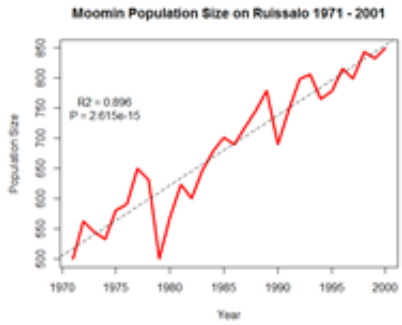
R Base Graphics: An Idiot's Guide

One of the most powerful functions of R is it's ability to produce a wide range of graphics to quickly and easily visualise data. Plots can be replicated, modified and even publishable with just a handful of commands.

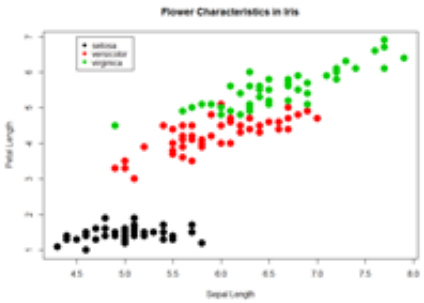
Making the leap from chiefly graphical programmes, such as Excel and Sigmaplot. may seem tricky. However, with a basic knowledge of R, just investing a few hours could completely revolutionise your data visualisation and workflow. Trust me - it's worth it.

Last year, I presented an informal course on the basics of R Graphics University of Turku. In this blog post, I am providing some of the slides and the full code from that practical, which shows how to build different plot types using the basic (i.e. pre-installed) graphics in R, including:

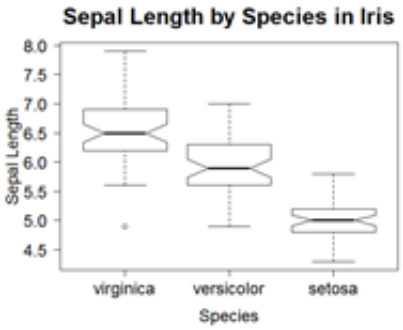
1. Basic Histogram



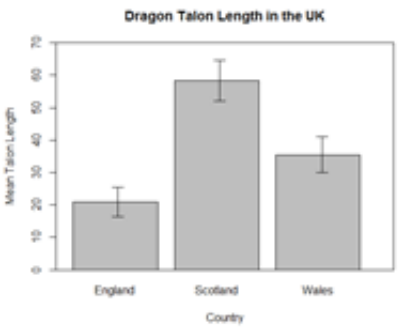
2. Line Graph with Regression



3. Scatterplot with Legend



4. Boxplot with reordered/ formatted axes



5. Boxplot with Error Bars

Exciting, eh?

This post is BIG, but DETAILED. So, use the links below to jump ahead. I hope someone out there finds this useful - all code and datafiles are available here.

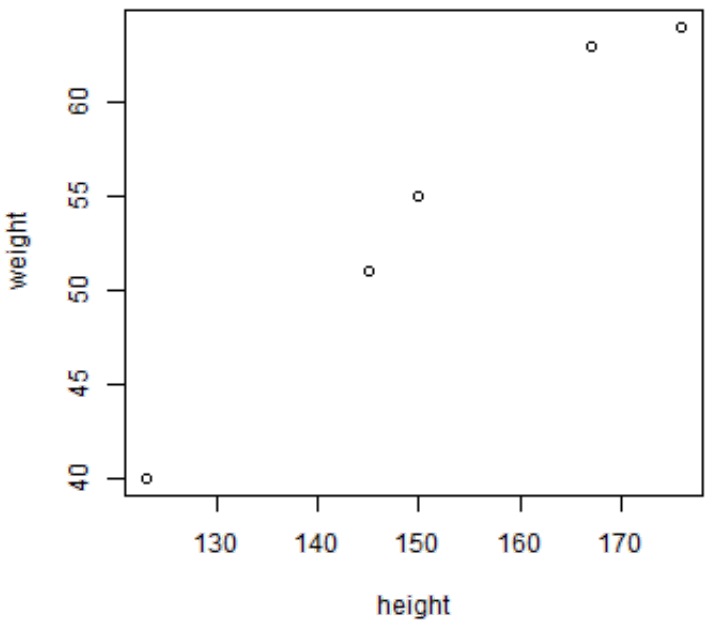
Menu:

0. Preface: What am I supposed to know again?

Oh you. Before you get started, you should be familiar with the follow concepts:

Vectors!

```
height <- c(145, 167, 176, 123, 150)
weight <- c(51, 63, 64, 40, 55)

plot(height,weight)
```



Data frames!

```
tarsus <- read.table("tarsus.txt", header = T)
tarsus
```

```
##    TarsusLength Weight
## 1            23    231
## 2            26    258
## 3            25    254
## 4            21    211
## 5            27    268
## 6            28    284
## 7            27    271
## 8            26    258
## 9            26    264
## 10           25    251
## 11           26    258
## 12           24    244
## 13           25    251
## 14           25    248
## 15           23    234
## 16           21    211
```

To call a variable in the dataframe, use the $ notation.

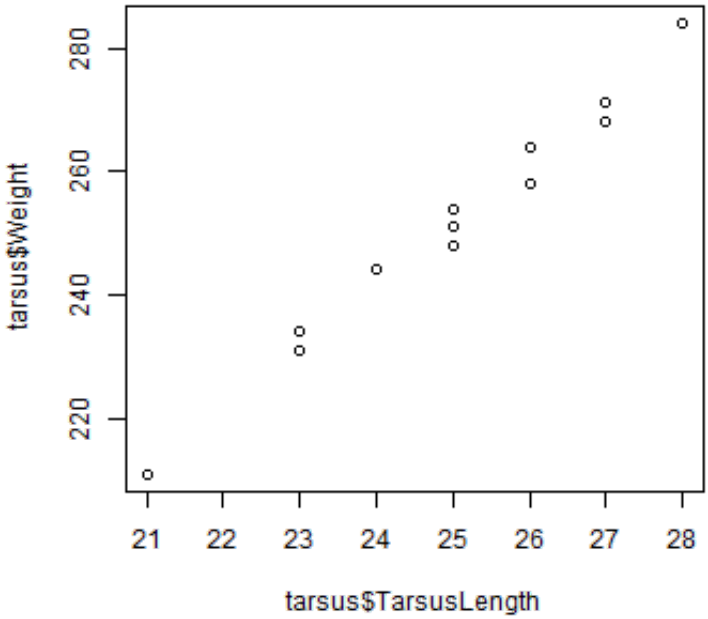
```
tarsus$TarsusLength
```

```
##  [1] 23 26 25 21 27 28 27 26 26 25 26 24 25 25 23 21
```

```
tarsus$Weight
```

```
##  [1] 231 258 254 211 268 284 271 258 264 251 258 244 251
248 234 211
```

```

plot(tarsus$TarsusLength,tarsus$Weight)
```

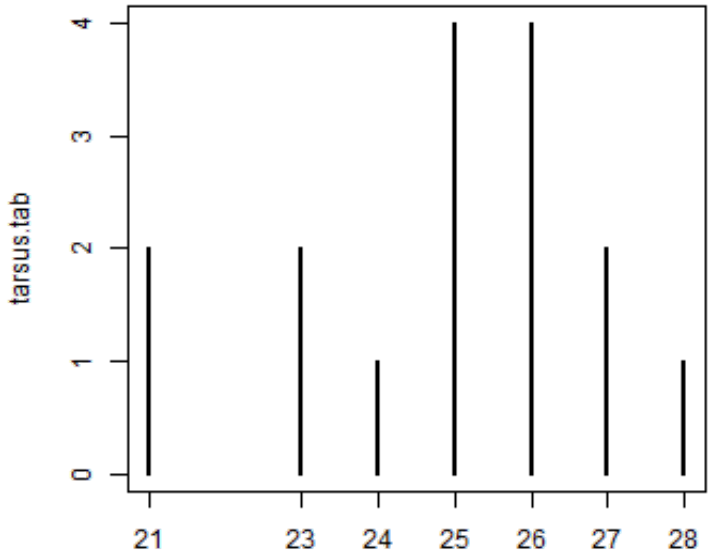


Tables!

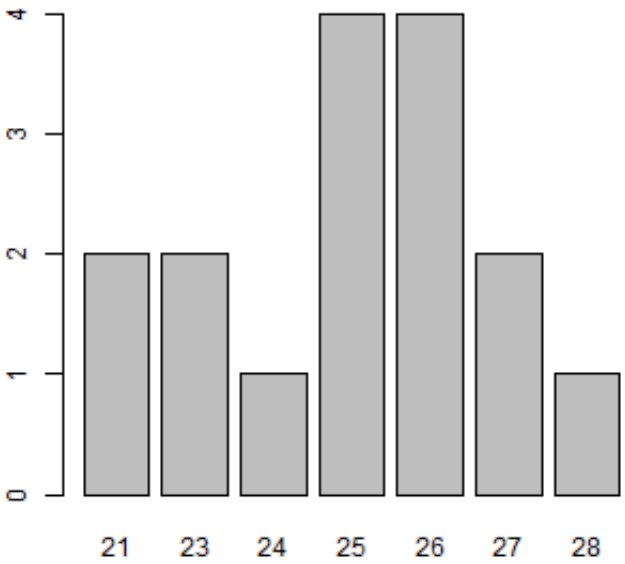
```
tarsus.tab <- table(tarsus$TarsusLength)

tarsus.tab
```

```
##
## 21 23 24 25 26 27 28
##  2  2  1  4  4  2  1
```

```
plot(tarsus.tab)
```

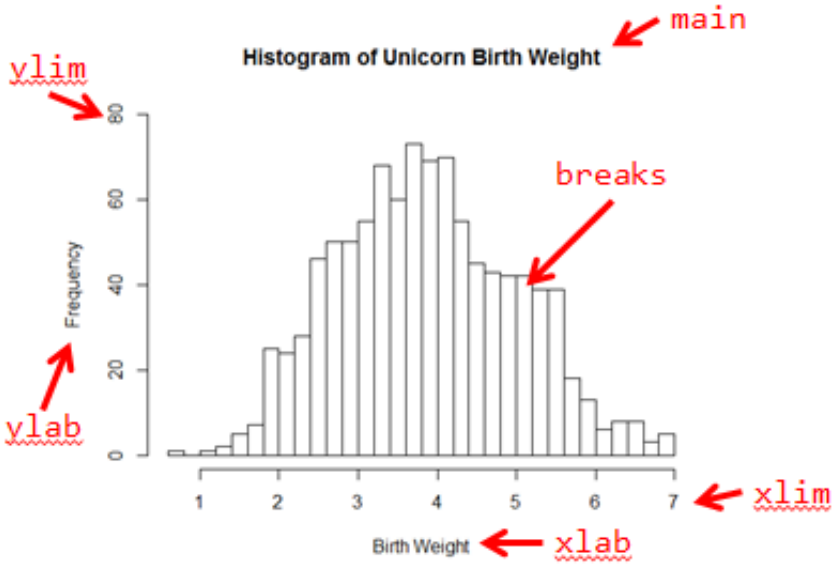



```
barplot(tarsus.tab)
```



1. Basic Histogram

What customisations are we going to learn in this section?




```
#~~ FINAL PLOT:

hist(unicorns$birthweight,                          # x value
     breaks = 40,                                   # number of cells
     xlab = "Birth Weight",                         # x-axis label
     main = "Histogram of Unicorn Birth Weight",    # plot title
     ylim = c(0,80))                                # limits of the y axis (min,max)

```

Let's begin. For this part, we will use data on birthweight measured in male and female unicorns.

