Aprendizagem Estatística em Altas Dimensões [MAE0501/MAE5904/IBI5904]

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Sumário

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Importando os dados / Limpando / Inspecionando

O objetivo geral do problema é prever se a pessoa possui ou não diabetes mellitus, com base em uma série de variáveis preditoras. O desafio foi posto declaradamente como um problema de aprendizagem.

O banco de dados possui todas suas observações constituídas de pessoas do gênero feminino, com idade superior a 21 anos, de ascendência do povo Pima (grupo de nativos norte-americanos). Os dados, que são atualmente abertos e gratuitos para download CC0 1.0, são provenientes do Instituto Nacional de Diabetes e Distúrbios Digestivos e do Rim (NIDDK) dos EUA e mantidos pela UC Irvine Machine Learning Repository (University of California-Irvine).

```r
diabetes <- read.csv("diabetes.csv")
head(diabetes) %>% kable(caption="Dados.")
```

Tabela 1: Dados.

Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
6	148	72	35	0	33,6	0,63	50	1
1	85	66	29	0	26,6	0,35	31	0
8	183	64	0	0	23,3	0,67	32	1
1	89	66	23	94	28,1	0,17	21	0
0	137	40	35	168	43,1	2,29	33	1
5	116	74	0	0	25,6	0,20	30	0

```r
summary(diabetes)
```

```
##   Pregnancies        Glucose      BloodPressure    SkinThickness
##  Min.   : 0.000   Min.   :  0.0   Min.   :  0.00   Min.   : 0.00
##  1st Qu.: 1.000   1st Qu.: 99.0   1st Qu.: 62.00   1st Qu.: 0.00
##  Median : 3.000   Median :117.0   Median : 72.00   Median :23.00
##  Mean   : 3.845   Mean   :120.9   Mean   : 69.11   Mean   :20.54
##  3rd Qu.: 6.000   3rd Qu.:140.2   3rd Qu.: 80.00   3rd Qu.:32.00
##  Max.   :17.000   Max.   :199.0   Max.   :122.00   Max.   :99.00
##     Insulin           BMI        DiabetesPedigreeFunction      Age
##  Min.   :  0.0   Min.   : 0.00   Min.   :0.0780           Min.   :21.00
##  1st Qu.:  0.0   1st Qu.:27.30   1st Qu.:0.2437           1st Qu.:24.00
##  Median : 30.5   Median :32.00   Median :0.3725           Median :29.00
##  Mean   : 79.8   Mean   :31.99   Mean   :0.4719           Mean   :33.24
##  3rd Qu.:127.2   3rd Qu.:36.60   3rd Qu.:0.6262           3rd Qu.:41.00
##  Max.   :846.0   Max.   :67.10   Max.   :2.4200           Max.   :81.00
##     Outcome
##  Min.   :0.000
##  1st Qu.:0.000
##  Median :0.000
##  Mean   :0.349
##  3rd Qu.:1.000
##  Max.   :1.000
```

Renomeando a variável

‘Outcome’ para ‘diabetes’

```
colnames(diabetes)[9] <- "diabetes"
```

Reshape

Diabetes? => 0 : No / 1 : Yes

```
diabetes$diabetes <- as.factor(diabetes$diabetes)

levels(diabetes$diabetes) <- c("No","Yes")
```

Visualização dos Dados

Estrutura dos Dados

```
str(diabetes)
```

```
## 'data.frame':    768 obs. of  9 variables:
##  $ Pregnancies             : int  6 1 8 1 0 5 3 10 2 8 ...
##  $ Glucose                 : int  148 85 183 89 137 116 78 115 197 125 ...
##  $ BloodPressure           : int  72 66 64 66 40 74 50 0 70 96 ...
##  $ SkinThickness           : int  35 29 0 23 35 0 32 0 45 0 ...
##  $ Insulin                 : int  0 0 0 94 168 0 88 0 543 0 ...
##  $ BMI                     : num  33.6 26.6 23.3 28.1 43.1 25.6 31 35.3 30.5 0 ...
##  $ DiabetesPedigreeFunction: num  0.627 0.351 0.672 0.167 2.288 ...
##  $ Age                     : int  50 31 32 21 33 30 26 29 53 54 ...
##  $ diabetes                : Factor w/ 2 levels "No","Yes": 2 1 2 1 2 1 2 1 2 2 ...
```

