Curso 8

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## What is prediction?

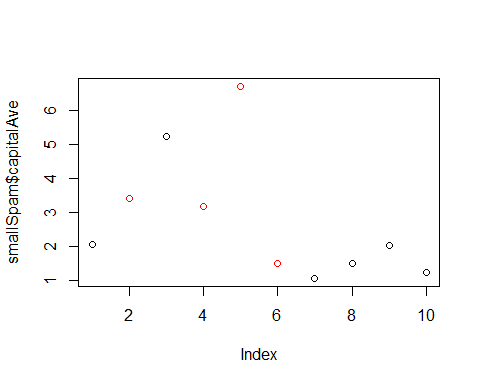
Queremos predecir cuando un email va a ser SPAM y cuando nop.

library(kernlab)  
library(caret)

## In and out of sample errors

Son los errores de la toma de muestra o datos de entrenamiento y los errores de testeo

data(spam); set.seed(133)  
smallSpam <- spam[sample(dim(spam)[1],size = 10),]  
spamLabel <- (smallSpam$type=="spam")\*1 + 1  
plot(smallSpam$capitalAve, col = spamLabel)



rule1 <- function(x){  
 prediction <- rep(NA, length(x))  
 prediction[x > 3] <- "spam"  
 prediction[x <= 3] <- "nonspam"  
 return(prediction)  
}  
table(rule1(smallSpam$capitalAve), smallSpam$type) #Podriamos crear reglas mas sofisticadas para hacer un match 100% pero pierde simplicidad el modelo

##   
## nonspam spam  
## nonspam 5 1  
## spam 1 3

sum(rule1(smallSpam$capitalAve)== smallSpam$type)

## [1] 8

table(rule1(spam$capitalAve), spam$type)

##   
## nonspam spam  
## nonspam 2314 716  
## spam 474 1097

sum(rule1(spam$capitalAve)== spam$type)

## [1] 3411

Hacer reglas mas precisas para capturar el ruido en pequeños set de data nos permite realizar predicciones mas precisas para esos datos pero resulta de un modelo sobreajustado que realizara peores predicciones para datos mas grandes. La idea es no capturar el ruido o la variacion de los datos.

## Caret

Es un paquete que contiene las tecnicas de machine learning que se utilizan comumente, para generar las predicciones con el comando predict debemos utilizar los siguientes input para cada tipo de tecnica.

data(spam)  
inTrain <- createDataPartition(y = spam$type, p = 0.75, list = FALSE)  
training <- spam[inTrain,]  
testing <- spam[-inTrain,]  
set.seed(32342)  
modelFit <- train(type ~ ., data = training, method = "glm")  
modelFit #Elige el mejor modelo que se ajusta en este caso bootstrapp con resampling

## Generalized Linear Model   
##   
## 3451 samples  
## 57 predictor  
## 2 classes: 'nonspam', 'spam'   
##   
## No pre-processing  
## Resampling: Bootstrapped (25 reps)   
## Summary of sample sizes: 3451, 3451, 3451, 3451, 3451, 3451, ...   
## Resampling results:  
##   
## Accuracy Kappa   
## 0.9201966 0.8311913

modelFit$finalModel

##   
## Call: NULL  
##   
## Coefficients:  
## (Intercept) make address all   
## -1.536e+00 -2.496e-01 -1.468e-01 6.151e-02   
## num3d our over remove   
## 1.959e+00 6.213e-01 6.425e-01 2.975e+00   
## internet order mail receive   
## 9.736e-01 9.952e-01 1.978e-01 -7.870e-01   
## will people report addresses   
## -1.849e-01 -8.838e-02 -3.289e-02 8.362e-01   
## free business email you   
## 8.757e-01 8.457e-01 5.796e-02 1.029e-01   
## credit your font num000   
## 1.071e+00 2.834e-01 2.041e-01 2.728e+00   
## money hp hpl george   
## 2.808e-01 -1.776e+00 -1.815e+00 -1.025e+01   
## num650 lab labs telnet   
## 4.375e-01 -2.243e+00 -2.159e-01 -1.261e-01   
## num857 data num415 num85   
## 3.117e+00 -5.252e-01 7.367e-01 -2.008e+00   
## technology num1999 parts pm   
## 9.453e-01 2.318e-01 -5.774e-01 -6.598e-01   
## direct cs meeting original   
## -4.833e-01 -4.097e+01 -3.671e+00 -7.235e-01   
## project re edu table   
## -1.988e+00 -8.644e-01 -2.238e+00 -3.551e+00   
## conference charSemicolon charRoundbracket charSquarebracket   
## -4.249e+00 -1.338e+00 -7.095e-01 -6.132e-01   
## charExclamation charDollar charHash capitalAve   
## 2.739e-01 6.668e+00 2.634e+00 1.151e-02   
## capitalLong capitalTotal   
## 7.544e-03 8.363e-04   
##   
## Degrees of Freedom: 3450 Total (i.e. Null); 3393 Residual  
## Null Deviance: 4628   
## Residual Deviance: 1315 AIC: 1431