Let's read the data into R:

```
unicorns <- read.table("unicorns.txt" ,header = T)
head(unicorns)
```

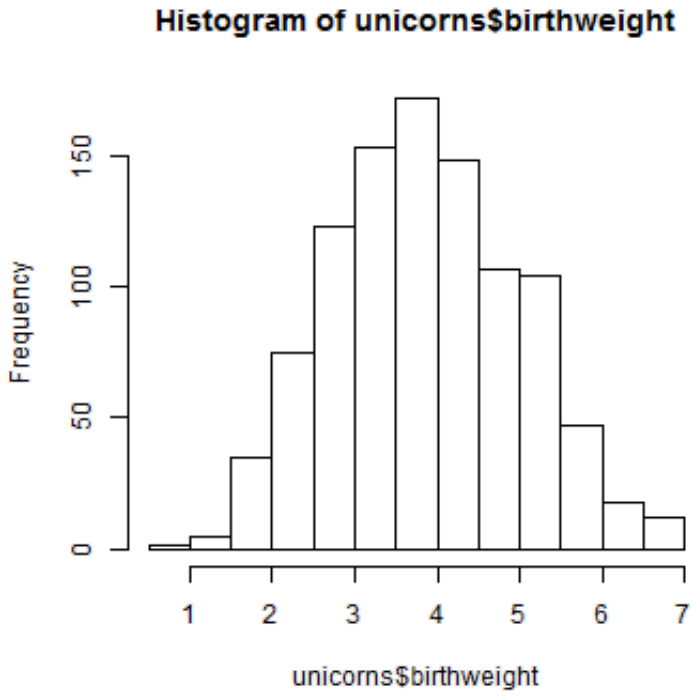
```
##   birthweight  sex longevity
## 1       4.478 Male         1
## 2       5.753 Male         0
## 3       3.277 Male         0
## 4       3.929 Male         0
## 5       3.973 Male         0
## 6       4.913 Male         0
```

```
str(unicorns)
```

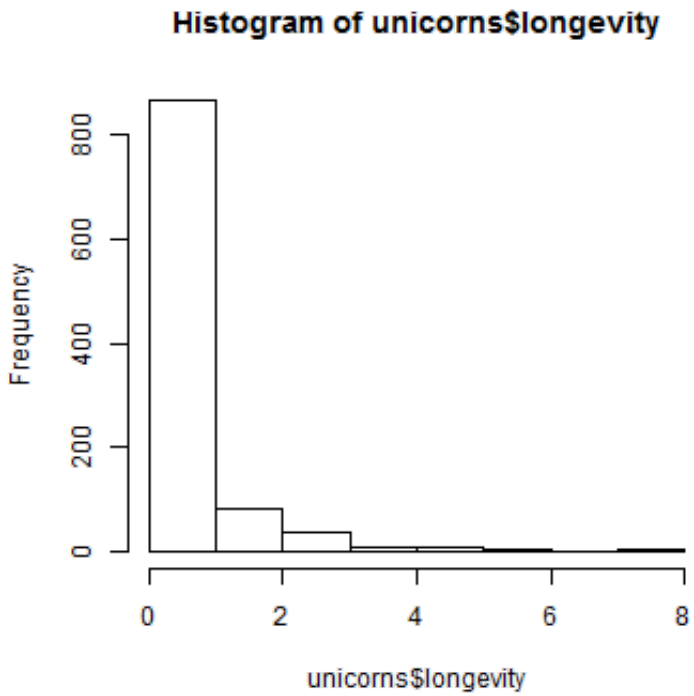
```
## 'data.frame':    1000 obs. of  3 variables:
##  $ birthweight: num  4.48 5.75 3.28 3.93 3.97 ...
##  $ sex        : Factor w/ 2 levels "Female","Male": 2 2
2 2 2 2 2 2 2 2 ...
##  $ longevity  : int  1 0 0 0 0 0 1 0 0 1 ...
```

We can create a basic histogram of unicorn birthweight and longevity using hist():

```
hist(unicorns$birthweight)              # normal distribution
```

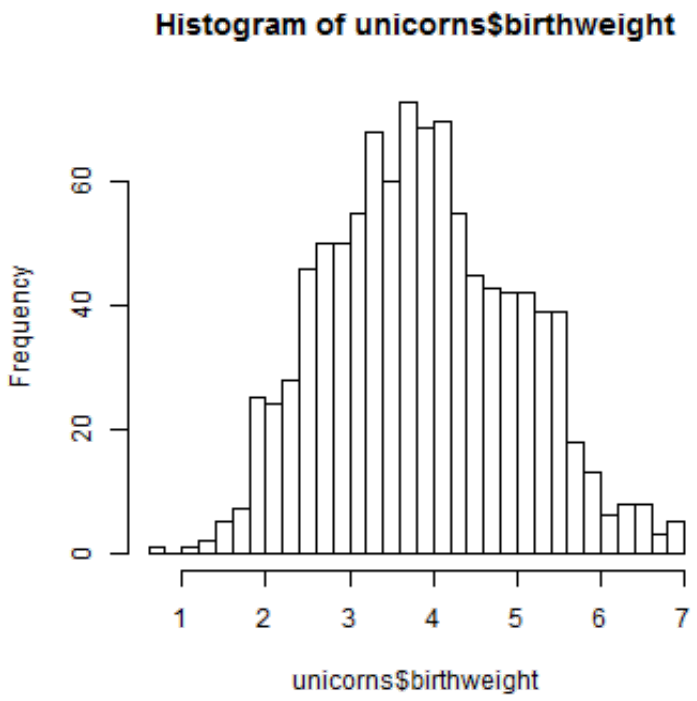



```
hist(unicorns$longevity)                # poisson
distribution
```

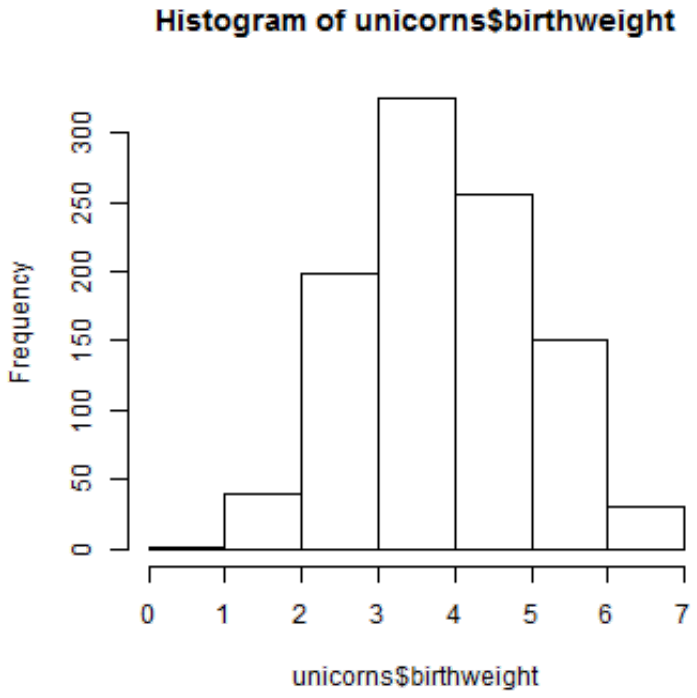


And we can specify the number of cells for the histogram using: breaks = N:

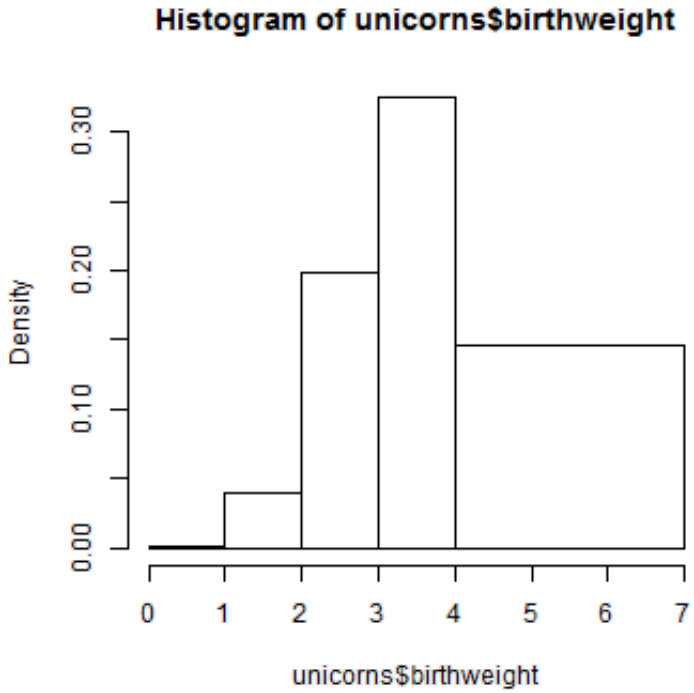
```
hist(unicorns$birthweight, breaks = 40)
```




```
hist(unicorns$birthweight, breaks = c(0,1,2,3,4,5,6,7))
```

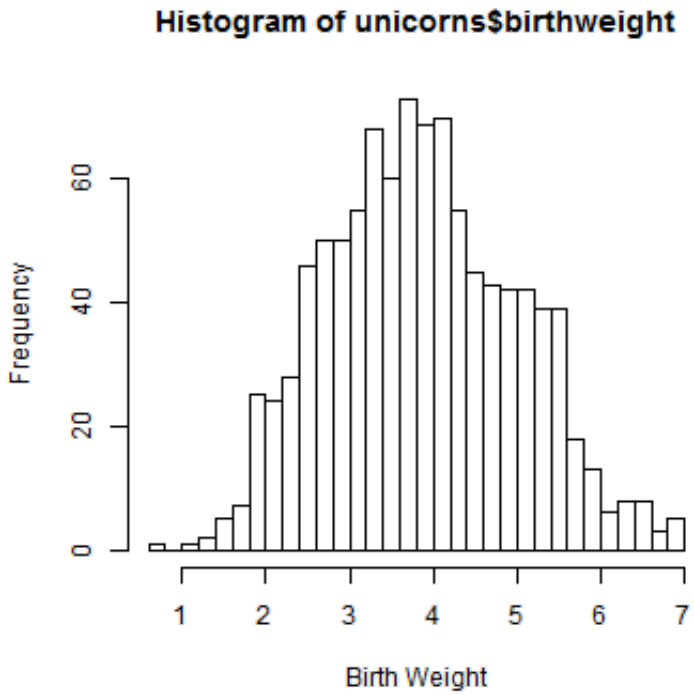



```
hist(unicorns$birthweight, breaks = c(0,1,2,3,4,7))
```



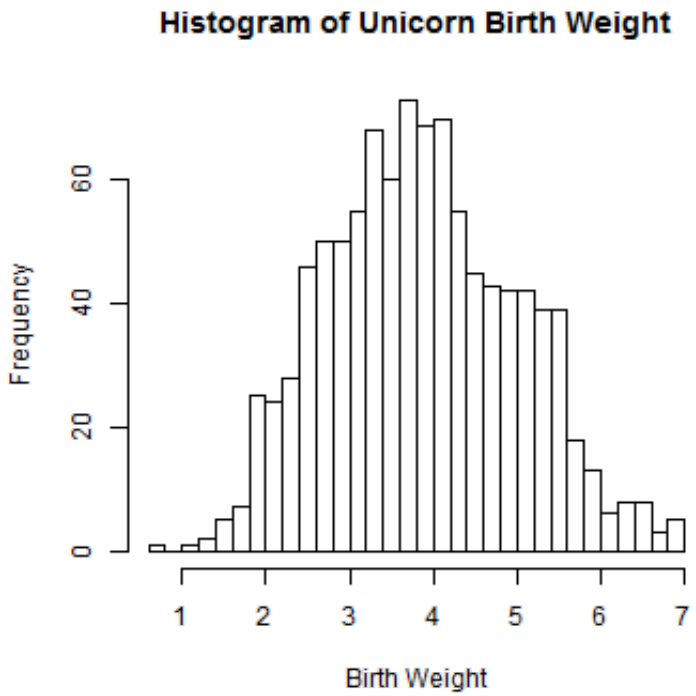
Relabel the x-axis using: xlab = “Text”

```
hist(unicorns$birthweight, breaks = 40, xlab = "Birth
Weight")
```



Relabel the main title using: main = “Text”

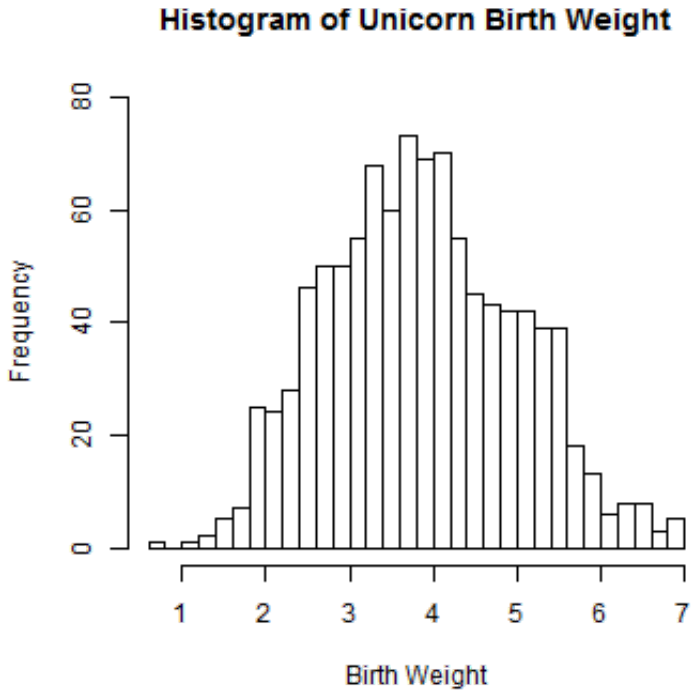
```
hist(unicorns$birthweight,
     breaks = 40,
     xlab = "Birth Weight",
     main = "Histogram of Unicorn Birth Weight")
```



NB: In our code, the lines are starting to get quite long. When there is a comma, R knows that there is more information on the next line!