Dimensão

```
dim(diabetes)
```

```
## [1] 768   9
```

Análise Descritiva

Correlação entre cada variável

```r
library(PerformanceAnalytics)
```

```
## Warning: package 'PerformanceAnalytics' was built under R version 4.0.3
```

```
## Loading required package: xts
```

```
## Warning: package 'xts' was built under R version 4.0.2
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

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

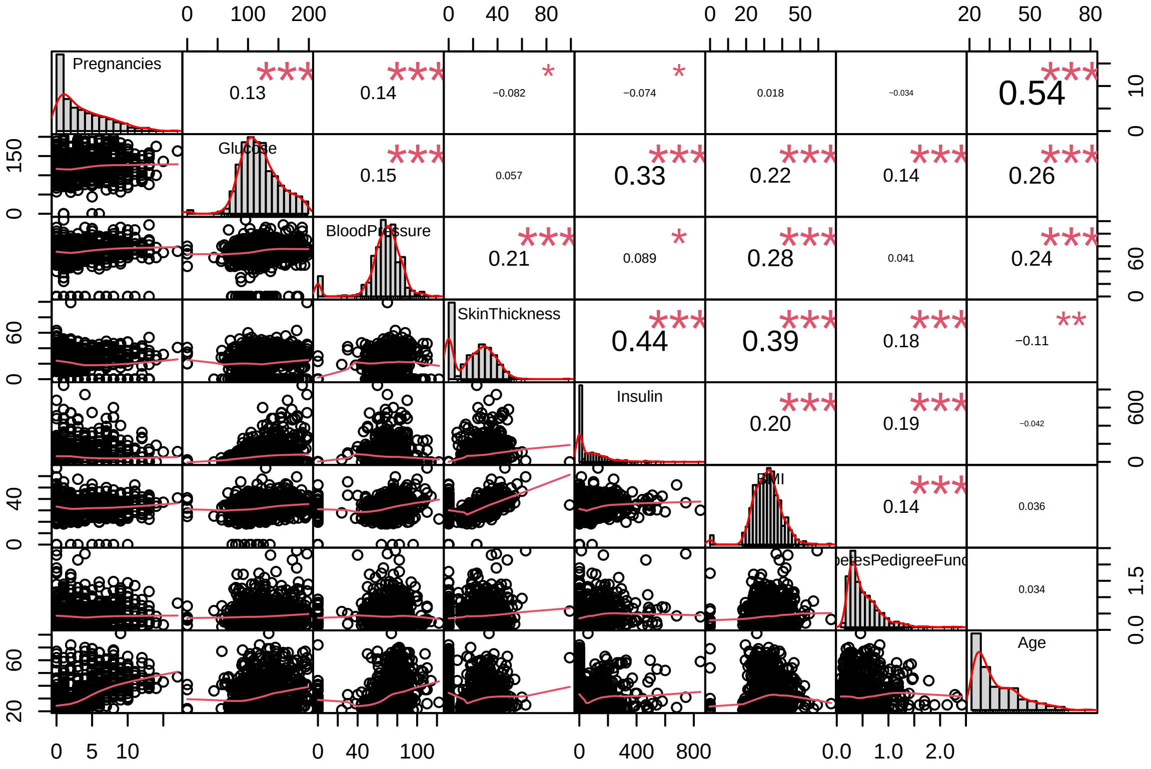
```
##
## Attaching package: 'xts'
```

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

