# How to recode variables

```
dat$Species = as.factor(ifelse(iris$Species=="virginica",1,0))
# to recode cleanly, you could use for instance:
dat$Species = car::recode(dat$Species, "0='other'; 1='virginica'")
# or:
levels(dat$Species) = c("other","virginica")
```

# Classification

## 1-. K-Nearest Neighbors (KNN) (01_Example Chp3 Exercise bank)

**Note: KNN strongly depends on K chosen**

- **Small K: Overfitting (low bias/large variance)**
- **Large K: Underfitting (high bias/low oiance)**

**So we need to select K to achieve a trade-off**

**Note: It is important to scale the data**

```
library(class) # It has function knn
```

**Splitting training & test (necessary for knn)**

```
x_train, x_test, y_train, y_test
```

**Passing them to knn**

```
K = alpha # Number of neighbors
ko = knn(x_train, x_test, y_train, K)
```

**Note: the training variable for the knn should be numeric**

**Note: it predicts automatically (i.e. not necessary to apply function predict)**

## Confusion matrix

**1-. Using library(caret) (Recommended)**

```
library(caret)
```

**confusionMatrix**(data = dat, reference = y.test) # they should have same levels to be compared!!

**It gives us:**

1-. Confusion Matrix

2-. Accuracy rate (also failure rate i.e. 1 – Accuracy)

3-. A **95% CI** for the **accuracy rate**

4-. Sensitivity and Specificity (using attribute $class)

**2-. Using table**

```
tb = table(pred, y_test)
tb
# Calculating accuracy or failure rate
sum(diag(tb))/sum(tb)
```

**# How to calculate specificity**

**spec = tb[1,1]/sum(tb[,1])**

**# Sensitivity**

**sens = tb[2,2]/sum(tb[,2])**

## How to find the suitable K that maximizes the accuracy rate:

We will perform a grid search using different values of K

```
Kmax = 30 (for instance)
acc = numeric(Kmax)
for(k in 1:Kmax){
  # Fitting knn
  ko = knn(x.train, x.test, y.train, k)
  # Building table
  tb = table(ko, y.test)
  # Storing error rates
```

```
  acc[k] = sum(diag(tb))/sum(tb)
}

# We can find the minimum or plot them

plot(acc, t = 'b', pch = …, cex = …)

or

k.best = which.max(acc)
```

## 2-. Logistic Regression (02_Exercise Chp 3)

**Note: if Y is a binary classification Logistic Regression should be used as a REFERENCE (i.e. when Y has more than one class, doesn't work well…)**

```
# How to code it

glm(interest ~., data = dat, subset = train, family = binomial(link = logit))
```

**Note: We will classify in terms of a cut-off** (threshold) (remember binomial classifies successes and failures)

**Predicting with it:**

**1-. Obtaining a vector of TRUE/FALSE**

```
Pred_vector = (predict(fit, newdata=data[-x_train,],
            type = "response") > Threshold )
```

**2-. Obtaining the probability associated with each row**

```
Pred_numeric = predict(fit, newdata=dat[-is,], type="response")
```

**Boxplot**

We can plot a boxplot to appreaciate the overlap between classes. **Why?**

If there **is no overlap** we can ensure that these classes behave differently, and so they can be classified.

```
boxplot(pred_numeric, y_test)
```

**Table**

```
Tb = table(pred_vector , y.test)
```

**We can perform a grid search to find a balance in the trade-off between sensibility and specificity (ROC CURVE ANALYSIS)**

```
alpha = seq(0.05, 0.95, by = 0.05)
err = numeric(length(alpha))
for (i in 1:length(alpha)){
  pred.y = as.numeric(pred_numeric>alpha[i])
  tb = table(pred.y, y.test)
  err[i] = (1-sum(diag(tb))/sum(tb)))
}
```

## 3-. ROC CURVE *(06_exercise Chp 3 and 05_Exercise)*

**Useful to find a trade-off between specificity and sensitivity**

**1-. If alpha is small (Highly sensitive):**

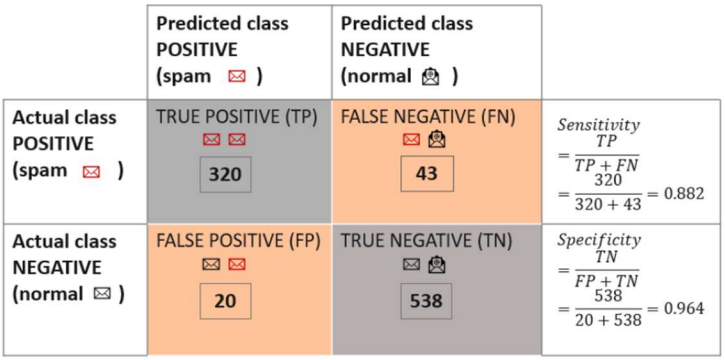
- Pi^hat is likely to be above the cut-off
- Zi^hat is likely to be 1
- Also likely to detect "false alarms"

**1-. If alpha is large (Highly specificity/not very sensitive):**

- Pi^hat is likely to be below the cut-off
- Zi^hat is likely to be 0

Ahead of anything we will introduce the concepts of sensitivity and specificity in terms of the confusion matrix.