The y-axis stops short of the highest value in the histogram. Lets specify new limits using: ylim = c(minimum, maximum)

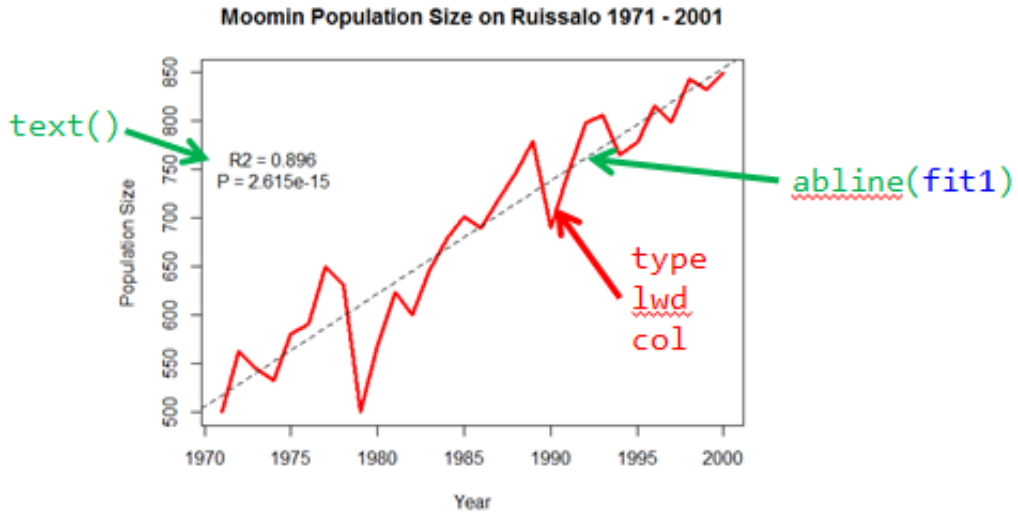
```
hist(unicorns$birthweight,
     breaks = 40,
     xlab = "Birth Weight",
     main = "Histogram of Unicorn Birth Weight",
     ylim = c(0,80))
```



2. Basic Line Graph with Regression

Moomins are a common pest species in Finland. We have data on their population on the island of Ruissalo from 1971 to 2000.

Which customisations will we learn here?



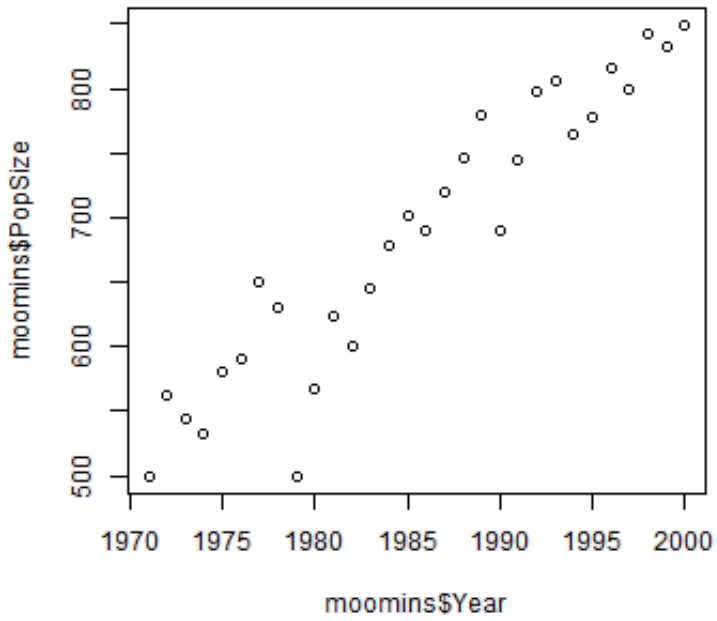

```
184 #~~ FINAL PLOT Script
185
186 plot(moomins$Year, moomins$PopSize,                          # x variable, y variable
187      type = "l",                                             # draw a line graphs
188      col = "red",                                            # red line colour
189      lwd = 3,                                                # line width of 3
190      xlab = "Year",                                          # x axis label
191      ylab = "Population Size",                               # y axis label
192      main = "Moomin Population Size on Ruissalo 1971 - 2001")    # plot title
193 fit1 <- lm (PopSize ~ Year, data = moomins)                  # carry out a linear regression
194 abline(fit1, lty = "dashed")                                 # add the regression line to the plot
195 text(x=1974,y=750,labels="R2 = 0.896\nP = 2.615e-15")        # add a label to the plot at coordinates (x,y)
196
```

```
moomins <- read.table("Moomin Density.txt", header = T)
head(moomins)
```

```
##   Year PopSize
## 1 1971     500
## 2 1972     562
## 3 1973     544
## 4 1974     532
## 5 1975     580
## 6 1976     590
```

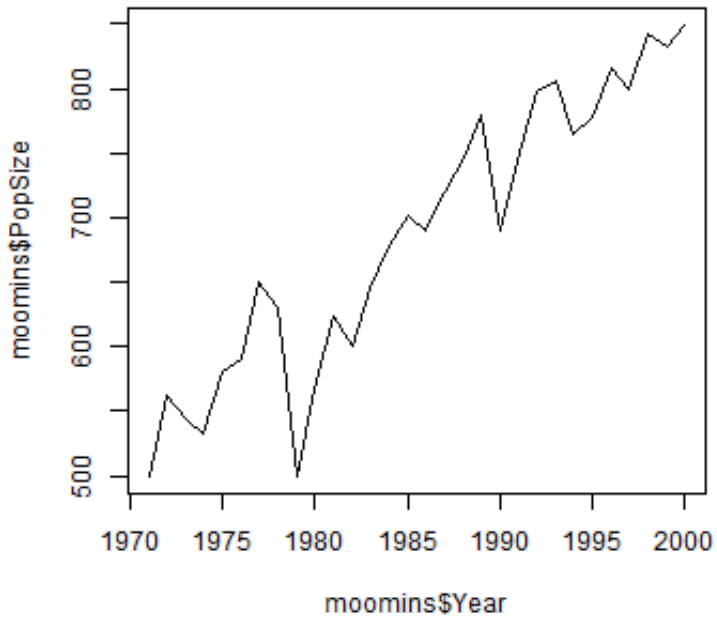
We can easily create a plot using the command `plot`.

```
plot(moomins$Year, moomins$PopSize)
```



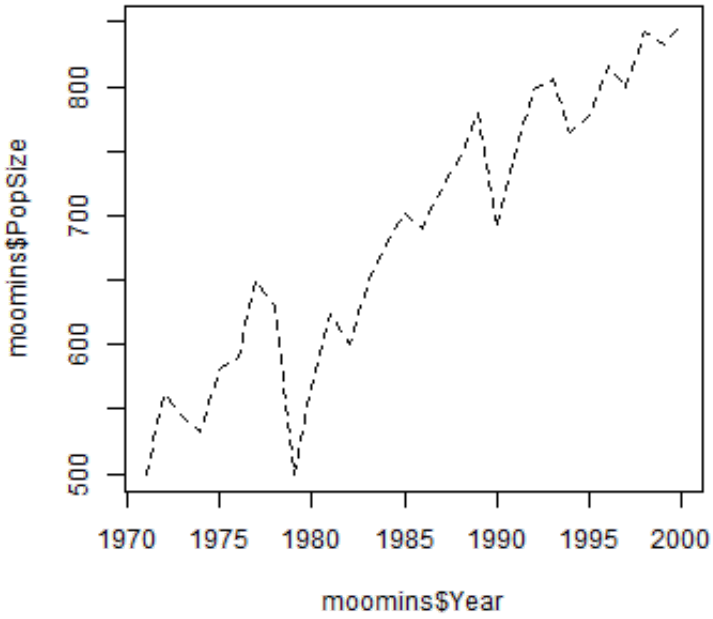
There are several types of plot within the plot function. Use “type”:

```
plot(moomins$Year, moomins$PopSize, type = "l")     # Try
"o" "p" "l" "b"
```

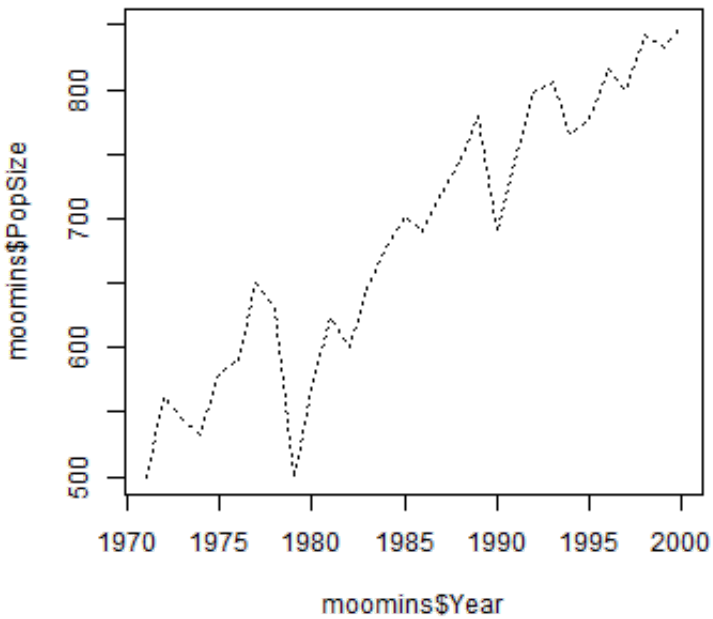


We can also change the line type using “lty”

```
plot(moomins$Year, moomins$PopSize, type = "l", lty =
"dashed")
```

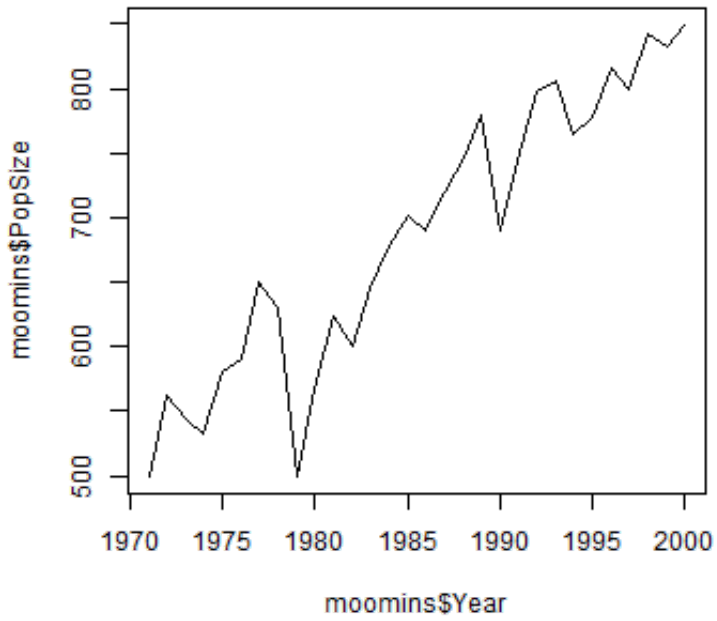



```
plot(moomins$Year, moomins$PopSize, type = "l", lty =
"dotted")
```



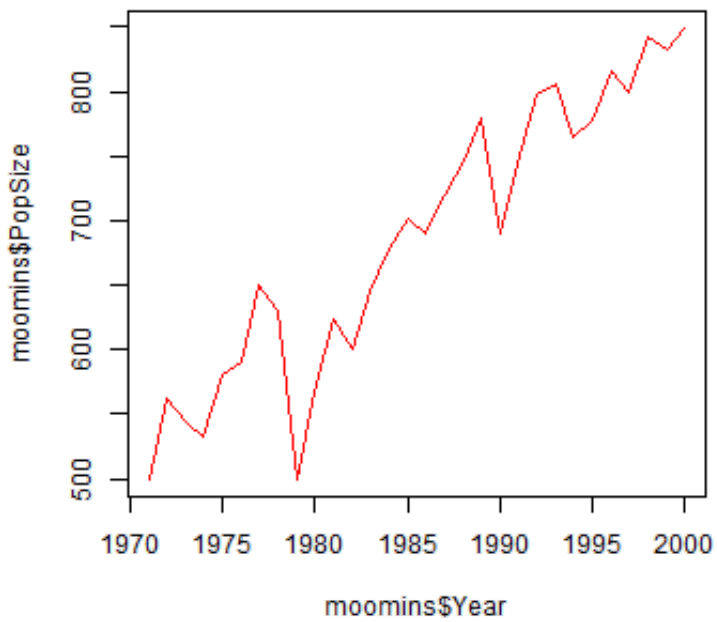
The solid line looks best, so lets stick with it.

```
plot(moomins$Year, moomins$PopSize, type = "l")
```