```
##
## Attaching package: 'PerformanceAnalytics'
```

```
## The following object is masked from 'package:graphics':
##
##     legend
```

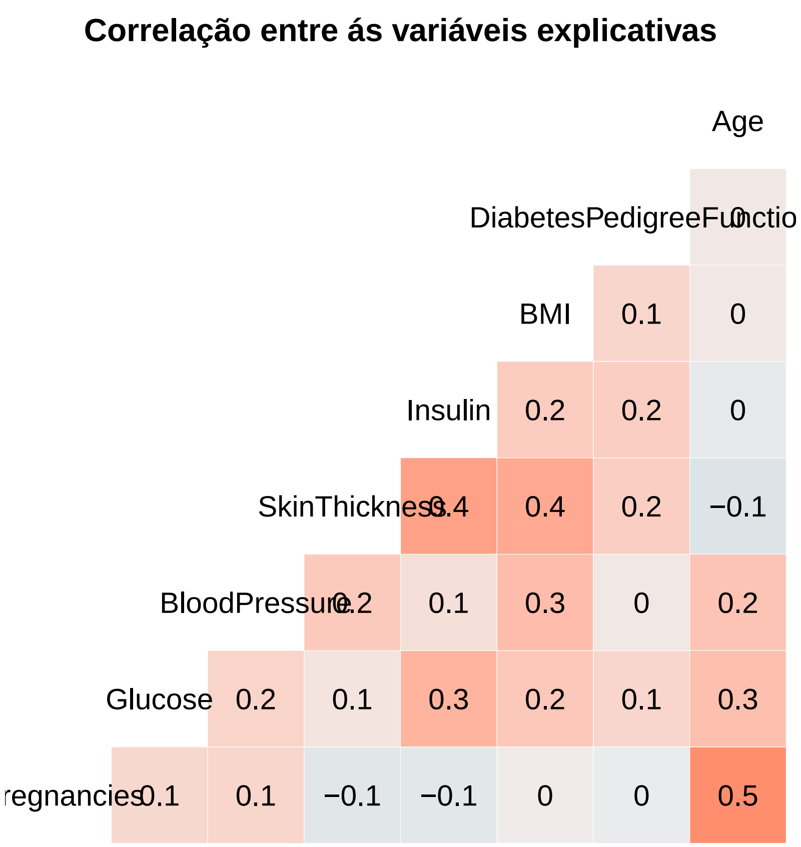
```r
chart.Correlation(diabetes[,-9], histogram=TRUE, col="grey10", pch=1, main="Correlação entre ás variáve
```



```
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
ggcorr(diabetes[,-9], name = "corr", label = TRUE)+

  theme(legend.position="none")+

labs(title="Correlação entre ás variáveis explicativas")+

theme(plot.title=element_text(face='bold',color='black',hjust=0.5,size=12))
```


Correlação entre ás variáveis explicativas

Modelagem

train / test

```r
library(tidyverse)
library(modelr)
```

```
##
## Attaching package: 'modelr'
```

```
## The following object is masked from 'package:permute':
##
##     permute
```

```r
library(dplyr)

# para reprodução
set.seed(23)

nrows <- NROW(diabetes)
```

```
index <- sample(1:nrows, 0.7 * nrows)   # shuffle and divide



# train <- diab                         # 768 test data (100%)

train <- diabetes[index,]                   # 537 test data (70%)

test <- diabetes[-index,]                   # 231 test data (30%)
```

Proporção de diabetes (Benign / Malignant)

train

```
prop.table(table(train$diabetes))
```

```
##
##        No       Yes
## 0.6405959 0.3594041
```

test

```
prop.table(table(test$diabetes))
```

```
##
##        No       Yes
## 0.6753247 0.3246753
```

RandomForest

```
library(caret)
```

```
## Warning: package 'caret' was built under R version 4.0.2
```

```
##
## Attaching package: 'caret'
```

```
## The following object is masked from 'package:vegan':
##
##     tolerance
## The following object is masked from 'package:survival':
##
##     cluster
```

