeans", nstart = 25, k.max=12)
```

## KMEANS Clustering



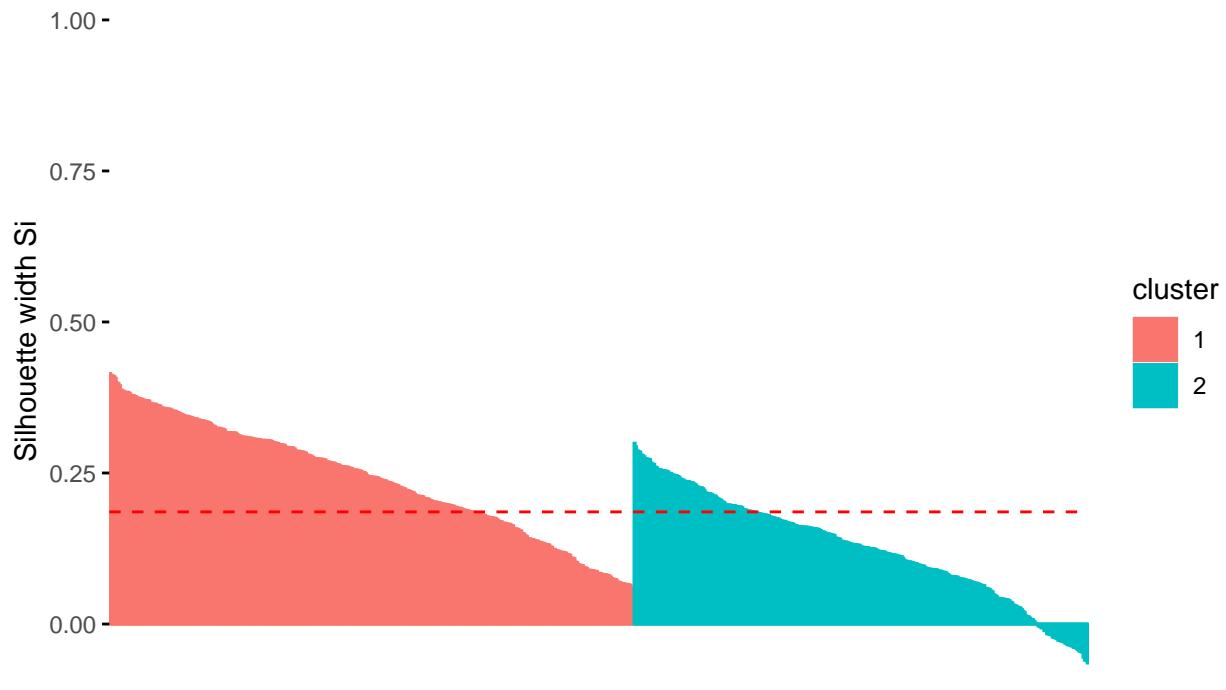
```
# Gap statistic plot  
fviz_gap_stat(res.km$gap_stat)
```



```
# Silhouette plot
fviz_silhouette(res.km)
```

```
##   cluster size ave.sil.width
## 1        1  375       0.24
## 2        2  325       0.13
```

Clusters silhouette plot  
 Average silhouette width: 0.19



```
# Optimal number of clusters using gap statistics
res.km$nbclust
```

```
## [1] 2
```

```
# Enhanced k-means clustering (forzando 11 conglomerados)
res.km11 <- eclust(df, FUNcluster = "kmeans", nstart = 25, k = 11)
```

```
# Gap statistic plot
fviz_gap_stat(res.km11$gap_stat)
```

```
# Silhouette plot
fviz_silhouette(res.km11)
```

```
library(cluster)

# Fijamos la semilla aleatoria
set.seed(123)

df <- scale(datos[,c("hba1c", "DMSES.Diet", "age")])