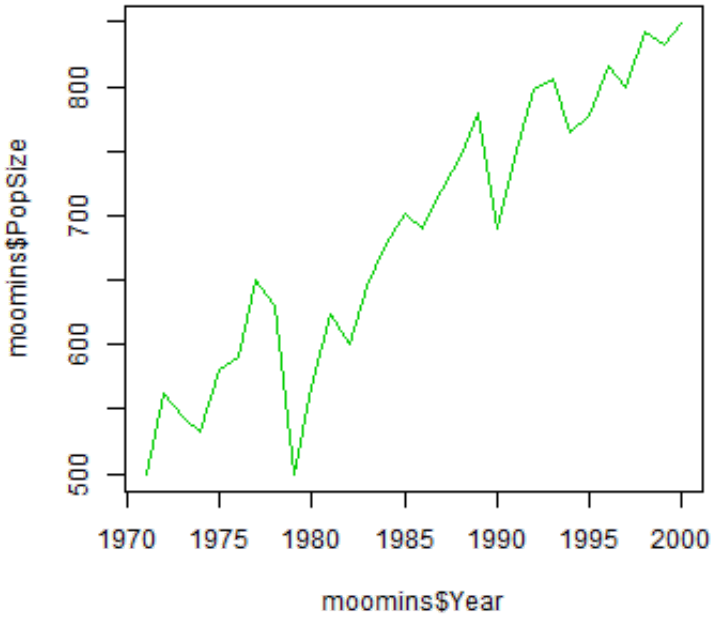
Let's start to add colour using “col”.

```
plot(moomins$Year, moomins$PopSize, type = "l", col =
"red")    # R Colour Chart
```



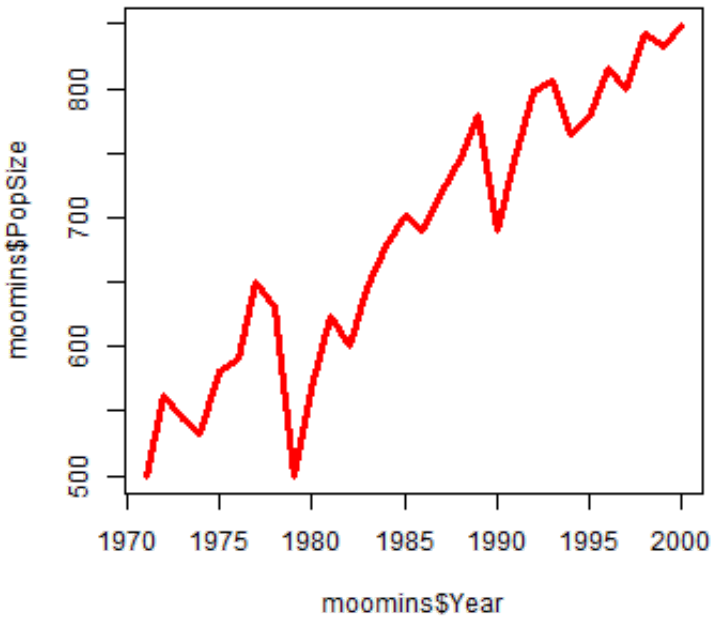
NB. numbers can also be used as colours!

```
plot(moomins$Year, moomins$PopSize, type = "l", col = 3)
```



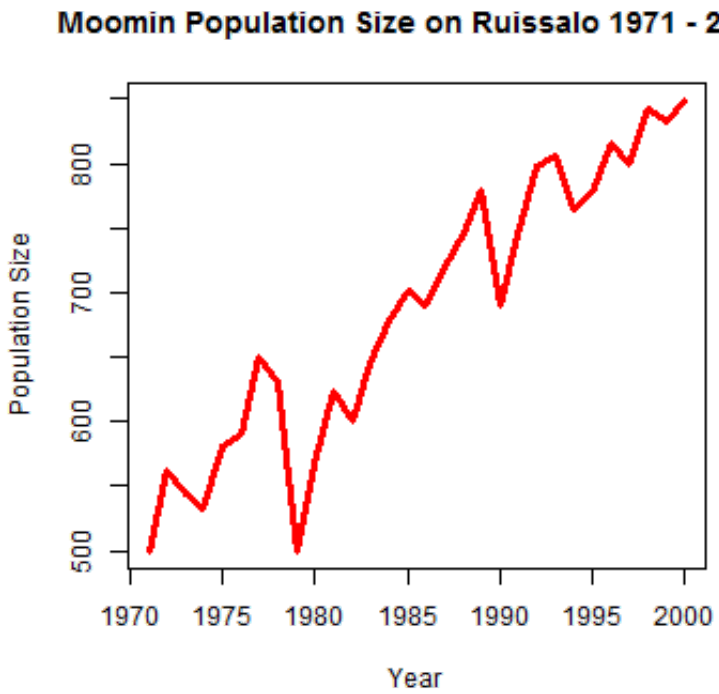
Let's make the line a little thicker using “lwd” (line width)

```
plot(moomins$Year, moomins$PopSize, type = "l", col =
"red", lwd = 3)
```



Finally, lets sort out the axis titles plot title:

```
plot(moomins$Year, moomins$PopSize,
     type = "l",
     col = "red",
     lwd = 3,
     xlab = "Year",
     ylab = "Population Size",
     main = "Moomin Population Size on Ruissalo 1971 -
2001")
```

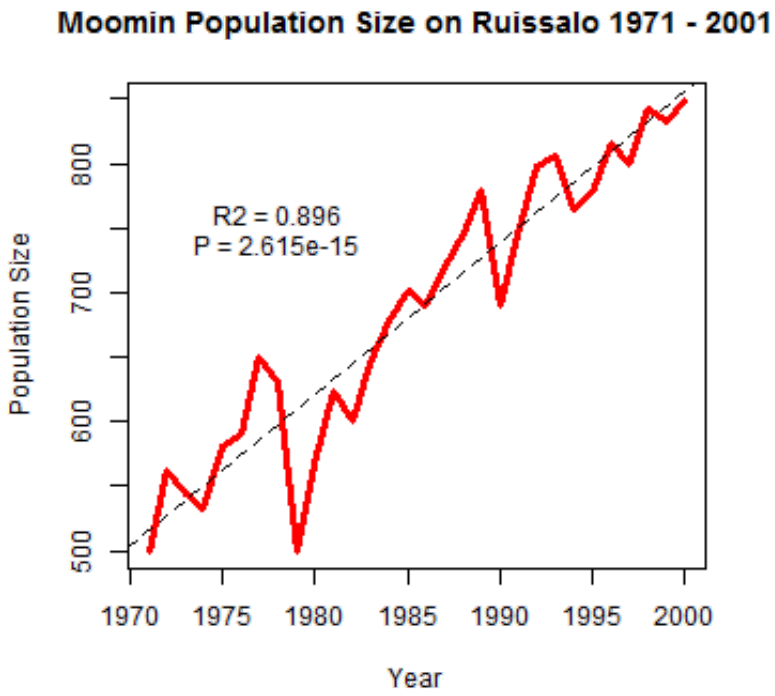


Is the Moomin population increasing in size? We can add a basic linear regression to the plot using `abline`. NB. we can also use lty, lwd, col here.

```
plot(moomins$Year, moomins$PopSize,
     type = "l",
     col = "red",
     lwd = 3,
     xlab = "Year",
     ylab = "Population Size",
     main = "Moomin Population Size on Ruissalo 1971 -
2001")

fit1 <- lm (PopSize ~ Year, data = moomins)
summary(fit1)
```

```
##
## Call:
## lm(formula = PopSize ~ Year, data = moomins)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -109.52  -17.76    1.65   20.37   63.83
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -22493.93    1489.99   -15.1  5.6e-15 ***
## Year            11.67       0.75    15.6  2.6e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1
##
## Residual standard error: 35.6 on 28 degrees of freedom
## Multiple R-squared:  0.896,  Adjusted R-squared:  0.893
## F-statistic:  242 on 1 and 28 DF,  p-value: 2.61e-15
```

```
abline(fit1, lty = "dashed")    #abline(a = intercept, b =
slope)

#~~ We can add some text to the plot giving the R2 value
and the P value using "text" and specifying the x and y
coordinates for the text.

text(x  =1978, y = 750,labels="R2 = 0.896\nP = 2.615e-15")
```

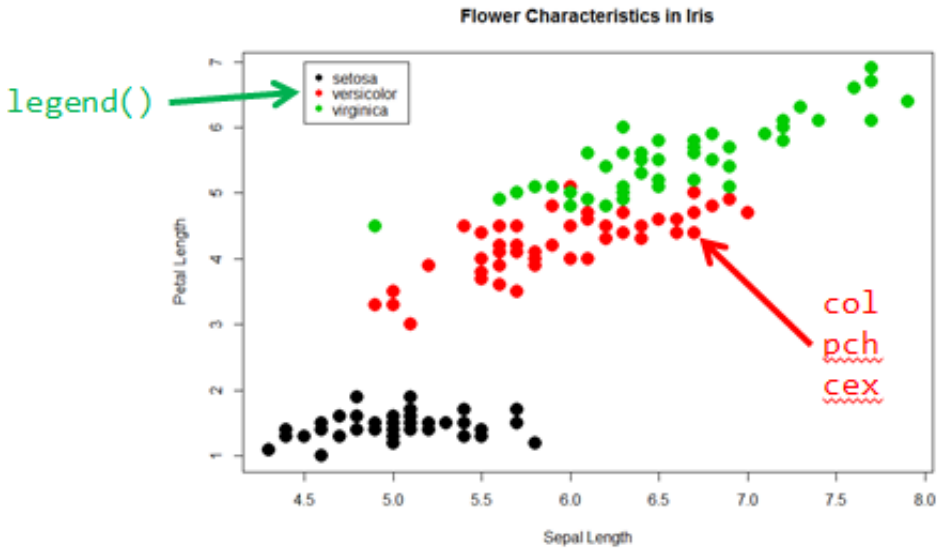


Final script:

```
plot(moomins$Year, moomins$PopSize,
# x variable, y variable
     type = "l",
# draw a line graphs
     col = "red",
# red line colour
     lwd = 3,
# line width of 3
     xlab = "Year",
# x axis label
     ylab = "Population Size",
# y axis label
     main = "Moomin Population Size on Ruissalo 1971 -
2001")    # plot title

fit1 <- lm (PopSize ~ Year, data = moomins)                #
carry out a linear regression
abline(fit1, lty = "dashed")                               #
add the regression line to the plot
text(x = 1978, y = 750, labels = "R2 = 0.896\nP = 2.615e-
15")   # add a label to the plot at (x,y)
```

3. Scatterplot with Legend

What will we learn here?




```
# FINAL PLOT

plot(iris$Sepal.Length, iris$Petal.Length,          # x variable, y variable
     col = iris$Species,                            # colour by species
     pch = 16,                                      # type of point to use
     cex = 2,                                       # size of point to use
     xlab = "Sepal Length",                         # x axis label
     ylab = "Petal Length",                         # y axis label
     main = "Flower Characteristics in Iris")       # plot title

legend (x = 4.5, y = 7, legend = levels(iris$Species), col = c(1:3), pch = 16)
# legend with titles of iris$Species and colours 1 to 3, point type pch at coords (x,y)
```

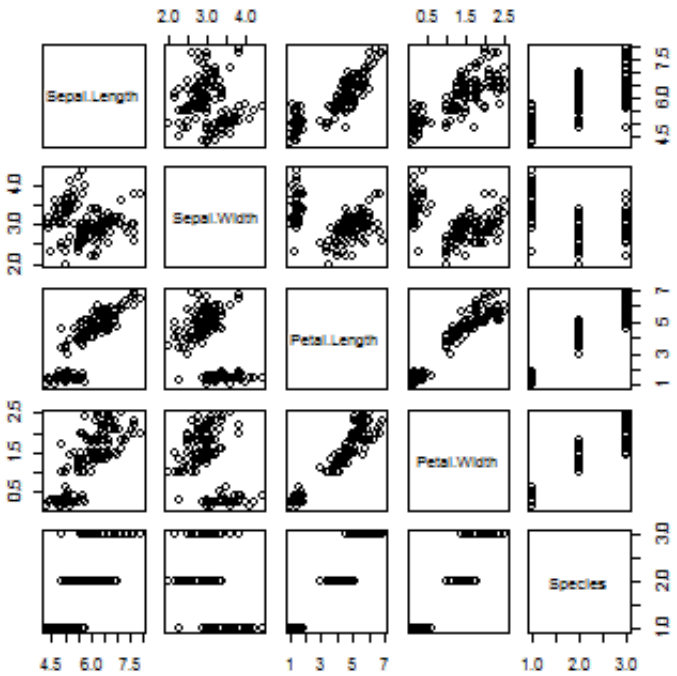
R comes with many datasets preinstalled. Let's load a dataset of Flower characteristics in 3 species of Iris.

```
data(iris)
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
```

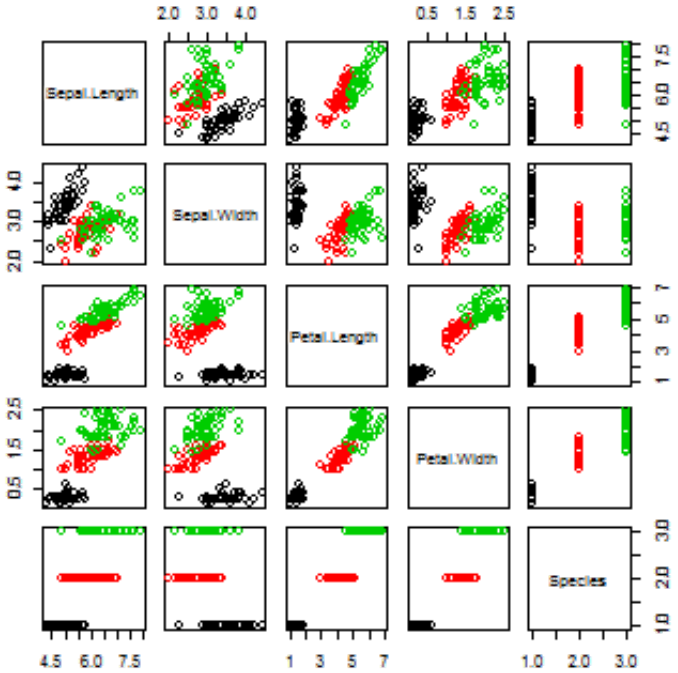
There is a lot of data here! Let's explore using the 'pairs' function

```
pairs(iris)
```