predictions <- predict(modelFit, newdata = testing)  
confusionMatrix(predictions,testing$type )

## Confusion Matrix and Statistics  
##   
## Reference  
## Prediction nonspam spam  
## nonspam 665 64  
## spam 32 389  
##   
## Accuracy : 0.9165   
## 95% CI : (0.899, 0.9319)  
## No Information Rate : 0.6061   
## P-Value [Acc > NIR] : < 2.2e-16   
##   
## Kappa : 0.823   
##   
## Mcnemar's Test P-Value : 0.001557   
##   
## Sensitivity : 0.9541   
## Specificity : 0.8587   
## Pos Pred Value : 0.9122   
## Neg Pred Value : 0.9240   
## Prevalence : 0.6061   
## Detection Rate : 0.5783   
## Detection Prevalence : 0.6339   
## Balanced Accuracy : 0.9064   
##   
## 'Positive' Class : nonspam   
##

## K-Folds

Separa datos por K-Folds

set.seed(1532523)  
folds <- createFolds(y = spam$type, k = 10, list = TRUE, returnTrain = TRUE) #Me entrega el train si eligo false me entra el test  
sapply(folds,length)

## Fold01 Fold02 Fold03 Fold04 Fold05 Fold06 Fold07 Fold08 Fold09 Fold10   
## 4141 4141 4141 4141 4141 4141 4140 4141 4141 4141

## Resample

Separa datos por Resample, este metodo puede repetir observaciones

set.seed(1532523)  
samples <- createResample(y = spam$type, times = 10, list = TRUE)  
sapply(samples,length)

## Resample01 Resample02 Resample03 Resample04 Resample05 Resample06 Resample07   
## 4601 4601 4601 4601 4601 4601 4601   
## Resample08 Resample09 Resample10   
## 4601 4601 4601

# Timeslices

Separa datos por Timeslices, busco predecir los datos a traves de ventanas de tiempo. Con el siguiente codigo quiero utilizar 20 datos para predecir los 10 siguientes

set.seed(1532523)  
tme <- 1:1000  
timeslices <- createTimeSlices(y = tme, initialWindow = 20, horizon = 10)  
names(timeslices)

## [1] "train" "test"

timeslices$train[[1]]

## [1] 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

timeslices$test[[1]]

## [1] 21 22 23 24 25 26 27 28 29 30

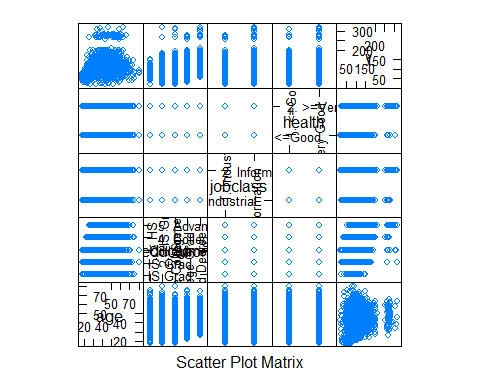
# Plotting predictors

library(ISLR); library(ggplot2); library(caret)

data(Wage); summary(Wage)

