

Exercie 1: Linear Decision Boundaries

Part A

Lets load and important the iris data set

```
data(iris)
summary(iris)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## Min. :4.300 Min. :2.000 Min. :1.000 Min. :0.100
## 1st Qu.:5.100 1st Qu.:2.800 1st Qu.:1.600 1st Qu.:0.300
## Median :5.800 Median :3.000 Median :4.350 Median :1.300
## Mean :5.843 Mean :3.057 Mean :3.758 Mean :1.199
## 3rd Qu.:6.400 3rd Qu.:3.300 3rd Qu.:5.100 3rd Qu.:1.800
## Max. :7.900 Max. :4.400 Max. :6.900 Max. :2.500
## Species
## setosa :50
## versicolor:50
## virginica :50
##
##
##
```

```
# Lets look at the head of the iris data set
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
```

```
# Number of rows of the iris dataset (number of individual observations)
nrow(iris)
```

```
## [1] 150
```

```
# All of the columns are numeric except for the species column
```

```
# They are continuous because they correspond to length and width (except for species) # The species are categorical
sapply(iris, class)
```

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

```
# The only categorical variable is species in this iris dataset
sapply(iris, class)
```

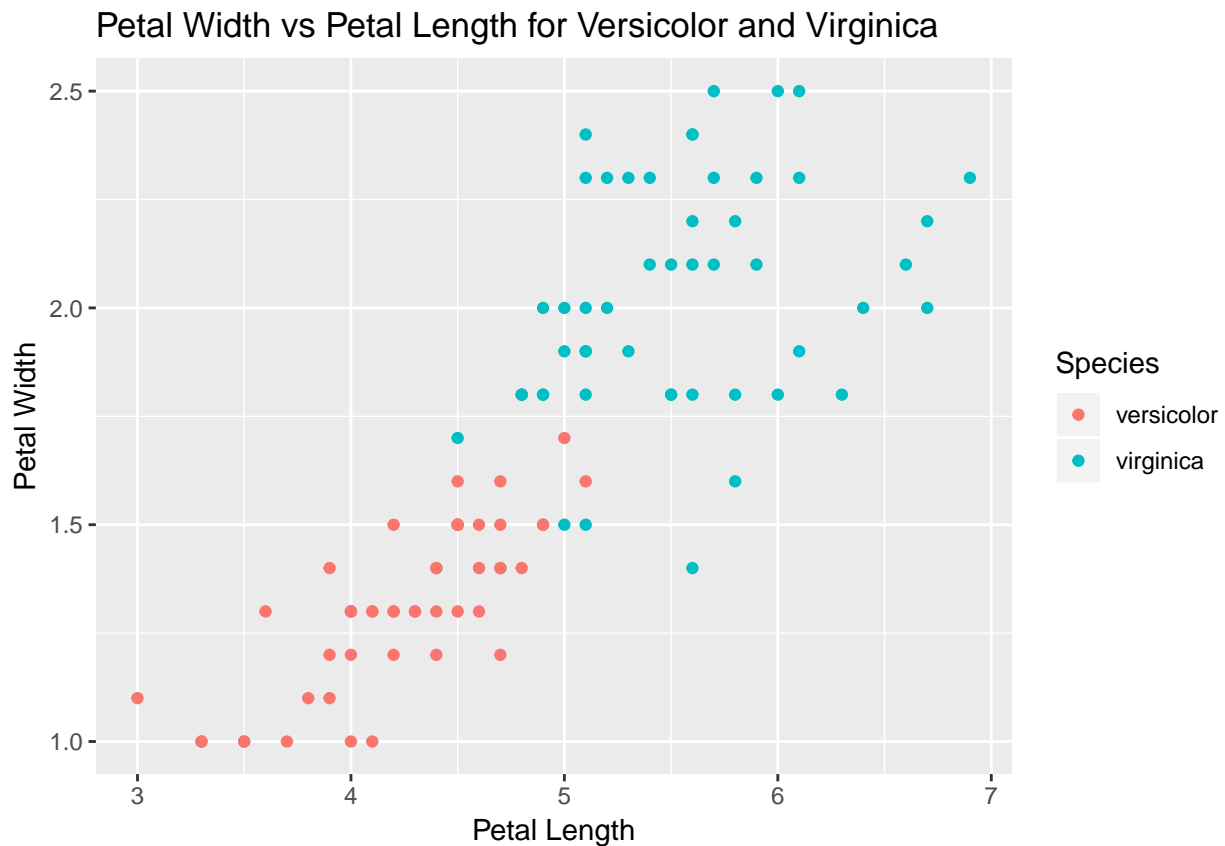
```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## "numeric" "numeric" "numeric" "numeric" "factor"
```

From our observations it looks like there are 50 samples of three species: setosa, versicolor and virginica. Each of the samples has measurements of sepal length, sepal width and petal length.