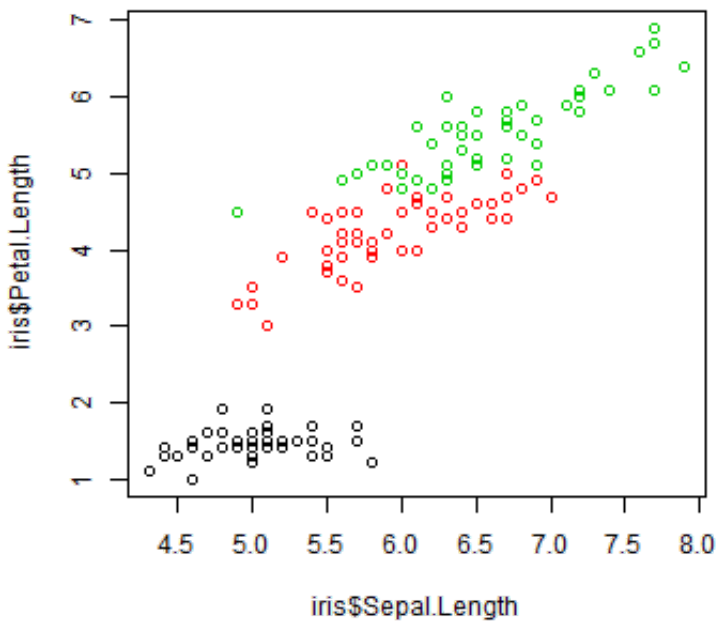
This doesn't tell us much about the species differences. We can tell R to plot using a different colour for the three species of iris:

```
pairs(iris, col = iris$Species)
```

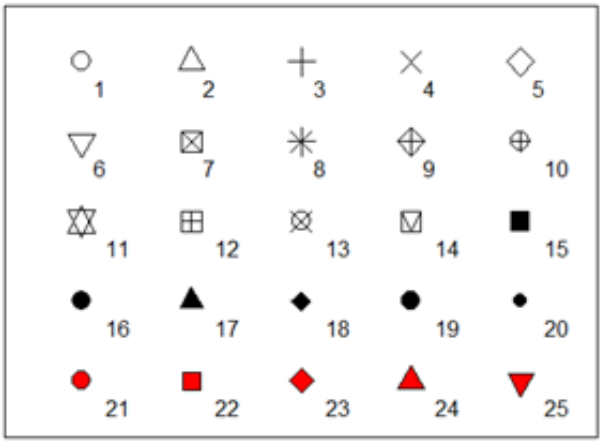


Sepal.Length and Petal.Length look interesting! Let's start by looking at that. Again, we will specify colour as the Species.

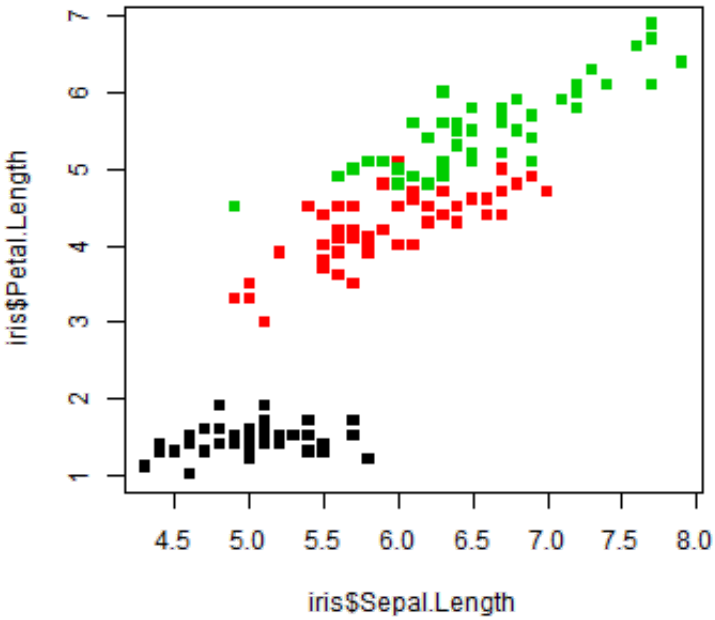
```
plot(iris$Sepal.Length, iris$Petal.Length, col =
iris$Species)
```



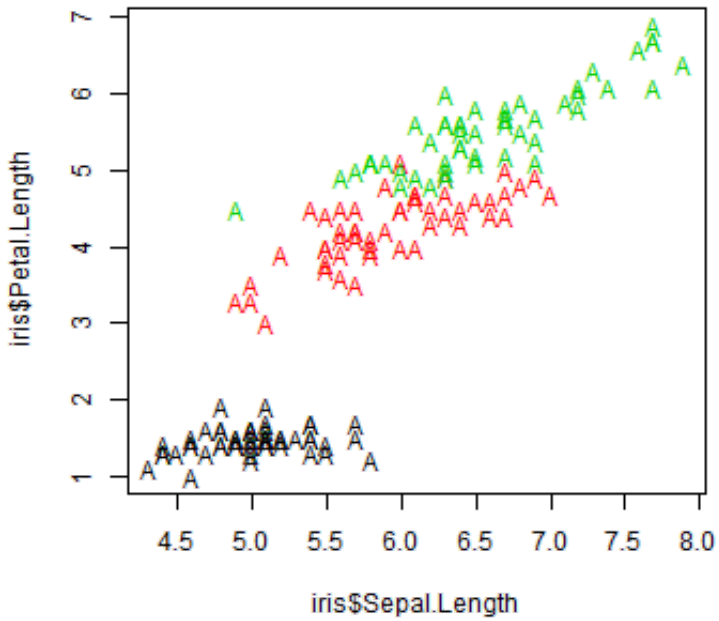
These points are difficult to see! Let's pick some different ones using “pch”




```
plot(iris$Sepal.Length, iris$Petal.Length, col =
iris$Species, pch = 15)
```

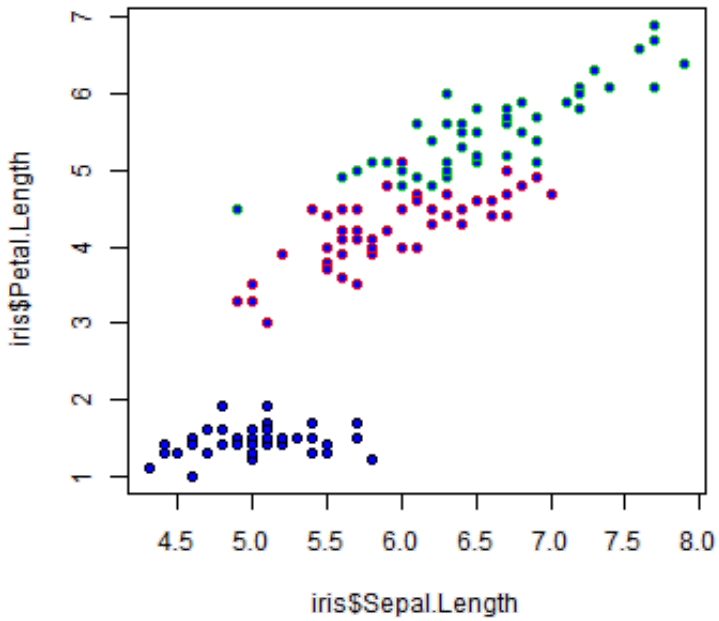



```
plot(iris$Sepal.Length, iris$Petal.Length, col =
iris$Species, pch = "A")
```



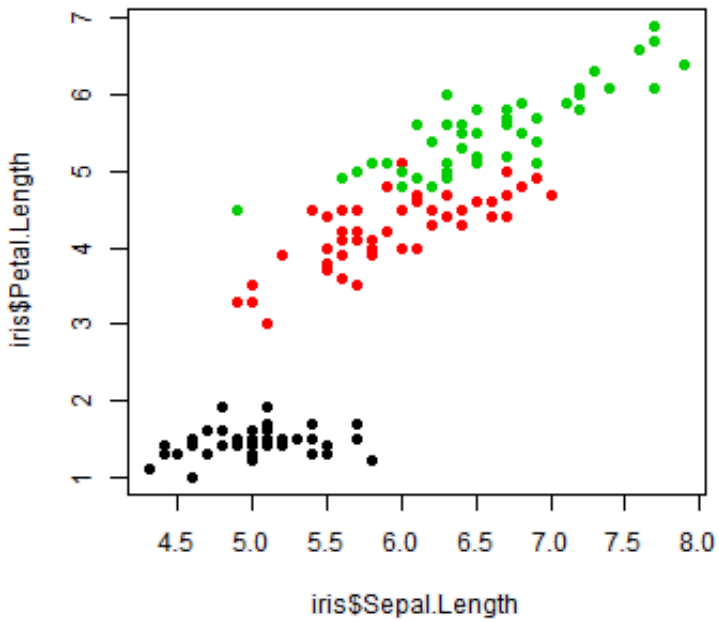
pch 21:25 also specify an edge colour (col) and a background colour (bg)

```
plot(iris$Sepal.Length, iris$Petal.Length, col =
iris$Species, pch = 21, bg = "blue")
```



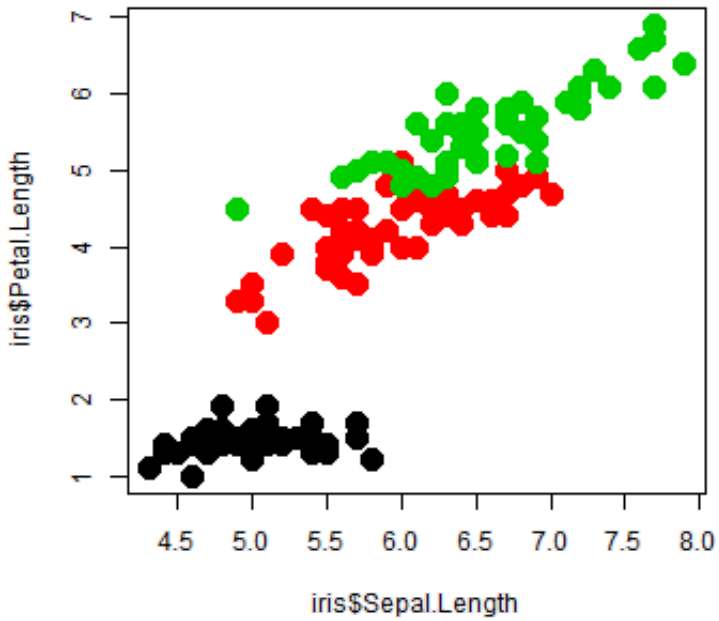
lets settle on solid circles (`pch = 16`)

```
plot(iris$Sepal.Length, iris$Petal.Length, col =
iris$Species, pch = 16)
```



We can change the size of the points with “cex”

```
plot(iris$Sepal.Length, iris$Petal.Length,
     col = iris$Species,
     pch = 16,
     cex = 2)
```



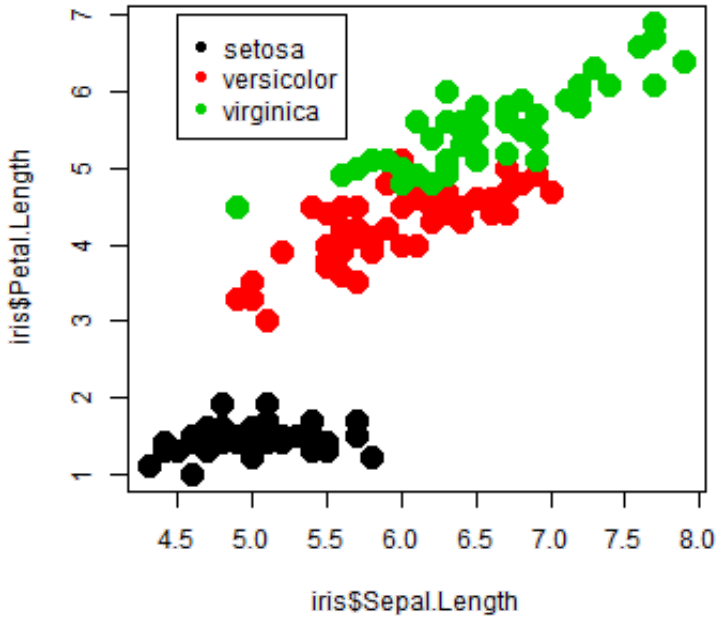
It's difficult to tell these points apart, so perhaps we should make a legend. This is one of the major drawbacks with R. iris$Species is a factor, and R will automatically order factors in alphabetical order.

```
levels(iris$Species)
```