```
## The following object is masked from 'package:purrr':
##
##     lift
```

```
library(randomForest)
```

```
## Warning: package 'randomForest' was built under R version 4.0.3
```

```
## randomForest 4.6-14
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:psych':
##
##     outlier
```

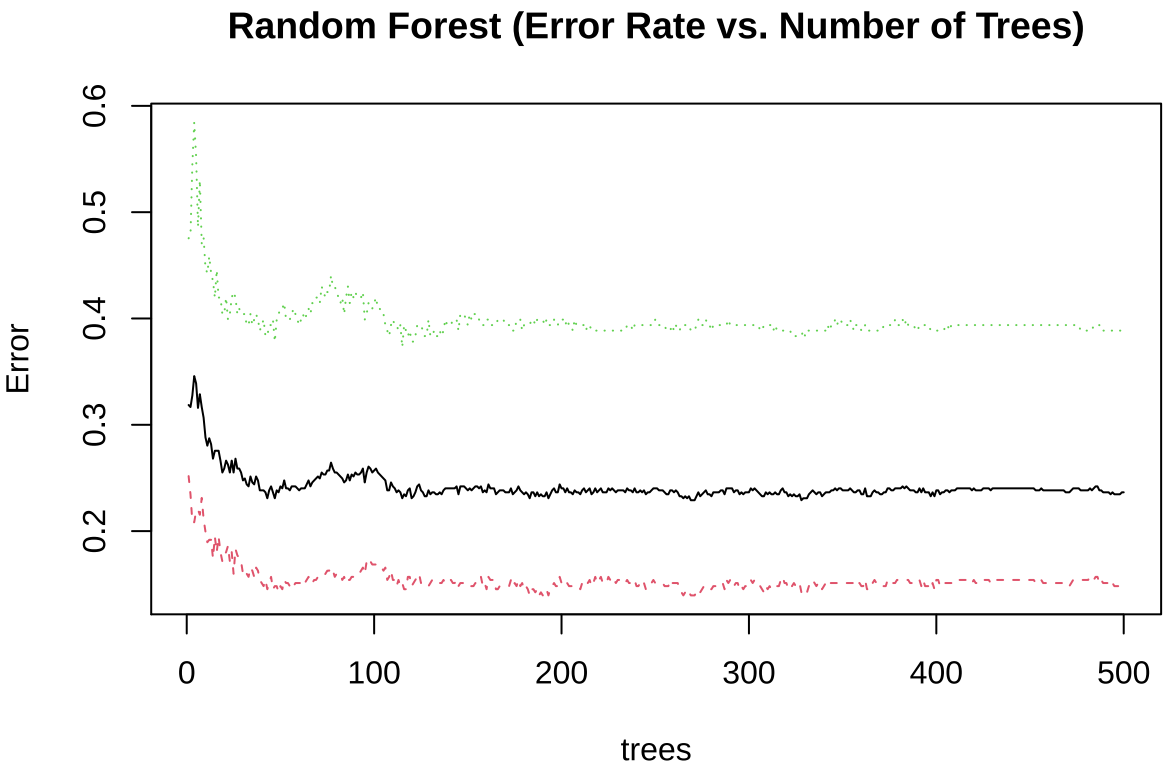
```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
learn_rf <- randomForest(diabetes~., data=train, ntree=500, proximity=T, importance=T)

pre_rf   <- predict(learn_rf, test[,-9])

cm_rf    <- confusionMatrix(pre_rf, test$diabetes)

