# ReadMe

## Machine Learning Practice

```
#install.packages("caret")
library(caret)
```

```
## Warning: package 'caret' was built under R version 4.0.5
```

```
## Loading required package: lattice
```

```
## Loading required package: ggplot2
```

```
library(ggplot2)
```

```
# attach the iris dataset to the environment
data(iris)
# rename the dataset
dataset <- iris
```

```
# create a list of 80% of the rows in the original dataset we can use for training
validation_index <- createDataPartition(dataset$Species, p=0.80, list=FALSE)
# select 20% of the data for validation
validation <- dataset[-validation_index,]
# use the remaining 80% of data to training and testing the models
dataset <- dataset[validation_index,]
```

```
# We can get a quick idea of how many instances (rows) and how many attributes (columns) the data conta

# dimensions of dataset
dim(dataset)
```

```
## [1] 120   5
```

```
# list types for each attribute
sapply(dataset, class)
```

```
## Sepal.Length  Sepal.Width Petal.Length  Petal.Width      Species
##    "numeric"    "numeric"    "numeric"    "numeric"     "factor"
```

```
# take a peek at the first 5 rows of the data
head(dataset)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
## 7          4.6         3.4          1.4         0.3  setosa
```

```
# list the levels for the class
levels(dataset$Species)
```

```
## [1] "setosa"     "versicolor" "virginica"
```

```
# summarize the class distribution
percentage <- prop.table(table(dataset$Species)) * 100
cbind(freq=table(dataset$Species), percentage=percentage)
```

```
##            freq percentage
## setosa       40   33.33333
## versicolor   40   33.33333
## virginica    40   33.33333
```

```
summary(dataset)
```

```
##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
##  Min.   :4.300   Min.   :2.200   Min.   :1.000   Min.   :0.100
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.500   1st Qu.:0.300
##  Median :5.800   Median :3.000   Median :4.500   Median :1.400
##  Mean   :5.848   Mean   :3.069   Mean   :3.772   Mean   :1.213
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
##  Max.   :7.900   Max.   :4.400   Max.   :6.700   Max.   :2.500
##        Species
##  setosa    :40
##  versicolor:40
##  virginica :40
##
##
##
```

## Testing and Machine Learning bit

```
# Run algorithms using 10-fold cross validation
control <- trainControl(method="cv", number=10)
metric <- "Accuracy"
# Run algorithms using 10-fold cross validation
control <- trainControl(method="cv", number=10)
metric <- "Accuracy"
```

Let's evaluate 5 different algorithms:

Linear Discriminant Analysis (LDA) Classification and Regression Trees (CART). k-Nearest Neighbors (kNN). Support Vector Machines (SVM) with a linear kernel. Random Forest (RF)