res.dist <- get_dist(df, method = "euclidean")
head(round(as.matrix(res.dist), 2))[, 1:5]
```

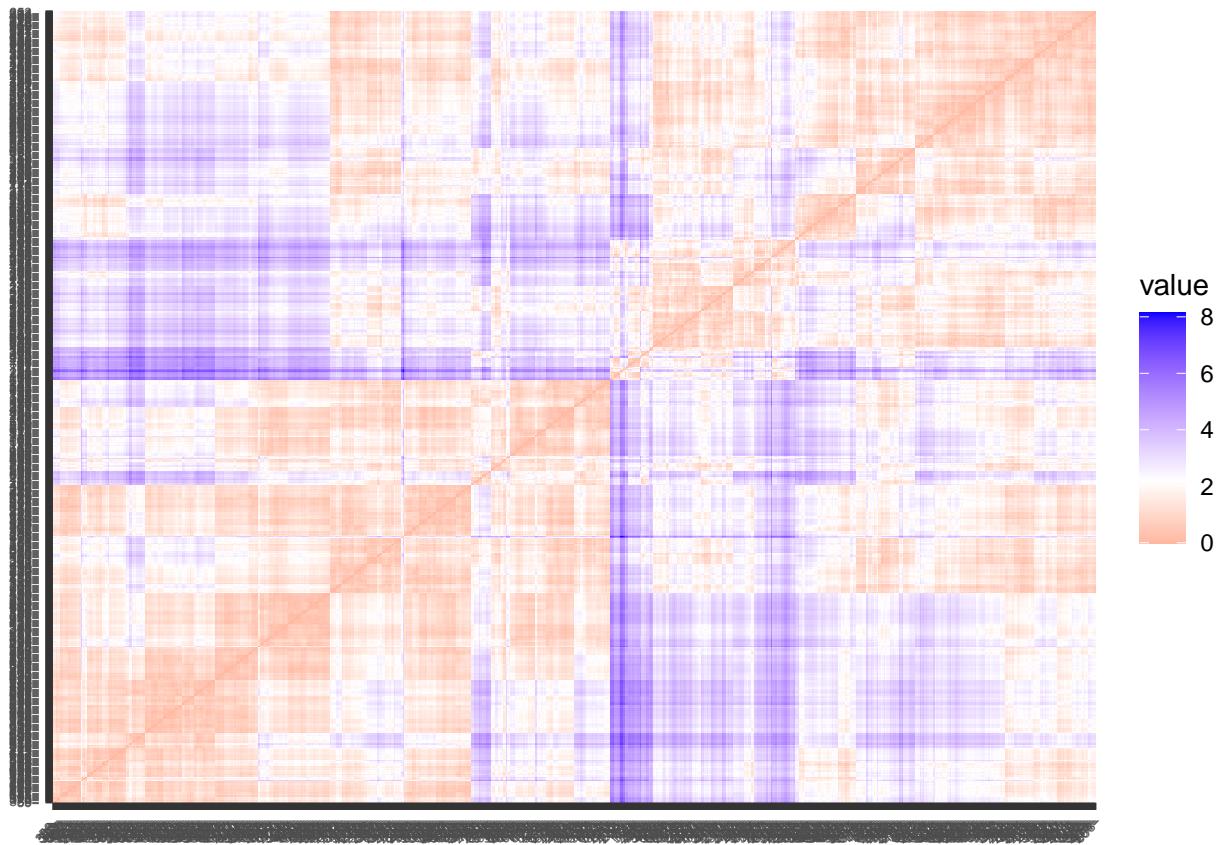
```
##      1     2     3     4     5
```

```

## 1 0.00 1.58 2.16 2.17 2.43
## 2 1.58 0.00 1.90 1.79 2.47
## 3 2.16 1.90 0.00 3.55 4.07
## 4 2.17 1.79 3.55 0.00 1.82
## 5 2.43 2.47 4.07 1.82 0.00
## 6 1.32 1.13 2.76 0.92 1.70