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

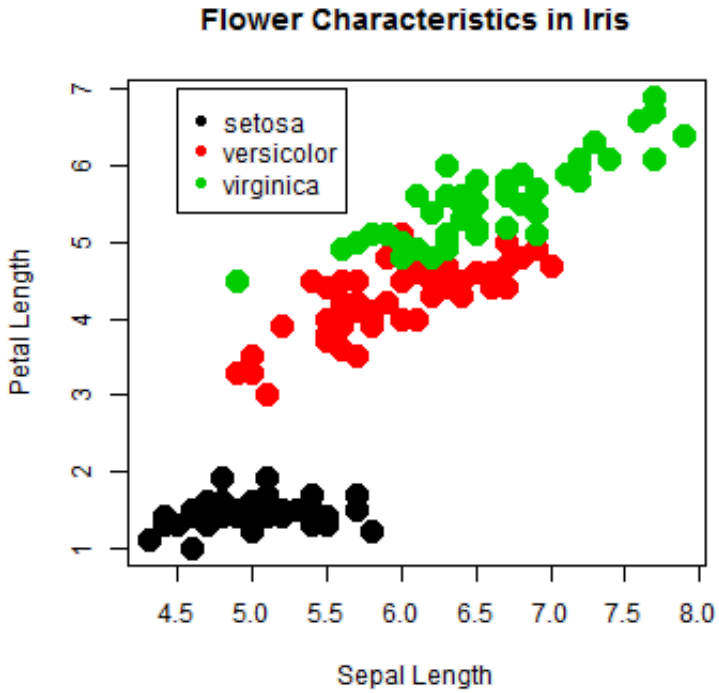
Therefore, setosa, versicolor and virginica will correspond to 1, 2 and 3 on the plot default colours. Keep this in mind for the next part!

```
plot(iris$Sepal.Length, iris$Petal.Length,
     col = iris$Species,
     pch = 16,
     cex = 2)
legend(x = 4.5, y = 7, legend = levels(iris$Species), col =
c(1:3), pch = 16)
```



FINAL PLOT

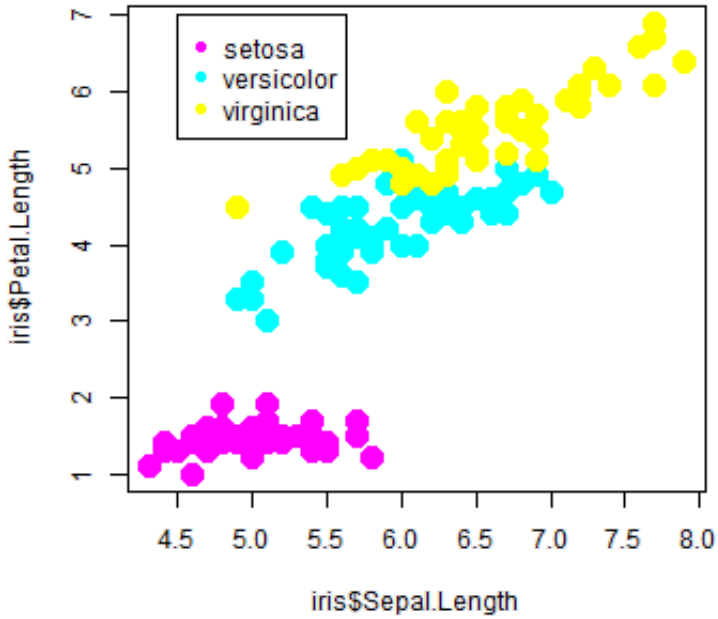
```
plot(iris$Sepal.Length, iris$Petal.Length,          # x
variable, y variable
     col = iris$Species,                            # colour
by species
     pch = 16,                                      # type of
point to use
     cex = 2,                                       # size of
point to use
     xlab = "Sepal Length",                         # x axis
label
     ylab = "Petal Length",                         # y axis
label
     main = "Flower Characteristics in Iris")       # plot
title

legend (x = 4.5, y = 7, legend = levels(iris$Species), col
= c(1:3), pch = 16)
```




```
#~~ legend with titles of iris$Species and colours 1 to 3,
point type pch at coords (x,y)
```

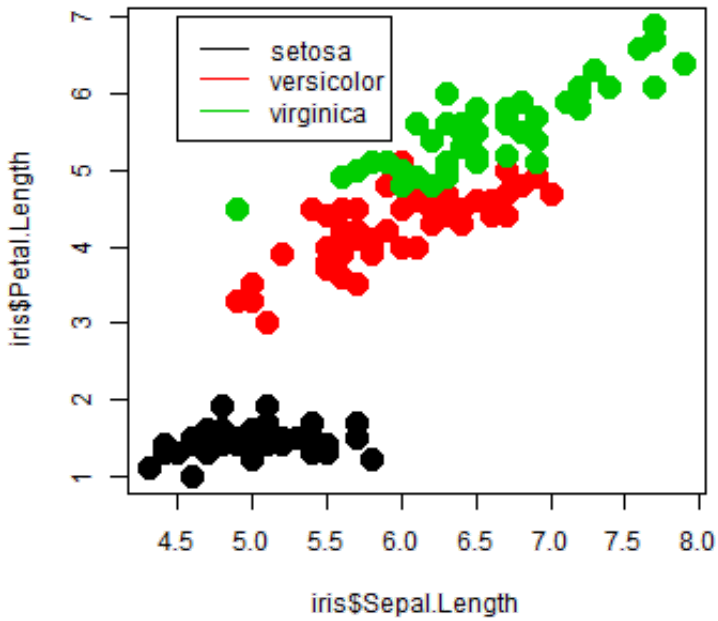
SIDE NOTE 1: specifying colours: It is also possible to specify colours in your data frame.

```
iris$Colour <- ""
iris$Colour[iris$Species=="setosa"] <- "magenta"
iris$Colour[iris$Species=="versicolor"] <- "cyan"
iris$Colour[iris$Species=="virginica"] <- "yellow"

plot(iris$Sepal.Length, iris$Petal.Length, col =
iris$Colour, pch = 16, cex = 2)
legend(x = 4.5, y = 7,
       legend = c("setosa","versicolor","virginica"),
       col = c("magenta","cyan","yellow"),
       pch=16)
```



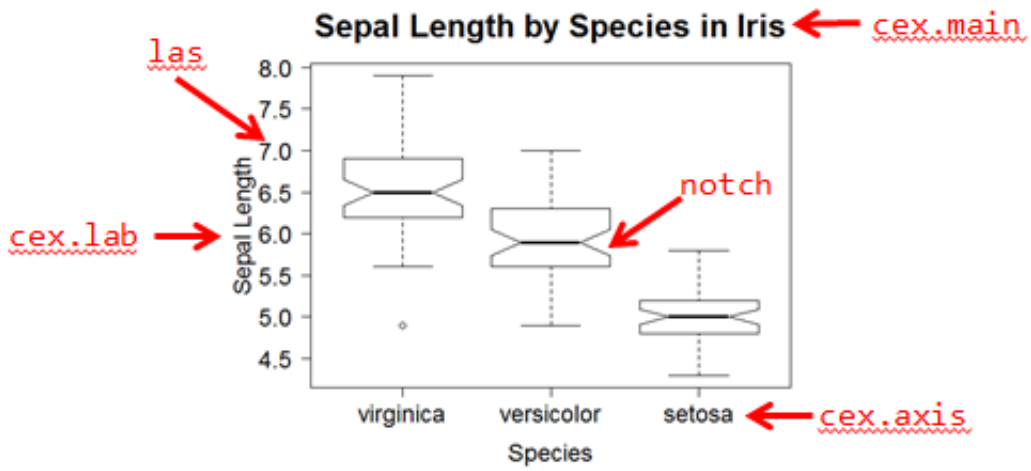
SIDE NOTE 2: It would also be possible to specify lines in the legend by using “lty” instead of “pch”

```
plot(iris$Sepal.Length, iris$Petal.Length, col =
iris$Species, pch = 16, cex = 2)
legend(4.5, 7,
       legend = c("setosa","versicolor","virginica"),
       col = c(1:3),
       lty = "solid")
```



4. Boxplot with reordered and formatted axes

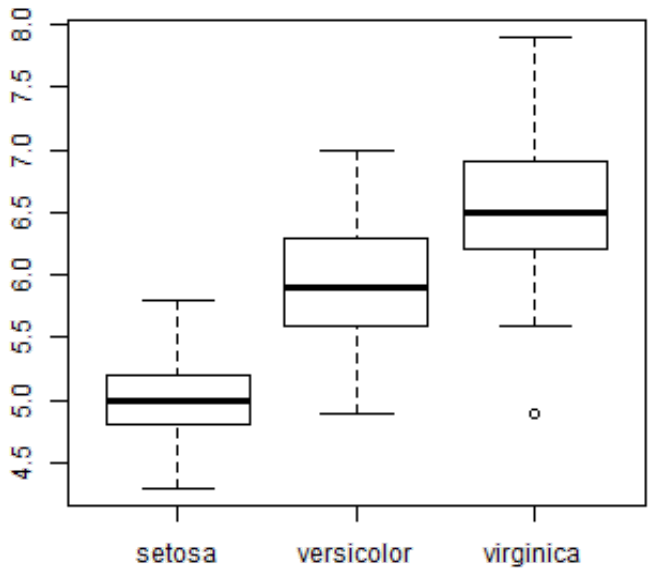
What will be tackle here?




```
354 #~~ FINAL PLOT
355
356 iris$Species<-factor(iris$Species, levels = c("virginica","versicolor","setosa"))
357
358 boxplot(iris$Sepal.Length ~ iris$Species,              # x variable, y variable
359         notch = T,                                    # Draw notch
360         las = 1,                                      # Orientate the axis tick labels
361         xlab = "Species",                             # X-axis label
362         ylab = "Sepal Length",                        # Y-axis label
363         main = "Sepal Length by Species in Iris",     # Plot title
364         cex.lab = 1.5,                                # Size of axis labels
365         cex.axis = 1.5,                               # Size of the tick mark labels
366         cex.main = 2)                                 # Size of the plot title
367
```

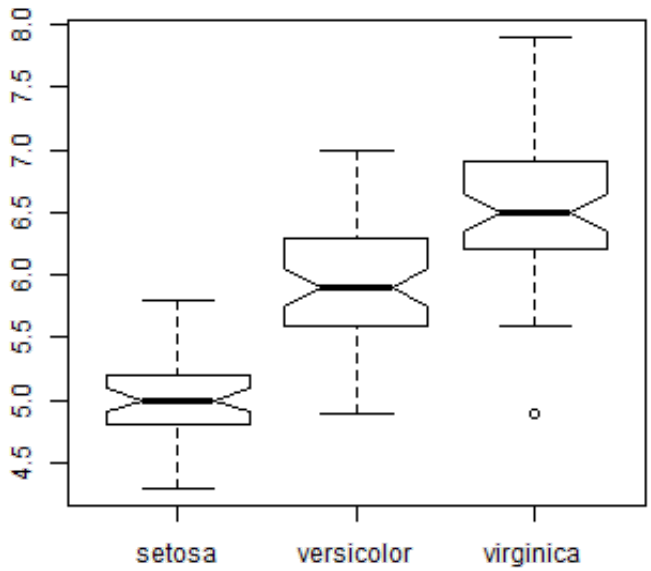
We will continue to use the Iris dataset for this section. Let's examine the distribution of Sepal Length for each species:

```
boxplot(iris$Sepal.Length ~ iris$Species)
```



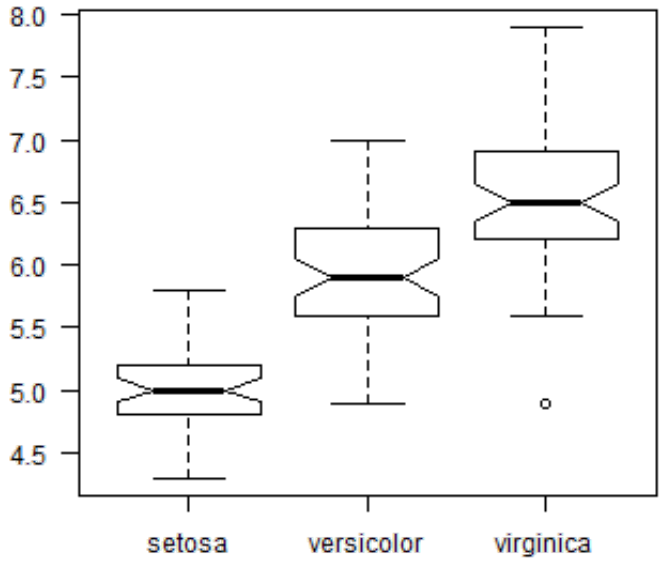
If you wish to compare the medians of the boxplot, you can use the function `notch`. If the notches of two plots do not overlap, this is 'strong evidence' that the two medians differ (see ?boxplot)

```
boxplot(iris$Sepal.Length ~ iris$Species, notch = T)
```



