

# Tutorial 1: Introduction to Machine Learning with Python¶

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## Tutorial 1: Introduction to Machine Learning with Python

The goal of this tutorial is to introduce a typical workflow in carrying out ML in R. Similarly to last week's Python tutorial, this includes:

1. accessing and organising data,
2. assessing the data,
3. visualising the data,
4. a) creating training, b) test datasets and c) learning a model using them and evaluating its performance.

### 1) Load Data

We load the same iris dataset as last week, which has 150 samples and 4 attributes. There are 3 classes (species).

In R we can load the Iris dataset from the `datasets` package:

```
library(datasets)
data(iris)
iris$Species <- as.character(iris$Species)
head(iris)
```

##	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
## 3	4.7	3.2	1.3	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

### 2) Statistics of the dataset

Now compute the mean, standard deviation, minimum and maximum of each attribute.

```
library(dplyr)

# Calculate the mean of each attribute
group.means <- iris %>%
  group_by(Species) %>%
  summarise_all(list(mean))
```

```

# Calculate the standard deviation of each attribute
group.sds <- iris %>%
  group_by(Species) %>%
  summarise_all(list(sd))

# Calculate the minimum of each attribute
group.mins <- iris %>%
  group_by(Species) %>%
  summarise_all(list(min))

# Calculate the maximum of each attribute
group.maxs <- iris %>%
  group_by(Species) %>%
  summarise_all(list(max))

```

### 3) Visualise the dataset

Make some exploratory plots here.

```

library(ggplot2)
library(GGally)

# A nice pairs plot of the 4 attributes and the class.
# The plot is colored by the species
ggpairs(iris, aes(color=Species, alpha=0.5), progress=FALSE)

```



We can see from the scatter plots that we should be able to separate the classes quite easily.

## 4) Classification using Least Squares

Here we will be carrying out classification using the least squares formulation on 2 classes of the dataset - setosa and versicolor.

a) Create separate datasets for the classes setosa and versicolor.

```
# Extract the rows that have the correct species
setosa <- iris[iris$Species=="setosa",]
```

```
versicolor <- iris[iris$Species=="versicolor",]
```

b) add a column to each dataset where the column is 1 if the class is setosa and -1 otherwise.

```
# Add a column to each dataframe with the appropriate label
setosa$output <- 1
versicolor$output <- -1
```

c) create training and test datasets, with 20% of the data for testing. This 80 training points and 20 testing points in total (half this per class).

```
# Splits a dataframe into training and test sets
train.test.split <- function(df, test.size=0.2) {
  train.idx <- sample(1:nrow(df),
                     as.integer((1.0-test.size)*nrow(df)),
                     replace=FALSE)
  return(list(train=df[train.idx,], test=df[-train.idx,]))
}

# Split each dataset
split.setosa <- train.test.split(setosa)
split.versicolor <- train.test.split(versicolor)

# Combine the two classes
training.data <- rbind(split.setosa$train, split.versicolor$train)
test.data <- rbind(split.setosa$test, split.versicolor$test)
```

d) apply the least squares solution to obtain an optimal solution for different combinations of the 4 available attributes.

```
# Creates all possible combinations of attributes
# attribute.combinations is a list whose elements are lists of attributes
attribute.names <- colnames(iris)[1:4]
attribute.combinations <- do.call(
  c,
  lapply(1:4, function(i) as.list(
    data.frame(combn(attribute.names, i), stringsAsFactors=FALSE)))
)
names(attribute.combinations) <- 1:length(attribute.combinations)

# Now fit the least squares model and make predictions
return.predictions <- function(attribute.names, training.data, test.data) {
  # Format training and test data (as matrices)
  X <- as.matrix(training.data[attribute.names])
  y <- as.matrix(training.data$output)
  X.test <- as.matrix(test.data[attribute.names])

  # Calculate optimal weights
  W.opt <- solve(t(X) %*% X, t(X) %*% y)
```

```

# Make predictions
predictions <- X.test %*% W.opt
return(predictions)
}

```

e) evaluate which input attributes are the best.

```

# Calculate the mean square error between some predictions and
# the corresponding testing data
return.mse <- function(predictions, test.data) {
  y.test <- as.numeric(test.data$output)
  error <- y.test - predictions
  square.error <- error**2.0
  mse <- mean(square.error)
  return(mse)
}

# Calculate the test MSE for each the elements of attribute.combinations
# by calling return.predictions and return.mse

# MSE as a dataframe
mse.df <- as.data.frame(
  sapply(
    attribute.combinations,
    function(a.names) return.mse(
      return.predictions(
        a.names, training.data, test.data),
        test.data
      )
    )
  )
colnames(mse.df)[[1]] <- "mean.square.error"

# attribute.combinations is a list of lists, but for plotting we want to flatten
# it into a single list
mse.df$attributes <- sapply(attribute.combinations, function(x) paste(x, collapse=", "))

# Plot the result
ggplot(mse.df, aes(x=reorder(attributes, mean.square.error), y=mean.square.error)) +
  geom_bar(stat="identity") +
  theme(axis.text.x=element_text(angle=60, hjust=1)) +
  xlab("Attributes") + ylab("Mean square error")

```