# Visualize the dissimilarity matrix
fviz_dist(res.dist, lab_size = 5)

```



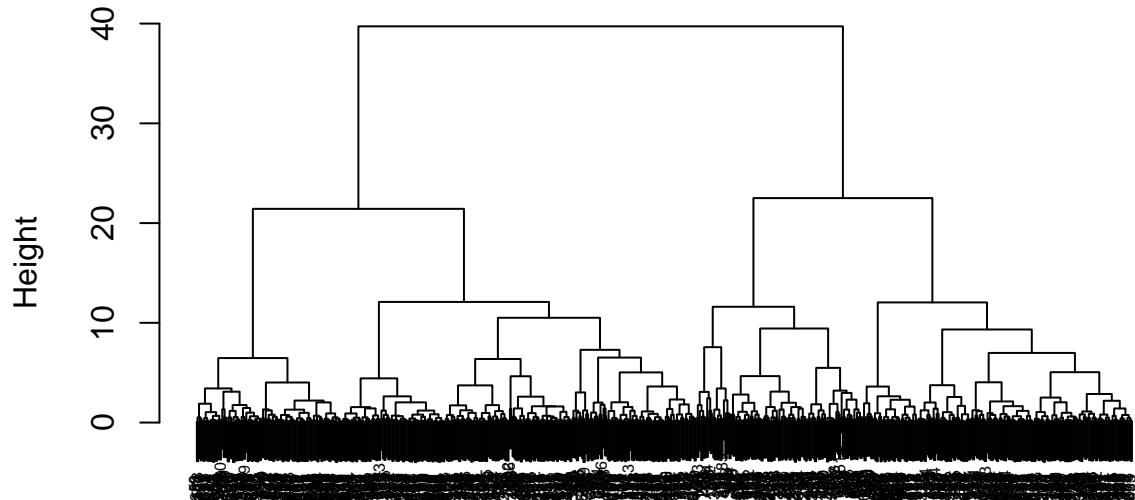
```

