

## Curso Livre II

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# Modulo III

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### Carregamento dos packages:

```
install.packages('mlr')
install.packages('mlbench')
install.packages('rpart.plot')
library(mlr)
library(mlbench)
library(rpart.plot)
```

### Tarefa :

1. Obtenha um conjunto de dados de câncer de mama usando os seguintes comandos (precisa instalar o pacote mlbench):

```
data(BreastCancer, package = "mlbench")
df = BreastCancer
df$Id = NULL
cl = df$Class
indx = sapply(df, is.factor)
df[indx] = lapply(df[indx], function(x) as.numeric(as.character(x)))
df$Class = cl
df$Bare.nuclei = NULL
```

2. Com os dados carregados, separe-os em conjunto de treinamento e de teste e use a biblioteca mlr como vimos:

```
set.seed(0)
trein_index <- sample(1:nrow(df), 0.8 * nrow(df))
test_index <- setdiff(1:nrow(df), trein_index)
trein <- df[trein_index,]
test <- df[test_index,]
```

3. Crie a tarefa de classificação (a variável alvo é "Class")

```
> taskclf <- makeClassifTask(data=trein, target = 'Class', positive = 'benign')
```

4. Treine os modelos que vimos na primeira aula (e outros, se desejar)

### Decision Tree Classifier

```
> tree <- makeLearner('classif.rpart', predict.type = 'prob')
> tree_trein <- train(learner = tree, task = taskclf)
> rpart.plot(tree_trein$learner.model, roundint = F)
```

### K-Nearest Neighbors (KNN)

```
> knn <- makeLearner('classif.knn')
> knn_trein <- train(learner = knn, task = taskclf)
```

### Logistic Regression

```
> reg_log <- makeLearner('classif.logreg', predict.type = 'prob')
> reg_log_trein <- train(learner = reg_log, task = taskclf)
```

5. Avalie os modelos treinados usando o conjunto de teste e veja qual teve melhor desempenho

### Decision Tree Classifier

```
> tree_predict <- predict(tree_trein, newdata = test)
> calculateROCMeasures(tree_predict)
```

	predicted		
true	benign	malignant	
benign	96	4	tpr: 0.96 fnr: 0.04
malignant	5	35	fpr: 0.12 tnr: 0.88
	ppv: 0.95	for: 0.1	lrp: 7.68 acc: 0.94
	fdr: 0.05	npv: 0.9	lrm: 0.05 dor: 168

Abbreviations:

tpr - True positive rate (Sensitivity, Recall)  
 fpr - False positive rate (Fall-out)  
 fnr - False negative rate (Miss rate)  
 tnr - True negative rate (Specificity)  
 ppv - Positive predictive value (Precision)  
 for - False omission rate  
 lrp - Positive likelihood ratio (LR+)  
 fdr - False discovery rate  
 npv - Negative predictive value  
 acc - Accuracy  
 lrm - Negative likelihood ratio (LR-)  
 dor - Diagnostic odds ratio

```
> calculateConfusionMatrix(tree_predict)
      predicted
true   benign malignant -err.-
benign    96         4      4
malignant  5        35      5
-err.-    5         4      9
```

**ppv (Precision) : 0.95**

**tpr (Recall): 0.96**

**acc (Acuracy): 0.94**

### K-Nearest Neighbors (KNN)

```
> knn_predict <- predict(knn_trein, newdata = test)
> calculateROCMeasures(knn_predict)
      predicted
true   benign  malignant
benign   98      2      tpr: 0.98 fnr: 0.02
malignant 5     35      fpr: 0.12 tnr: 0.88
          ppv: 0.95 for: 0.05 lrp: 7.84 acc: 0.95
          fdr: 0.05 npv: 0.95 lrm: 0.02 dor: 343
```

#### Abbreviations:

tpr - True positive rate (Sensitivity, Recall)  
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 acc - Accuracy  
 lrm - Negative likelihood ratio (LR-)  
 dor - Diagnostic odds ratio

```
> calculateConfusionMatrix(knn_predict)
      predicted
true   benign malignant -err.-
benign   98         2      2
malignant 5        35      5
-err.-    5         2      7
```

**ppv (Precision) : 0.95**

**tpr (Recall): 0.98**

**acc (Acuracy): 0.95**

## Logistic Regression

```
> reg_log_predict <- predict(reg_log_trein, newdata = test)
> calculateROCMeasures(reg_log_predict)

      predicted
true      benign      malignant
benign    100         0      tpr: 1      fnr: 0
malignant  9         31      fpr: 0.22  tnr: 0.78
          ppv: 0.92  for: 0      lrp: 4.44  acc: 0.94
          fdr: 0.08 npv: 1      lrm: 0      dor: Inf
```

### Abbreviations:

tpr - True positive rate (Sensitivity, Recall)  
 fpr - False positive rate (Fall-out)  
 fnr - False negative rate (Miss rate)  
 tnr - True negative rate (Specificity)  
 ppv - Positive predictive value (Precision)  
 for - False omission rate  
 lrp - Positive likelihood ratio (LR+)  
 fdr - False discovery rate  
 npv - Negative predictive value  
 acc - Accuracy  
 lrm - Negative likelihood ratio (LR-)  
 dor - Diagnostic odds ratio

```
> calculateConfusionMatrix(reg_log_predict)

      predicted
true      benign malignant -err.-
benign    100         0      0
malignant  9         31      9
-err.-     9         0      9
```

**ppv (Precision) : 0.92**

**tpr (Recall): 1**

**acc (Accuracy): 0.94**

### Todos :

Modelo\medida	ppv	tpr	acc
DecisionTree	0.95	0.96	0.94
KNN	0.95	0.98	0.95
LogisticReg	0.92	1	0.94

Repare que a logistic regression apresentou uma maior taxa de cobertura, equivalente a 1, consequentemente perde um pouco em sua precisão. Por ser

um modelo que mais acerta a classe do seu target, o modelo de Regressão Logística é o melhor, para esta situação.