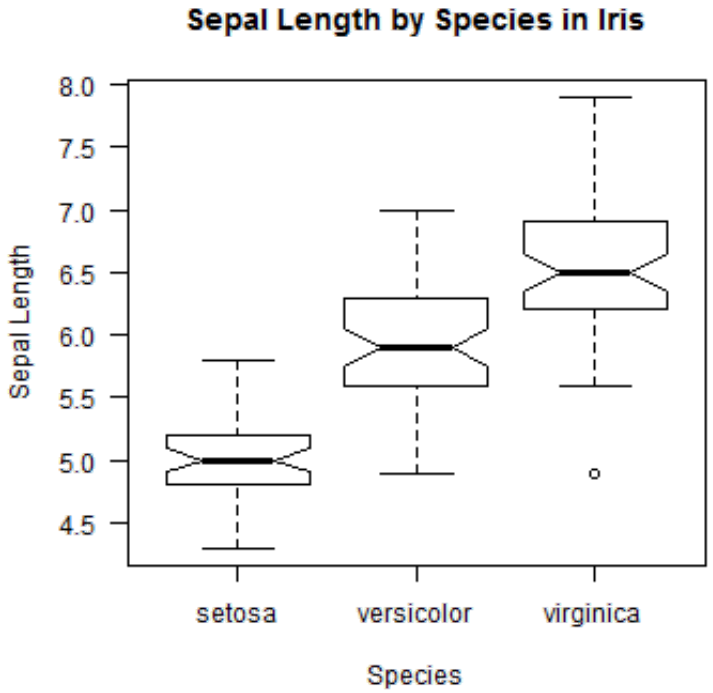
You may have noticed that the y-axis labels are always orientated to be perpendicular to the axis. We can rotate all axis labels using `las`. Play around with different values.

```
boxplot(iris$Sepal.Length ~ iris$Species, notch = T, las =
1)
```



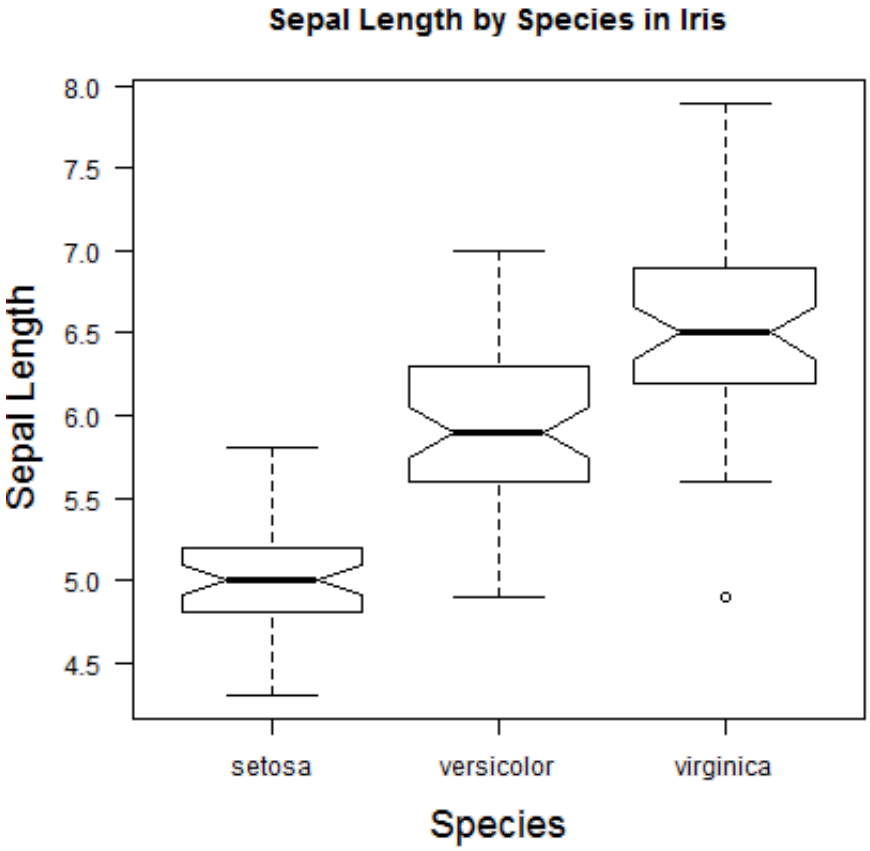
Let's add in all the axis and plot labels:

```
boxplot(iris$Sepal.Length ~ iris$Species,
        notch = T,
        las = 1,
        xlab = "Species",
        ylab = "Sepal Length",
        main = "Sepal Length by Species in Iris")
```



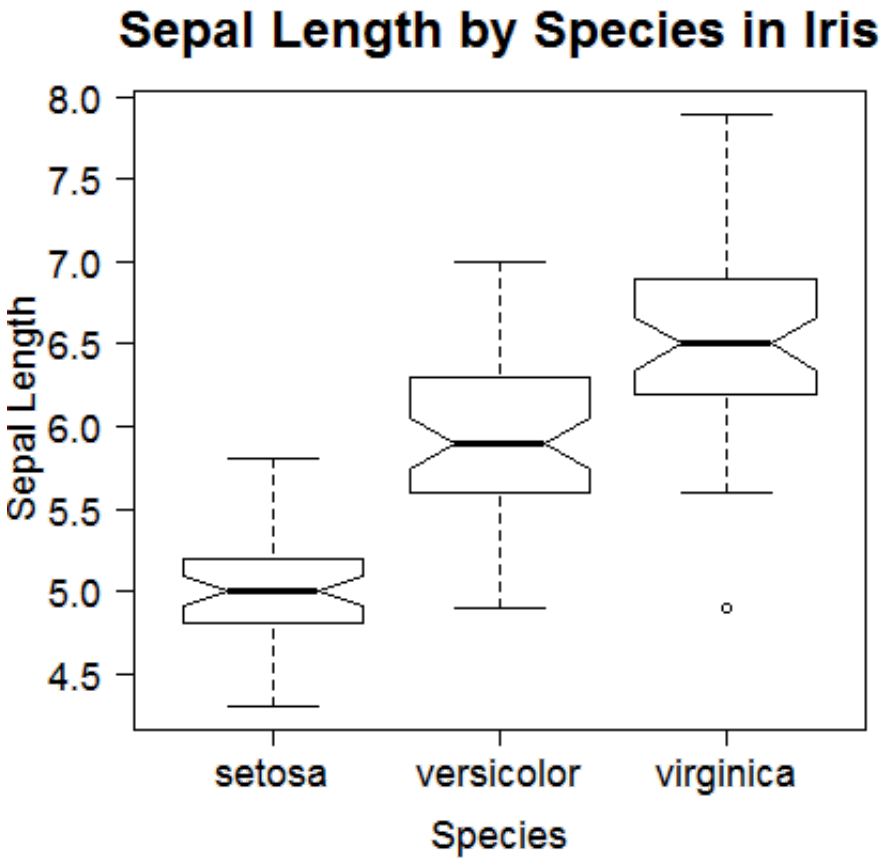
Like we can change the size of the points in the scatterplot, we can change the size of the axis labels and titles. Let's start with `cex.lab`, which controls the axis titles:

```
boxplot(iris$Sepal.Length ~ iris$Species,
        notch = T,
        las = 1,
        xlab = "Species", ylab = "Sepal Length", main =
"Sepal Length by Species in Iris",
        cex.lab=1.5)
```



Now we can add in “cex.axis” (changing the tickmark size) and “cex.main” (changing the plot title size)

```
boxplot(iris$Sepal.Length ~ iris$Species, notch = T, las =
1,
        xlab = "Species", ylab = "Sepal Length", main =
"Sepal Length by Species in Iris",
        cex.lab = 1.5,
        cex.axis = 1.5,
        cex.main = 2)
```



As we discussed earlier, R automatically puts factors in alphabetical order. But perhaps we would prefer to list the iris species as virginica, versicolor and setosa. First lets look at the levels of iris:

```
data(iris)
levels(iris$Species)
```

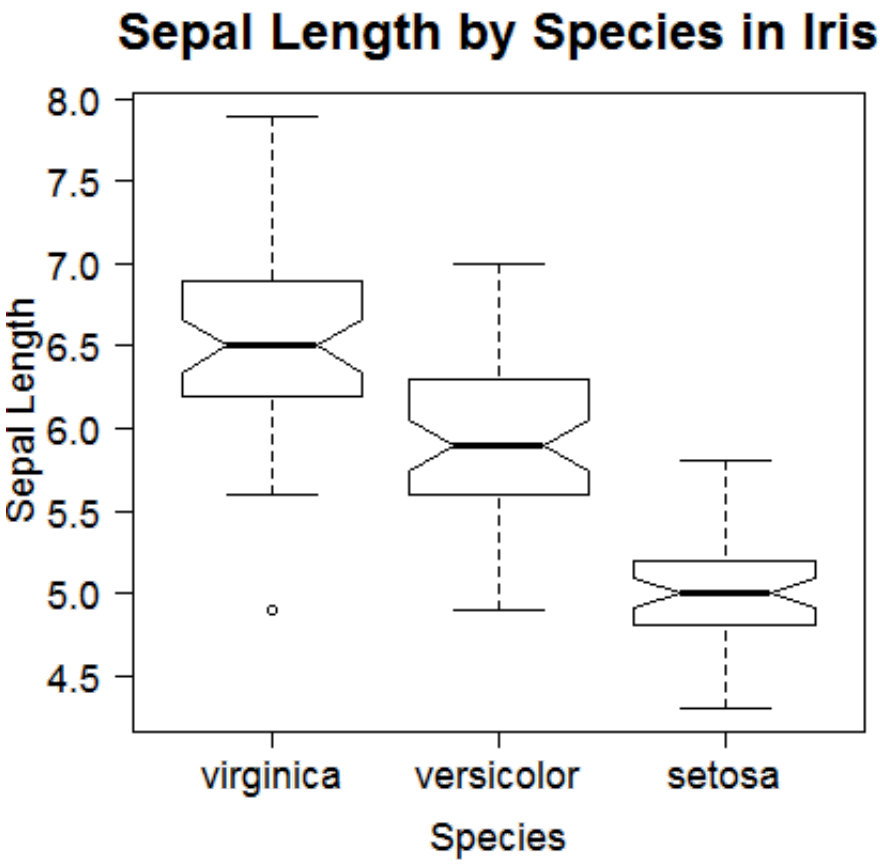
```
## [1] "setosa"     "versicolor" "virginica"
```

We reorder them with the following command:

```
iris$Species <- factor(iris$Species, levels =
c("virginica","versicolor","setosa"))
```

Let's see that FINAL PLOT:

```
boxplot(iris$Sepal.Length ~ iris$Species,               # x
variable, y variable
        notch = T,                                      #
Draw notch
        las = 1,                                        #
Orientate the axis tick labels
        xlab = "Species",                               # X-
axis label
        ylab = "Sepal Length",                          # Y-
axis label
        main = "Sepal Length by Species in Iris",       #
Plot title
        cex.lab = 1.5,                                  #
Size of axis labels
        cex.axis = 1.5,                                 #
Size of the tick mark labels
        cex.main = 2)                                   #
Size of the plot title
```



5. Barplot with error bars using summary data

Ugh. I warn you - this will not be pretty.Let's create a new data frame with information on three populations of dragon in the UK:

```
dragons <- data.frame(
  TalonLength = c(20.9, 58.3, 35.5),
  SE = c(4.5, 6.3, 5.5),
  Population = c("England", "Scotland", "Wales"))

dragons
```

```
##   TalonLength  SE Population
## 1        20.9 4.5    England
## 2        58.3 6.3   Scotland
## 3        35.5 5.5      Wales
```

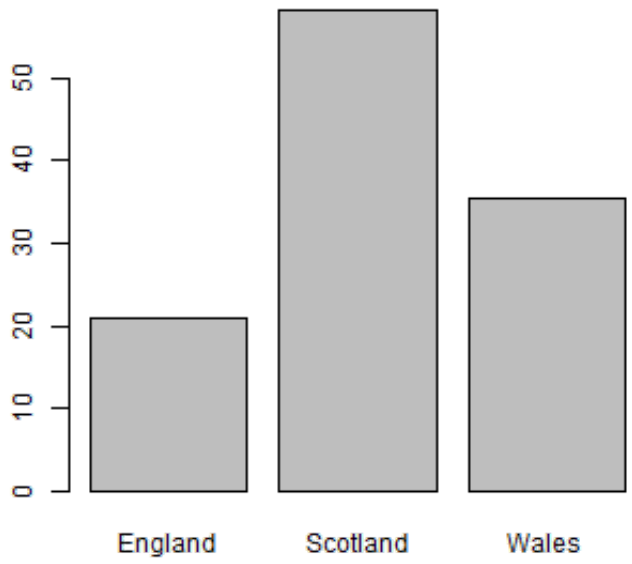
Let's make our barplot.

```
barplot(dragons$Population, dragons$TalonLength)
```

```
## Error: 'height' must be a vector or a matrix
```