# Compute hierarchical clustering
res.hc <- hclust(res.dist, method = "ward.D2")

# Visualize
plot(res.hc, cex = 0.5)

```

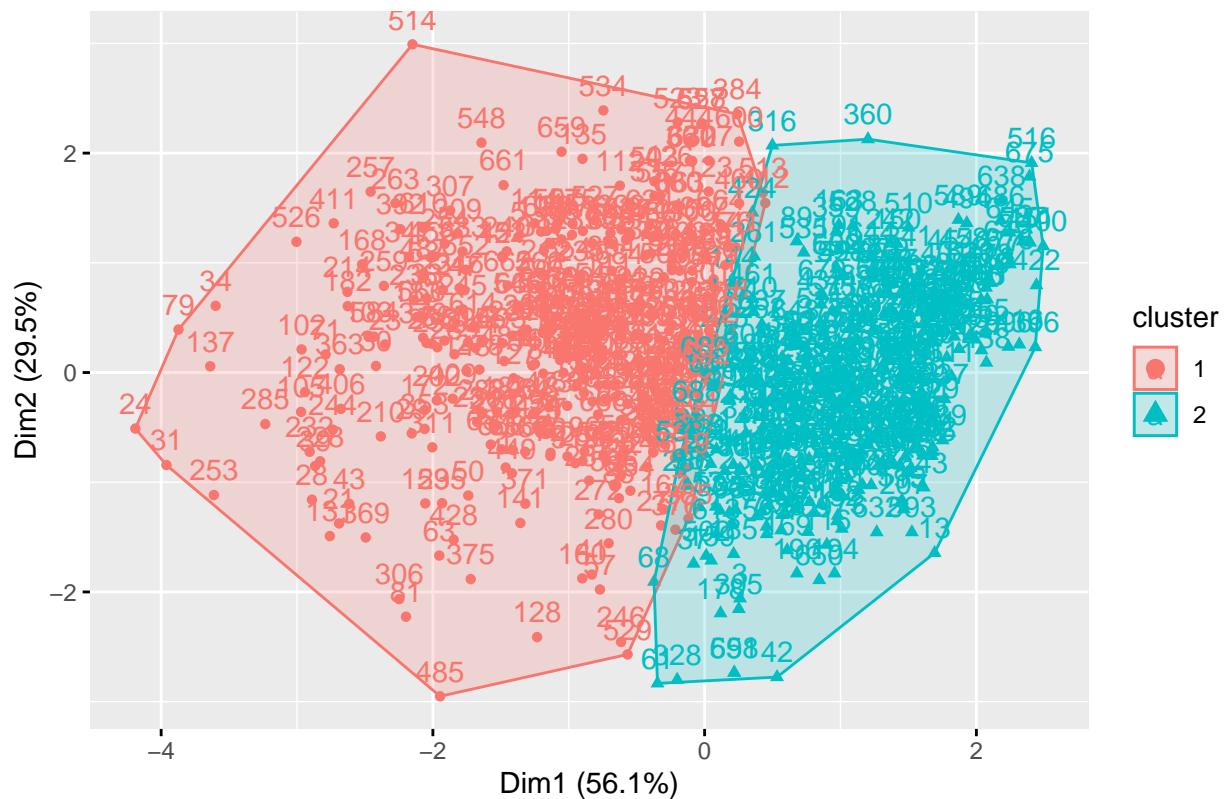
## Cluster Dendrogram



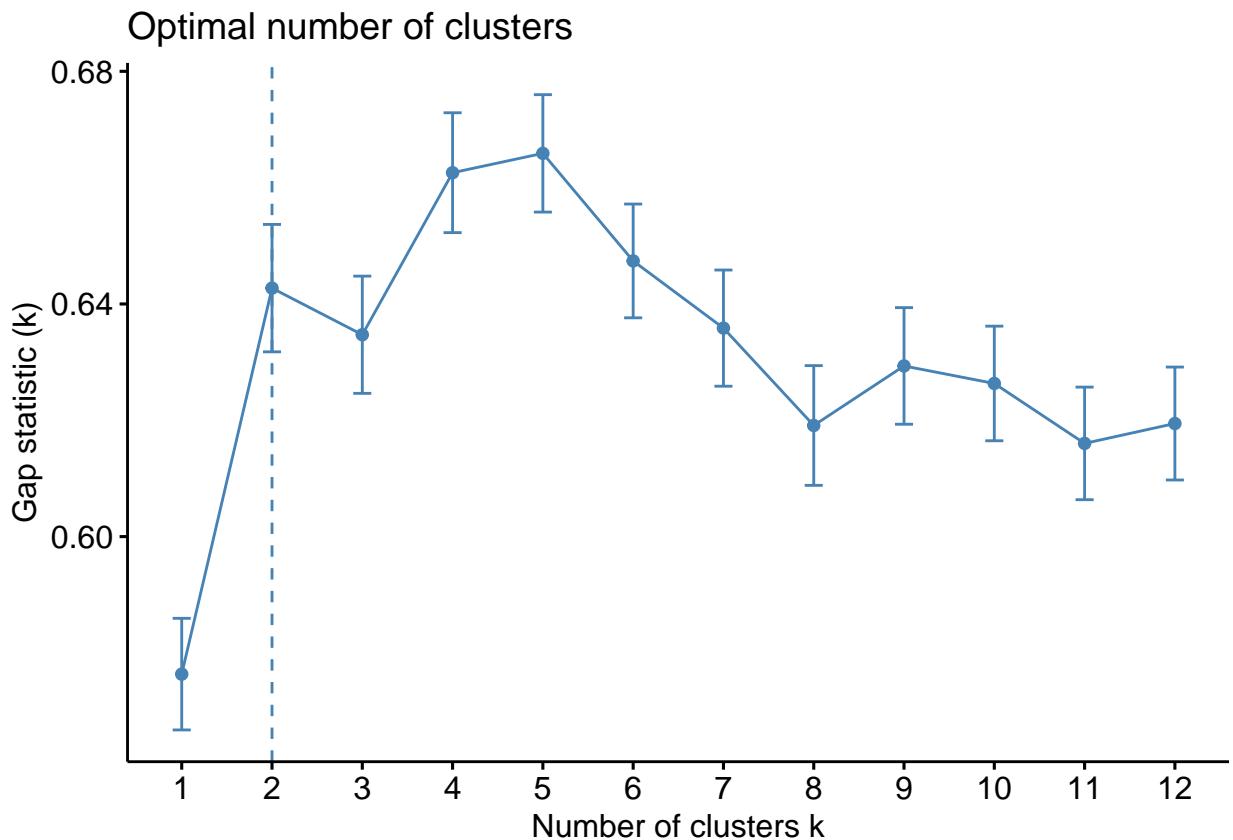
```
res.dist  
hclust (*, "ward.D2")
```