Let's plot the second and third iris classes:

```
# Lets pick the 2nd and 3rd classes: versicolor and virginica and let's plot the subset
plot1 <- iris %>% filter(Species == 'versicolor' | Species == 'virginica') %>%
ggplot(aes(x = Petal.Length, y = Petal.Width, color = Species)) + geom_point() +
labs(color = "Species") + xlab("Petal Length") + ylab("Petal Width") +
ggtitle("Petal Width vs Petal Length for Versicolor and Virginica")
```

plot1



Part B

The following function will take in five inputs (c_0 , c_1 , c_2) which are constants that will be estimated later in this exercise and (x_1 , x_2) which correspond to petal width and petal length. The output will return a value between a probability value between 0 and 1 where all values above 0.5 will correspond to the 3rd iris class and values below 0.5 to the 2nd iris class.

```
# inputs: c0, c1, c2, petal_width, petal_length
# outputs:
```

```
one_layer_neural_network <- function(c0, c1, c2, petal_width, petal_length) {

  # Linear function
  z <- c0 + c1*x1 + c2*x2

  #result
  result <- 1/(1 + exp(1)^(-z))
}
```

```

    return(result)
  }

```

Part C

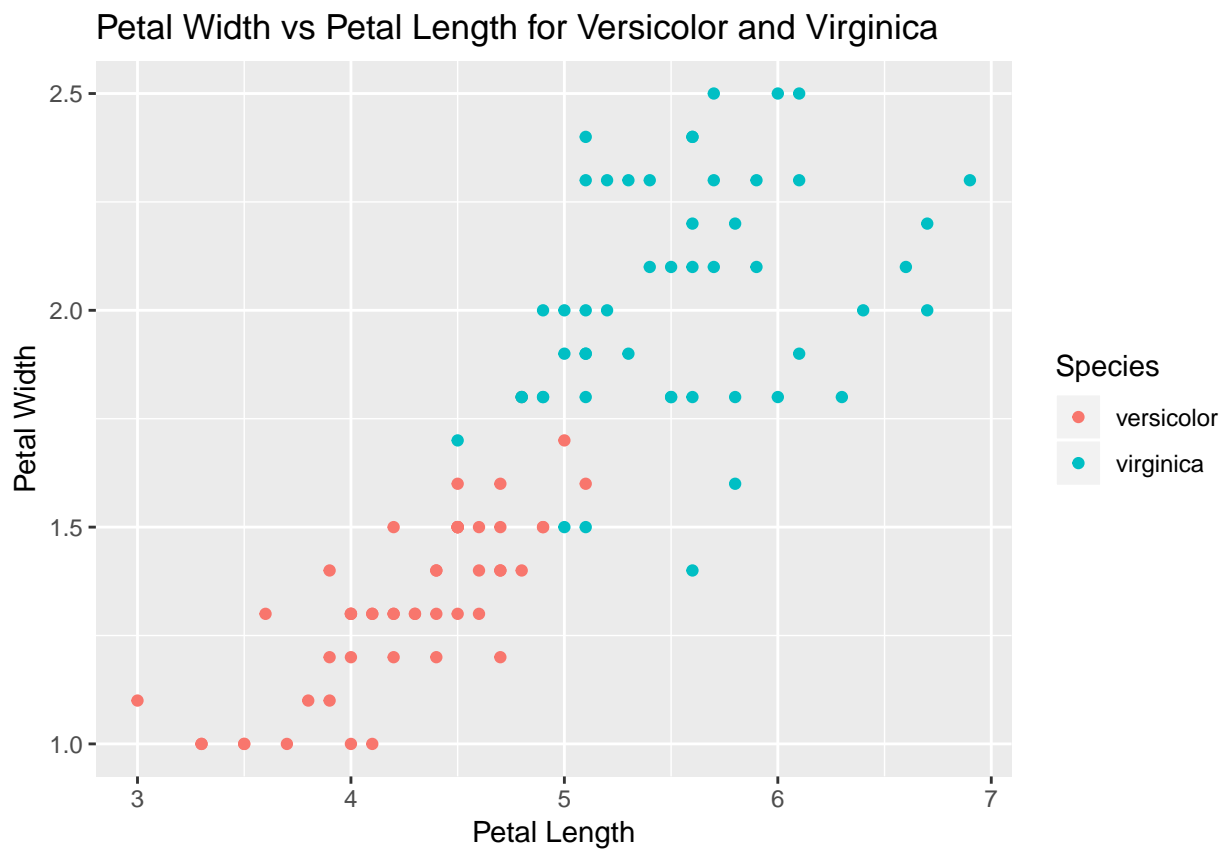
We are going to estimate the constant values such as...

```

# Lets pick the 2nd and 3rd classes: versicolor and virginica and let's plot the subset
plot2 <- iris %>% filter(Species == 'versicolor' | Species == 'virginica') %>%
  ggplot(aes(x = Petal.Length, y = Petal.Width, color = Species)) + geom_point() +
  labs(color = "Species") + xlab("Petal Length") + ylab("Petal Width") +
  ggtitle("Petal Width vs Petal Length for Versicolor and Virginica")

```

plot2



Part D ### Part E