- 2x2 confusion matrix (i.e. only two classes)
- 3x3 Confusion Matrix (i.e. 3 classes)




Recall: we can **calculate them** using

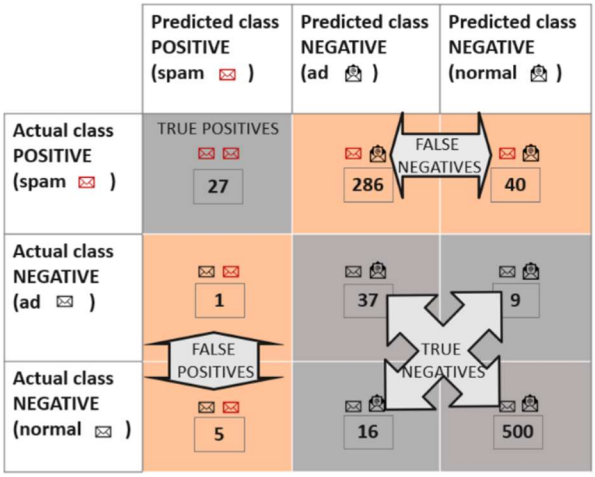
- ConfusionMatrix from caret
- Table

```
# How to calculate specificity

spec = tb[1,1]/sum(tb[,1])

# Sensitivity

sens = tb[2,2]/sum(tb[,2])
```




We will focus as well in **the Area under the curve** (ROC curve of course)

**Idea: the more we get 1 the better our model is**

```
Library(pROC)

Roc.g = roc(y.test, glm.p #needs probabilties here)$auc

plot(roc.g) # will give you the graph

# How to plot it

plot(spec, sens,

     xlim = c(1,0),

     type = 'b')

abline(h = 1, v = 1)
```

## 4-. Linear Discriminant Analysis (LDA) *(03_Exercise Chp3)*

**Note: Natural reference technique for classification problems WITH MORE THAN 3 CLASSES (Y RESPONSE)**

**First of all we need to check the assumptions of:**

- **Normality**
- **Equal variance**

**Library(MAAS)**

*Look code in exercise 03_Exercise Chpt3*

**How to assess normality (FOR EACH CLASS , SEPARATELY):**

**1-. Boxplot (informal):** we can assess normality here, looking if the boxplots of each class and attribute are symmetric.

**2-. Histogram (specifically and formal):** we need to address normality here as you know: paying attention to skews, symmetry, tails…

**3-. QQ-plots:** looking at substantial departures and if the fit a straight line…

**4-. Shapiro Test (do not rely on these too much):** if the p-value is large is normal and if not is not normal…

**How to assess equal variance**

**1-. Barlett's test:** if p is large then equal variance if p is small not equal variance. We do not need to differenciate classes over here

```
for(j in 1:4){print( bartlett.test(dat[,j]~dat$Species)$p.value )}
```

**Note:** in this exercise in particular the assumptions were not verified but we continued fitting lda…

**Fitting LDA**

```
lda.o = lda(Species~., data=dat)

(lda.o)
```

Gives us:

- Probability for each class
- Group means (if numerical)
- Coefficient of linear discriminant

**How to get predict**

```
lda.p = predict(lda.o, newdata=dat.test)
```

```
names(lda.p)
```

1. **Lda.p$class**: contains the classes predicted
2. **Lda.p$posterior** : contains an array of probabilities

**Confusionmatrix**

```
(tb = table(lda.p$class, dat.test$Species))

Accuracy = sum(diag(tb))/sum(tb)


# or

confusionMatrix(lda.p$class, reference = dat.test[,'Species'])
```

## 5-. Quadratic Discriminator Analysis (QDA)

**Note: more robus than LDA when LDA assumptions fail**

```
# QDA:

qda.o = qda(Species~., data=dat.train)

qda.p = predict(qda.o, newdata=dat.test)

(tb = table(qda.p$class, dat.test$Species))

sum(diag(tb))/sum(tb)


# or


confusionMatrix(qda.p$class, dat.test[,'Species'])
```

## 6-. Decision Trees *(01_02_Exercise Chp 4)*

**Note: Prunning might be requiered in some situations since trees tend to overfit (i.e. low biad large variance)**

**Note: as the trees grow more, the more overfitting you will have**

**Library(tree)**

**How to code a tree**

```
tree.out = tree(High~., data = dat, subset = i.train,
                na.action = na.pass # if you need to omit Nas)
```

**Summary**

summary(tree.out) gives you:

1. **Misclassification** error
2. **Names of variables used**
3. Number of terminal nodes/leaf nodes

**Plot a tree**

```
plot(tree.out) # Will plot the edges and structure of tree
text(tree.out, pretty = 0) # will set the names on top of each split
```

## Pruning a tree

**Note: we need to set a seed (if wanted) to get same results**

**Note: pruning reduces overfitting**

**Note: FUN = prune.misclass - classification**

**FUN = Prune.tree - regression**

```
cv.CS = cv.tree(tree.out, FUN=prune.misclass)
```

**names**(cv.CS)

**# - size:**

# number of terminal nodes in each tree in the cost-complexity pruning sequence.

**# - deviance:**

# total deviance of each tree in the cost-complexity pruning sequence.

**# - k:**

# the value of the cost-complexity pruning parameter of each tree in the sequence.

**Plotting size vs deviance**

```
plot(cv.CS$size,cv.CS$dev,t='b')
```

```
abline(v = cv.CS$size[which.min(cv.CS$dev)]) # Optimal pruning
```

**Plotting k vs deviance**

```
plot(cv.CS$k,cv.CS$dev,t='b')
```

**How to implement the pruning :**

1. use which.min(cv.CS$dev) to get the location of the optimum

   opt.size = **cv.CS$size[which.min(cv.CS$dev)]**

2. retrieve the corresponding tree size
3. pass this information on to pruning function

   **Note: prune.tree for regression**

   ptree = **prune.misclass(tree.out, best=opt.size)**

And now we could plot the ptree as explained above.

## Predicting with trees

**We can use:**

1. Class: to get the classes
2. Vector: to get the probabilities

```
tree.pred = predict(tree.out, CS.test, type="class")
```

```
tb1 = table(tree.pred,High.test)
```

## 7-. Random Forests *(04_Exercise Chp 4)*

**Note: random forests are important since with them we can rule out some attributes with ease. (i.e. using variable importance)**

**library(randomForest)**

**Coding a random Forest**

rf.out = **randomForest**(High~., CS)

**Predicting with a forest**

We can use:

1. **Class:** vector with predicted classes
2. **Prob:** vector with probabilities

rf.yhat = **predict**(rf.out, CS, type=**"class"**)

**Note: we can get the fitted values passing the original dataframe to the function predict**

**Matrix for the OOB observations:** (it has the class error associated)

(tb.rf2 = **rf.out$confusion**)

Ex:

| | No | Yes | class.error |
|---|---|---|---|
| No | 209 | 27 | 0.1144068 |
| Yes | 50 | 114 | 0.3048780 |

**Bagging**

**Note: Bagging can work even better than randomForests!! Remember: it decorrelates the trees (i.e. great reduction in variance , central limit theorem)**

**How to code and predict with bagging**

bag.out = **randomForest**(High~., CS, **mtry=P**)

**P:** numbers of attributes to be considered usually root(ncol())

bag.yhat = **predict**(bag.out, CS, type="class")

**Note: we can get here too the predicted values of the training set..**

**Variable importance** *(07_Exercise Chp 4):*

**Note: we can have an overview of which variables are the most influencial for the reference (i.e. which variables should be dropped)**

```
rf = randomForest(High~., data = CS)
rf$importance
```

We can **plot** it

```
varImpPlot(rf, pch=15, main="Ensemble method 1")
```

## 8-. Gradient Boosting *(07_Exercise Chp 4)*

**Watch out: it needs numerical variable as response variables!!**

**Note: we can get even better results than randomFORESTS**

**Note: the main idea is rule out useless variables**

```
Library(gbm)
```

**How to code it:**

```
gb.out = gbm(High~., data=CS,
             distribution="bernoulli", # use "gaussian" instead for regression
             n.trees=5000, # size of the ensemble
             interaction.depth=1) # depth of the trees, 1 = stumps
```

**Inspect output:**

```
par(mar=c(4.5,6,1,1))
summary(gb.out, las=1) Gives you variable importance
plot(gb.out, i="Price") Graph of Price
plot(gb.out, i="ShelveLoc") Graph of ShelveLoc
```

**Predict with it**

```
gb.p = (predict(gb.out, newdata=CS.test, n.trees=5000, type = "response")) > 0.5
```

**Roc Analysis**

**Note: for gbm we do not need to pass into roc function a vector of probabilties…**

```
roc.gb = roc(response=CS.test$High, predictor=gb.p)
```

## USING CARET

```
library(caret)
```

**Coding it**

```
gb.out = train(Salary~., data=dat.train, method='gbm',
distribution='bernoulli')
```

**Note: distribution = "gaussian" if we want to use regression**

**Predicting**

```
gb.fitted = predict(gb.out) # corresponding fitted values

gb.pred = predict(gb.out, dat.validation)
```

**Confusion Matrix**

```
confusionMatrix(reference=dat.validation$Salary, data=gb.pred,
                mode="everything")
```