```
# Enhanced k-means clustering  
res.km <- eclust(df, "kmeans", nstart = 25, k.max=12)
```

## KMEANS Clustering



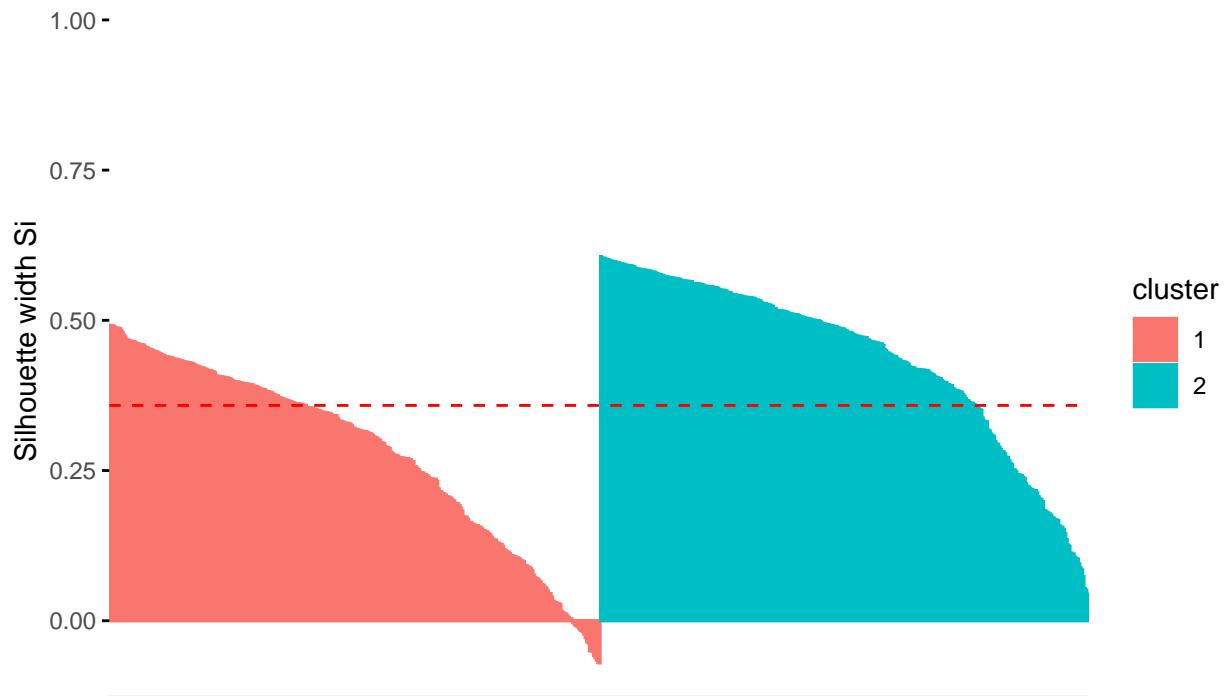
```
# Gap statistic plot
fviz_gap_stat(res.km$gap_stat)
```



```
# Silhouette plot  
fviz_silhouette(res.km)
```

```
##   cluster size ave.sil.width  
## 1       1   351      0.28  
## 2       2   349      0.44
```

Clusters silhouette plot  
Average silhouette width: 0.36



```
# Optimal number of clusters using gap statistics
res.km$nbclust
```

```
## [1] 2
```

#### 4.3 Análisis discriminante

```
# Alerta vs Diet
fit.cv <- lda(alerta ~ DMSES.Diet, data=datos, CV=TRUE)
# Assess the accuracy of the prediction
# percent correct for each category of G
ct <- table(datos$alerta, fit.cv$class)
diag(prop.table(ct, 1))
```

```
##           No         Sí
## 0.7957958 0.8283379
```

```
prop.table(ct, 1)
```

```
##
##           No         Sí
## 0.7957958 0.2042042
## 0.1716621 0.8283379
```

```

# total percent correct
sum(diag(prop.table(ct)))

## [1] 0.8128571

# Alerta vs Diet + age
fit.cv <- lda(alerta ~ DMSES.Diet + age, data=datos, CV=TRUE)
# Assess the accuracy of the prediction
# percent correct for each category of G
ct <- table(datos$alerta, fit.cv$class)
diag(prop.table(ct, 1))

##          No        Sí
## 0.8018018 0.8337875

prop.table(ct, 1)