cm_rf
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  128  26
##        Yes  28  49
##
##                 Accuracy : 0.7662
##                   95% CI : (0.7063, 0.8192)
##      No Information Rate : 0.6753
##      P-Value [Acc > NIR] : 0.00157
##
##                    Kappa : 0.4706
##
##   Mcnemar's Test P-Value : 0.89176
##
##              Sensitivity : 0.8205
##              Specificity : 0.6533
##           Pos Pred Value : 0.8312
##           Neg Pred Value : 0.6364
##               Prevalence : 0.6753
##           Detection Rate : 0.5541
##     Detection Prevalence : 0.6667
##        Balanced Accuracy : 0.7369
##
##         'Positive' Class : No
##
```

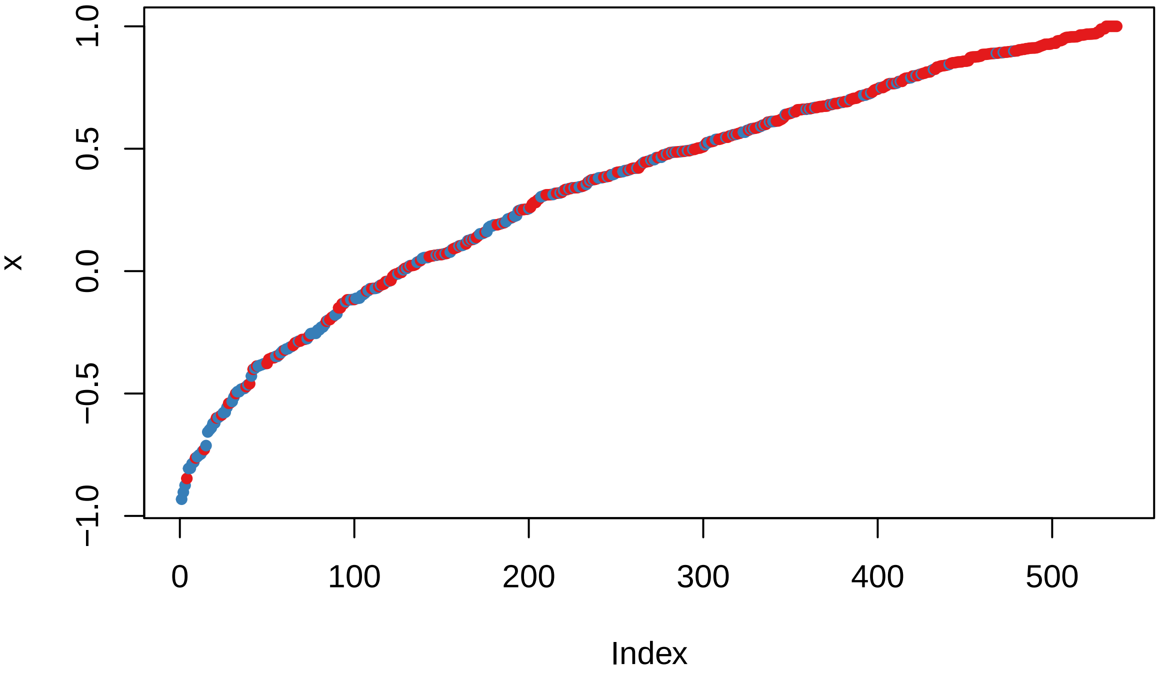
```
plot(learn_rf, main="Random Forest (Error Rate vs. Number of Trees)")
```



Prediction Plot

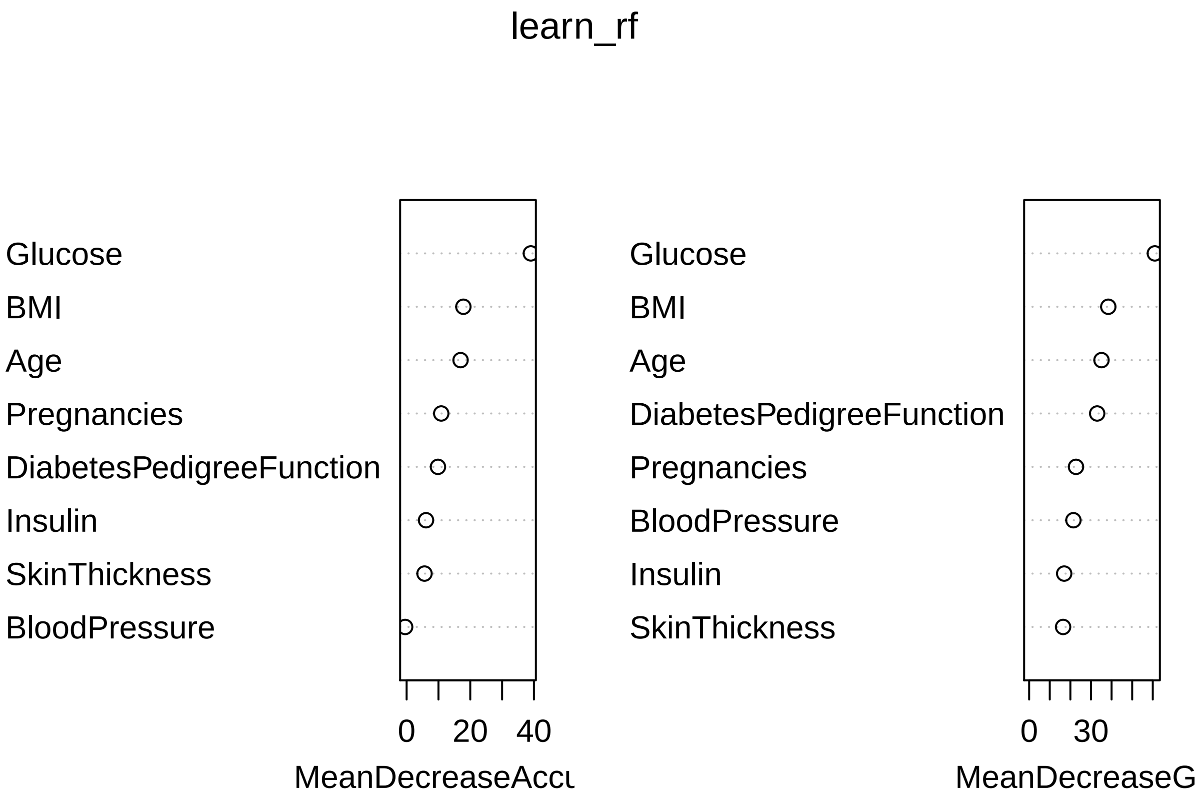
```
plot(margin(learn_rf,test$diabetes))
```

```
## Warning in RColorBrewer::brewer.pal(nlevs, "Set1"): minimal value for n is 3, returning requested pal
```



Variance Importance Plot

```
varImpPlot(learn_rf)
```


learn_rf
Glucose
BMI
Age
Pregnancies
DiabetesPedigreeFunction
Insulin
SkinThickness
BloodPressure
0
20
40
MeanDecreaseAccu
Glucose
BMI
Age
DiabetesPedigreeFunction
Pregnancies
BloodPressure
Insulin
SkinThickness
0
30
MeanDecreaseG