## year age maritl race   
## Min. :2003 Min. :18.00 1. Never Married: 648 1. White:2480   
## 1st Qu.:2004 1st Qu.:33.75 2. Married :2074 2. Black: 293   
## Median :2006 Median :42.00 3. Widowed : 19 3. Asian: 190   
## Mean :2006 Mean :42.41 4. Divorced : 204 4. Other: 37   
## 3rd Qu.:2008 3rd Qu.:51.00 5. Separated : 55   
## Max. :2009 Max. :80.00   
##   
## education region jobclass   
## 1. < HS Grad :268 2. Middle Atlantic :3000 1. Industrial :1544   
## 2. HS Grad :971 1. New England : 0 2. Information:1456   
## 3. Some College :650 3. East North Central: 0   
## 4. College Grad :685 4. West North Central: 0   
## 5. Advanced Degree:426 5. South Atlantic : 0   
## 6. East South Central: 0   
## (Other) : 0   
## health health\_ins logwage wage   
## 1. <=Good : 858 1. Yes:2083 Min. :3.000 Min. : 20.09   
## 2. >=Very Good:2142 2. No : 917 1st Qu.:4.447 1st Qu.: 85.38   
## Median :4.653 Median :104.92   
## Mean :4.654 Mean :111.70   
## 3rd Qu.:4.857 3rd Qu.:128.68   
## Max. :5.763 Max. :318.34   
##

inTrain <- createDataPartition(y = Wage$wage, p = 0.7, list = FALSE)  
training <- Wage[inTrain,]  
testing <- Wage[-inTrain,]  
featurePlot(x=training[,c("age","education","jobclass","health")], y = training$wage, plot = "pairs")



## Predicting with trees

El algoritmo busca crear un arbol que separe las decisiones dependiendo de ciertas caracterizticas de las variables en “hojas”, estas hojas contienen ciertas condiciones y nos entregan informacion de lo que queremos predecir

library(rattle)

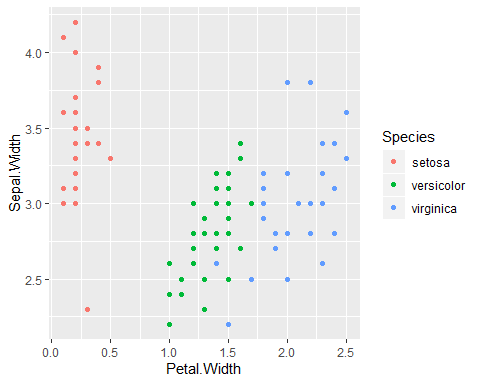
data(iris); names(iris)

## [1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"

table(iris$Species)

##   
## setosa versicolor virginica   
## 50 50 50

inTrain <- createDataPartition(y = iris$Species, p = 0.7, list = FALSE)  
training <- iris[inTrain,]  
testing <- iris[-inTrain,]  
qplot(Petal.Width, Sepal.Width, colour = Species, data = training) #Podemos ver una clara diferencia entre las especies



model <- train(Species ~ . , method = "rpart", data = training) #rpart es para hacer arboles de regresion  
print(model$finalModel) #Se puede ver por ejemplo que si el largo es menor a 2.45 es "setosa"

## n= 105   
##   
## node), split, n, loss, yval, (yprob)  
## \* denotes terminal node  
##   
## 1) root 105 70 setosa (0.33333333 0.33333333 0.33333333)   
## 2) Petal.Length< 2.45 35 0 setosa (1.00000000 0.00000000 0.00000000) \*  
## 3) Petal.Length>=2.45 70 35 versicolor (0.00000000 0.50000000 0.50000000)   
## 6) Petal.Width< 1.75 38 3 versicolor (0.00000000 0.92105263 0.07894737) \*  
## 7) Petal.Width>=1.75 32 0 virginica (0.00000000 0.00000000 1.00000000) \*

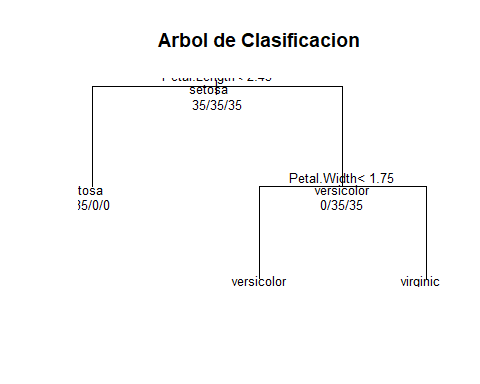
plot(model$finalModel, unirform = TRUE, main = "Arbol de Clasificacion")