##
##          No        Sí
## 0.8018018 0.1981982
## 0.1662125 0.8337875

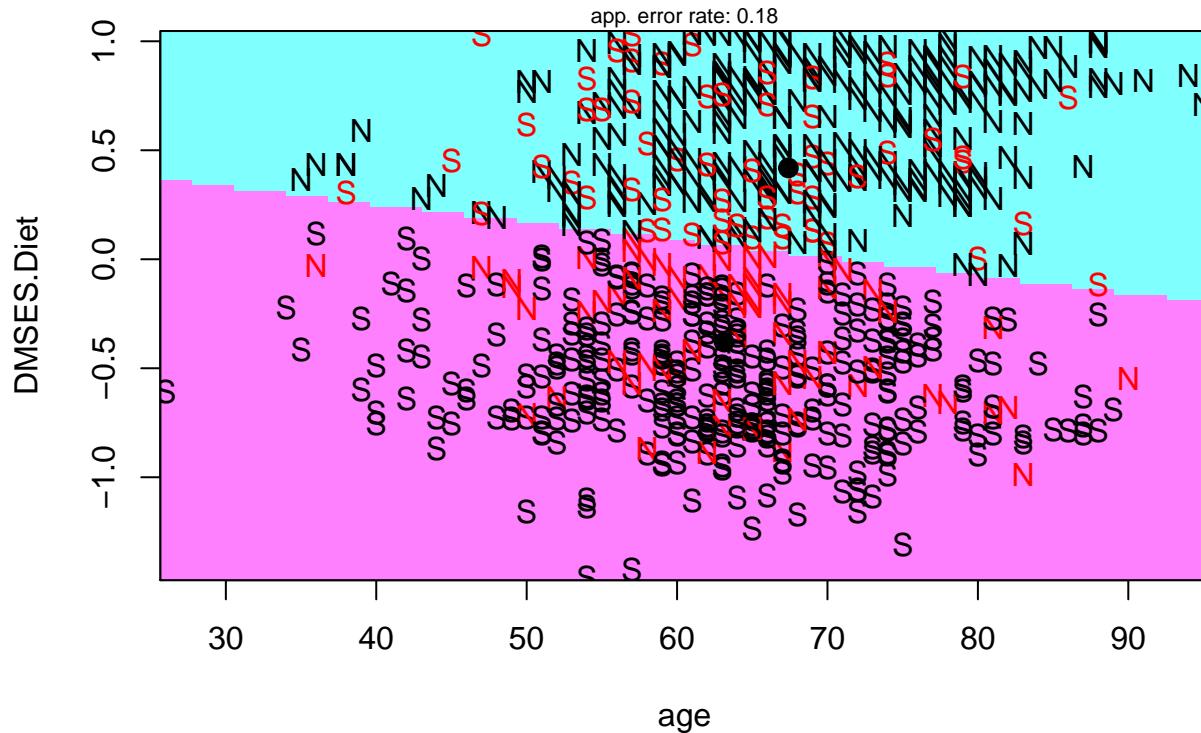
# total percent correct
sum(diag(prop.table(ct)))

## [1] 0.8185714

partimat(alerta ~ DMSES.Diet + age, data=datos, method="lda")

```

## Partition Plot



```
# Alerta vs otras variables
fit.cv <- lda(alerta ~ DMSES.Diet + age + ldl + hdl + trig + bmi, data=datos, CV=TRUE)
summary(fit.cv)
```

```
##          Length Class  Mode
## class       700   factor numeric
## posterior  1400   -none- numeric
## terms        3   terms call
## call         4   -none- call
## xlevels      0   -none- list
```

```
# Assess the accuracy of the prediction
# percent correct for each category of G
ct <- table(datos$alerta, fit.cv$class)
diag(prop.table(ct, 1))
```

```
##           No      Sí
## 0.8018018 0.8337875
```

```
prop.table(ct, 1)
```

```
##
##          No      Sí
## No  0.8018018 0.1981982
## Sí  0.1662125 0.8337875
```

```

# total percent correct
sum(diag(prop.table(ct)))

## [1] 0.8185714

prop.table(ct)

##          No         Sí
##  No 0.38142857 0.09428571
##  Sí 0.08714286 0.43714286

# Análisis discriminante cuadrático
datos.qda <- qda(alerta ~ DMSES.Diet + age, data=datos)
summary(datos.qda)

##      Length Class  Mode
## prior     2   -none- numeric
## counts    2   -none- numeric
## means     4   -none- numeric
## scaling   8   -none- numeric
## ldet      2   -none- numeric
## lev       2   -none- character
## N         1   -none- numeric
## call      3   -none- call
## terms     3   terms  call
## xlevels   0   -none- list

clq <- predict(datos.qda, datos[,c("DMSES.Diet","age")])$class
ct <- table(datos$alerta, clq)
prop.table(ct)

##      clq
##          No         Sí
##  No 0.37285714 0.10285714
##  Sí 0.08285714 0.44142857

```