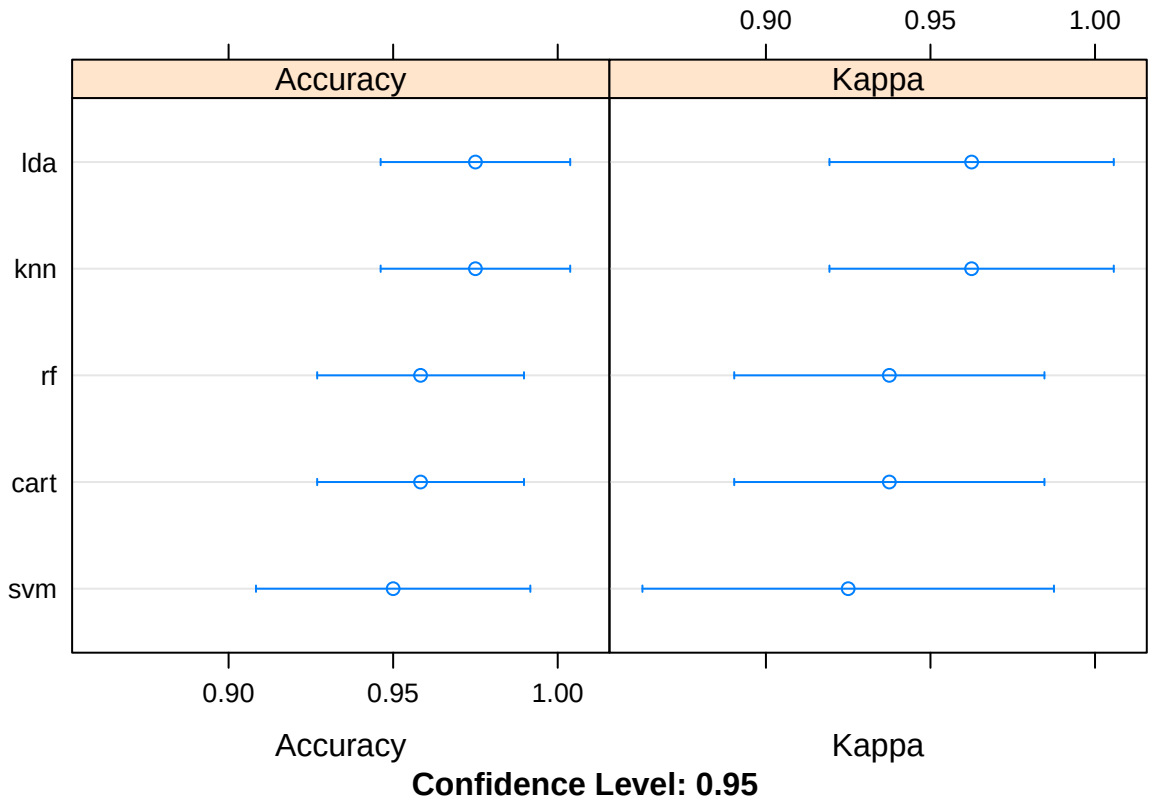
```
#install.packages("e1071")
```

```
# a) linear algorithms
set.seed(7)
fit.lda <- train(Species~., data=dataset, method="lda", metric=metric, trControl=control)
# b) nonlinear algorithms
# CART
set.seed(7)
fit.cart <- train(Species~., data=dataset, method="rpart", metric=metric, trControl=control)
# kNN
set.seed(7)
fit.knn <- train(Species~., data=dataset, method="knn", metric=metric, trControl=control)
# c) advanced algorithms
# SVM
set.seed(7)
fit.svm <- train(Species~., data=dataset, method="svmRadial", metric=metric, trControl=control)
# Random Forest
set.seed(7)
fit.rf <- train(Species~., data=dataset, method="rf", metric=metric, trControl=control)
```

```
# summarize accuracy of models
results <- resamples(list(lda=fit.lda, cart=fit.cart, knn=fit.knn, svm=fit.svm, rf=fit.rf))
summary(results)
```

```
##
## Call:
## summary.resamples(object = results)
##
## Models: lda, cart, knn, svm, rf
## Number of resamples: 10
##
## Accuracy
##           Min.   1st Qu.    Median      Mean 3rd Qu. Max. NA's
## lda  0.9166667 0.9375000 1.0000000 0.9750000       1    1    0
## cart 0.9166667 0.9166667 0.9583333 0.9583333       1    1    0
## knn  0.9166667 0.9375000 1.0000000 0.9750000       1    1    0
## svm  0.8333333 0.9166667 0.9583333 0.9500000       1    1    0
## rf   0.9166667 0.9166667 0.9583333 0.9583333       1    1    0
##
## Kappa
##       Min. 1st Qu. Median   Mean 3rd Qu. Max. NA's
## lda  0.875 0.90625 1.0000 0.9625       1    1    0
## cart 0.875 0.87500 0.9375 0.9375       1    1    0
## knn  0.875 0.90625 1.0000 0.9625       1    1    0
## svm  0.750 0.87500 0.9375 0.9250       1    1    0
## rf   0.875 0.87500 0.9375 0.9375       1    1    0
```

```
dotplot(results)
```




```
print(fit.lda)
```

```
## Linear Discriminant Analysis
##
## 120 samples
##   4 predictor
##   3 classes: 'setosa', 'versicolor', 'virginica'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 108, 108, 108, 108, 108, 108, ...
## Resampling results:
##
##   Accuracy  Kappa
##   0.975     0.9625
```

# Predict

```
# estimate skill of LDA on the validation dataset
predictions <- predict(fit.lda, validation)
confusionMatrix(predictions, validation$Species)
```

```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction   setosa versicolor virginica
##   setosa         10          0         0
##   versicolor      0         10         1
##   virginica       0          0         9
##
## Overall Statistics
##
##                Accuracy : 0.9667
##                  95% CI : (0.8278, 0.9992)
##     No Information Rate : 0.3333
##     P-Value [Acc > NIR] : 2.963e-13
##
##                   Kappa : 0.95
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: setosa Class: versicolor Class: virginica
## Sensitivity                 1.0000            1.0000           0.9000
## Specificity                 1.0000            0.9500           1.0000
## Pos Pred Value              1.0000            0.9091           1.0000
## Neg Pred Value              1.0000            1.0000           0.9524
## Prevalence                  0.3333            0.3333           0.3333
## Detection Rate              0.3333            0.3333           0.3000
## Detection Prevalence        0.3333            0.3667           0.3000
## Balanced Accuracy           1.0000            0.9750           0.9500
```