## Warning in plot.window(...): "unirform" is not a graphical parameter

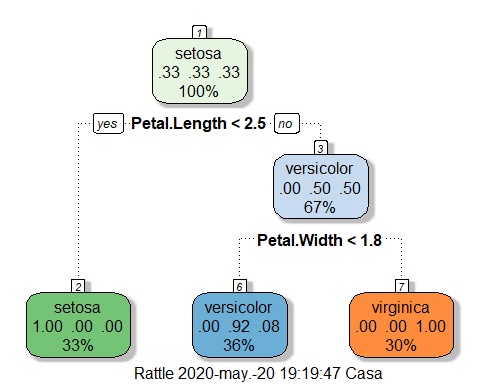
## Warning in plot.xy(xy, type, ...): "unirform" is not a graphical parameter

## Warning in title(...): "unirform" is not a graphical parameter

text(model$finalModel, use.n = TRUE, all = TRUE, cex = .8)



#Una mejor clasificacion o arbol puede usarse con el paquete de rattle  
fancyRpartPlot(model$finalModel)



predict(model, newdata = testing)

## [1] setosa setosa setosa setosa setosa setosa   
## [7] setosa setosa setosa setosa setosa setosa   
## [13] setosa setosa setosa versicolor versicolor versicolor  
## [19] versicolor versicolor versicolor versicolor virginica versicolor  
## [25] versicolor versicolor versicolor versicolor versicolor versicolor  
## [31] virginica virginica virginica virginica virginica virginica   
## [37] versicolor versicolor virginica virginica virginica virginica   
## [43] virginica virginica virginica   
## Levels: setosa versicolor virginica

## Bagging

Esta tecnica permite crear algoritmos (de arbol generalmente) con menor variacion ya que genera varios modelos y promedia los resultados lo que nos genera una menor varianza pero mantiene el bias

## Random Forest

Rnadom forest es una extension del bagging (generar muchos modelos y promediarlos), para los arboles de clasificacion. La diferencia es que cuando separamos los datos con bootstrap tambien hacemos boostrap a las variables. Con esto hacemos distintos tipos de arboles con distintas variables. Nos entrega mejor accuracy, tiene problemas de velocidad, interpretabilidad y estar sobreajustado (es importante usar validacion cruzada para este metodo). Cada arbol debe se creado por un boostrap Ç(una muestra aleatoria de la muestra), y en cada nodo se elige una cantidad de variables distintas.

library(randomForest)

data(iris); names(iris)

## [1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"

inTrain <- createDataPartition(y = iris$Species, p = 0.7, list = FALSE)  
training <- iris[inTrain,]  
testing <- iris[-inTrain,]  
model <- train(Species ~ ., data = training, method = "rf", prox = TRUE) #rf de "random forest"  
model

## Random Forest   
##   
## 105 samples  
## 4 predictor  
## 3 classes: 'setosa', 'versicolor', 'virginica'   
##   
## No pre-processing  
## Resampling: Bootstrapped (25 reps)   
## Summary of sample sizes: 105, 105, 105, 105, 105, 105, ...   
## Resampling results across tuning parameters:  
##   
## mtry Accuracy Kappa   
## 2 0.9669215 0.9492635  
## 3 0.9678971 0.9507815  
## 4 0.9657050 0.9474202  
##   
## Accuracy was used to select the optimal model using the largest value.  
## The final value used for the model was mtry = 3.

getTree(model$finalModel, k = 2)

## left daughter right daughter split var split point status prediction  
## 1 2 3 3 4.75 1 0  
## 2 4 5 3 2.45 1 0  
## 3 6 7 3 5.05 1 0  
## 4 0 0 0 0.00 -1 1  
## 5 8 9 4 1.65 1 0  
## 6 10 11 1 6.50 1 0  
## 7 0 0 0 0.00 -1 3  
## 8 0 0 0 0.00 -1 2  
## 9 0 0 0 0.00 -1 3  
## 10 0 0 0 0.00 -1 3  
## 11 0 0 0 0.00 -1 2

## Boosting

Se comienzan con tecnicas simple de prediccion, luego se les confiere un peso mas relevante a las observaciones que no han sido tomadas por las tecnicas y asi sucesivamente. Finalmente con cada peso calculado por el error creo un modelo final que me permita encontrar la mejor prediccion posible (El algoritmo mas famoso es el Adaboost).

data(Wage); names(Wage)

## [1] "year" "age" "maritl" "race" "education"   
## [6] "region" "jobclass" "health" "health\_ins" "logwage"   
## [11] "wage"

Wage <- subset(Wage, select = -c(logwage))  
inTrain <- createDataPartition(y = Wage$wage, p = 0.7, list = FALSE)  
training <- Wage[inTrain,]  
testing <- Wage[-inTrain,]  
model <- train(wage ~ ., method = "gbm", data = training, verbose = FALSE) ## GBM is boosting with trees

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 18: region6. East South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 19: region7. West South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 20: region8. Mountain has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 21: region9. Pacific has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
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## "bernoulli", : variable 18: region6. East South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 19: region7. West South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 20: region8. Mountain has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 21: region9. Pacific has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

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## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 18: region6. East South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 19: region7. West South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 20: region8. Mountain has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 21: region9. Pacific has no variation.

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## "bernoulli", : variable 15: region3. East North Central has no variation.

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## "bernoulli", : variable 16: region4. West North Central has no variation.

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## "bernoulli", : variable 18: region6. East South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 19: region7. West South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 20: region8. Mountain has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 21: region9. Pacific has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =  
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print(model)

## Stochastic Gradient Boosting   
##   
## 2102 samples  
## 9 predictor  
##   
## No pre-processing  
## Resampling: Bootstrapped (25 reps)   
## Summary of sample sizes: 2102, 2102, 2102, 2102, 2102, 2102, ...   
## Resampling results across tuning parameters:  
##   
## interaction.depth n.trees RMSE Rsquared MAE   
## 1 50 33.65938 0.3263938 23.35429  
## 1 100 33.02623 0.3381446 22.99872  
## 1 150 32.95339 0.3395242 23.04961  
## 2 50 32.91334 0.3443208 22.89835  
## 2 100 32.72305 0.3488339 22.89576  
## 2 150 32.75848 0.3480268 22.98555  
## 3 50 32.72856 0.3497609 22.84205  
## 3 100 32.80608 0.3464548 23.00133  
## 3 150 32.99734 0.3402497 23.19388  
##   
## Tuning parameter 'shrinkage' was held constant at a value of 0.1  
##   
## Tuning parameter 'n.minobsinnode' was held constant at a value of 10  
## RMSE was used to select the optimal model using the smallest value.  
## The final values used for the model were n.trees = 100, interaction.depth =  
## 2, shrinkage = 0.1 and n.minobsinnode = 10.

## Model Based Prediction

La idea basica es que los datos siguen un modelos probabilistico (normal por ejemplo), luego se usa el teorema de bayes para encontrar los clasificadores optimos de ese modelo probabilistico. Las ventajas es que se aprovechan de la estructura de los datos, puede ser conveniente computacionalmente, se ajusta razonablemente a problemas reales. Las desventajas es que hay que asumir un modelo de la data, si el model es incorrecto el accuracy baja mucho

data(iris); names(iris)

## [1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"

inTrain <- createDataPartition(y = iris$Species, p = 0.7, list = FALSE)  
training <- iris[inTrain,]  
testing <- iris[-inTrain,]  
model1 <- train(Species ~ . , data = training, method = "lda")# linear discimination analysis  
model2 <- train(Species ~ . , data = training, method = "nb") #Naive base classification  
plda <- predict(model1,testing); pnb <- predict(model2, testing)  
table(plda,pnb)

## pnb  
## plda setosa versicolor virginica  
## setosa 15 0 0  
## versicolor 0 15 0  
## virginica 0 0 15