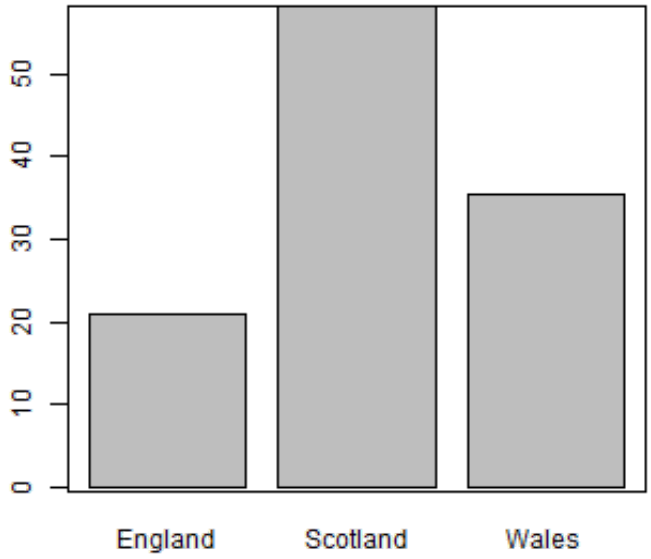
No, this didn't work. It would be better to add Titles to the x-axis:

```
barplot(dragons$TalonLength, names = dragons$Population)
```



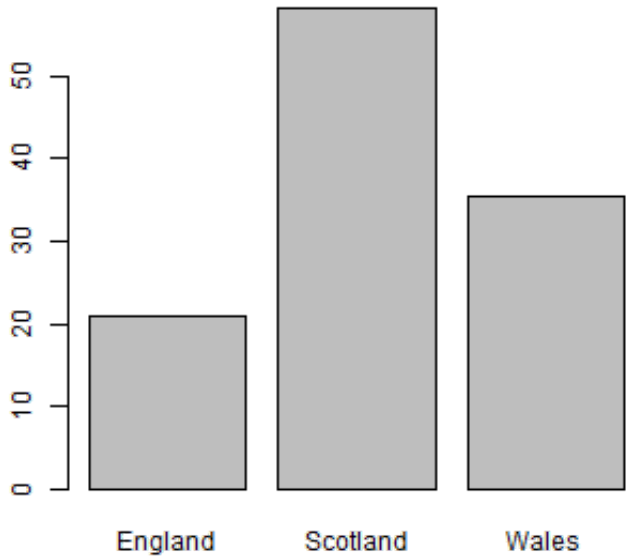
Would a box look better around this plot?

```
barplot(dragons$TalonLength, names = dragons$Population)
box()
```



Not really. Let's start again:

```
barplot(dragons$TalonLength, names = dragons$Population)
```



Let's reorder the columns by how beautiful the dragon habitat is (from best to worst). Naturally, this order is 'Scotland, Wales, England'.

```
levels(dragons$Population)
```

```
## [1] "England"  "Scotland" "Wales"
```

```
dragons$Population <- factor(dragons$Population,
levels=c("Scotland","Wales","England"))

barplot(dragons$TalonLength, names = dragons$Population)
```

No…. it's not working. I give up for now. What about error bars?

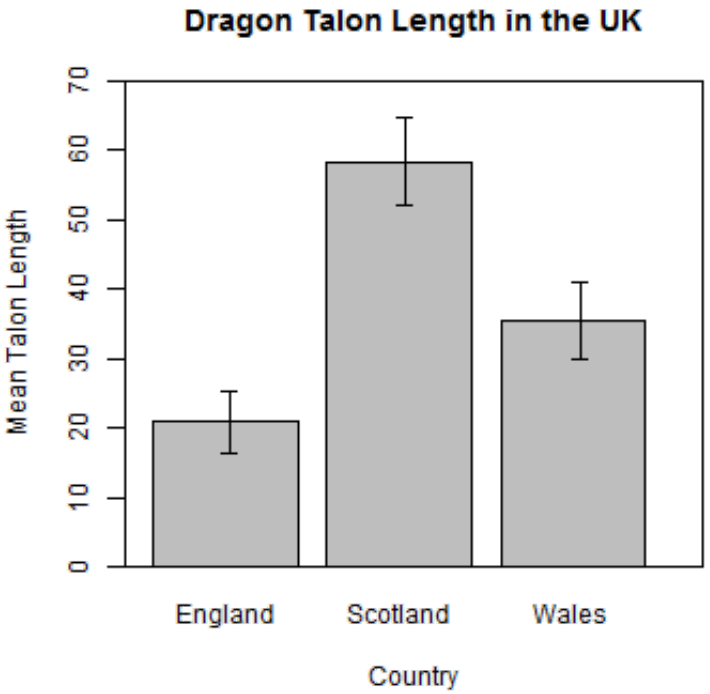
```
library(gplots)
```

```
## Loading required package: gtools Loading required
package: gdata gdata:
## Unable to locate valid perl interpreter gdata: gdata:
read.xls() will be
## unable to read Excel XLS and XLSX files gdata: unless
the 'perl=' argument
## is used to specify the location gdata: of a valid perl
intrpreter. gdata:
## gdata: (To avoid display of this message in the future,
please gdata:
## ensure perl is installed and available on the executable
gdata: search
## path.) gdata: Unable to load perl libaries needed by
read.xls() gdata: to
## support 'XLX' (Excel 97-2004) files.
##
## gdata: Unable to load perl libaries needed by read.xls()
gdata: to support
## 'XLSX' (Excel 2007+) files.
##
## gdata: Run the function 'installXLSXsupport()' gdata: to
automatically
## download and install the perl gdata: libaries needed to
support Excel XLS
## and XLSX formats.
##
## Attaching package: 'gdata'
##
## The following object is masked from 'package:stats':
##
## nobs
##
## The following object is masked from 'package:utils':
##
## object.size
##
## Loading required package: caTools Loading required
package: grid Loading
## required package: KernSmooth KernSmooth 2.23 loaded
Copyright M. P. Wand
## 1997-2009 Loading required package: MASS
##
## Attaching package: 'gplots'
##
## The following object is masked from 'package:stats':
##
## lowess
```

```
barplot(dragons$TalonLength, names = dragons$Population,
        ylim=c(0,70),xlim=c(0,4),yaxs='i', xaxs='i',
        main="Dragon Talon Length in the UK",
        ylab="Mean Talon Length",
        xlab="Country")
par(new=T)
plotCI (dragons$TalonLength,
        uiw = dragons$SE, liw = dragons$SE,
        gap=0,sfrac=0.01,pch="",
        ylim=c(0,70),
        xlim=c(0.4,3.7),
        yaxs='i', xaxs='i',axes=F,ylab="",xlab="")
```

```
## Warning: "axes" is not a graphical parameter
```

```
box()
```



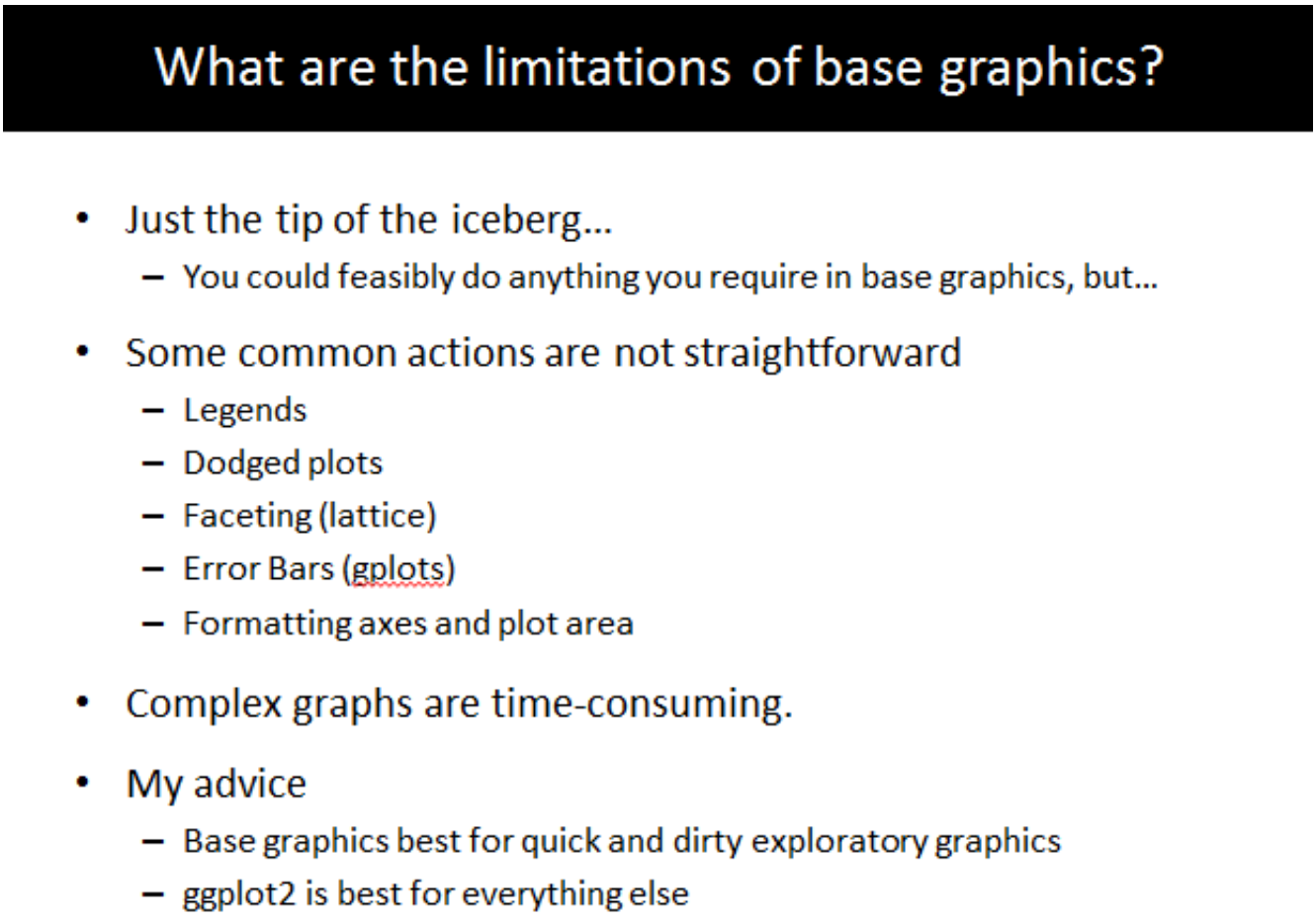
Aaaaaaaaaaargh!

FINAL PLOT

```
# Just do it in ggplot2!
```

Final words in base graphics

This is how I summed it up in the course:

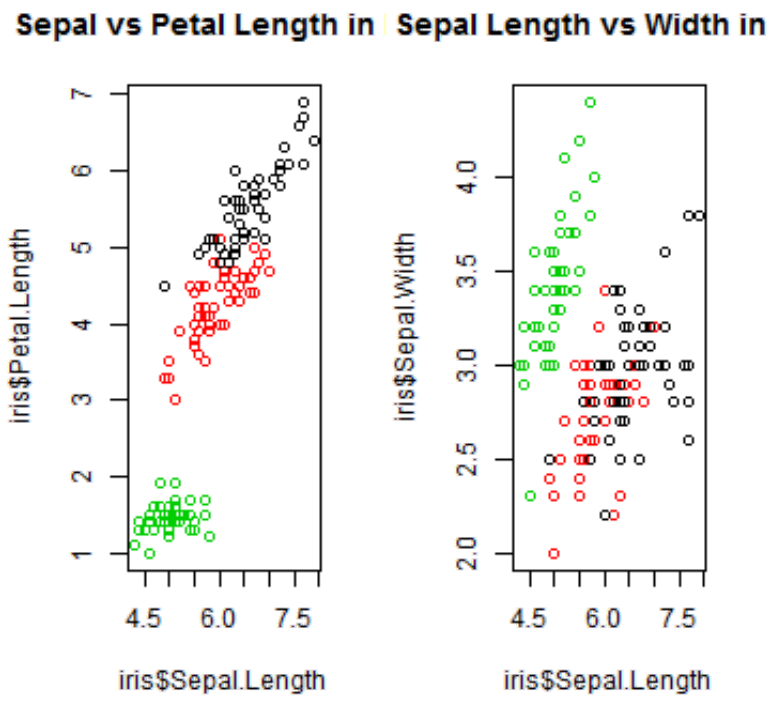


Extras!

Here is some code for some extra fun things in base graphics:

6. More than one plot in a window

```
par(mfrow=c(1,2))      # number of rows, number of columns

plot(iris$Sepal.Length, iris$Petal.Length,        # x
variable, y variable
     col = iris$Species,                          # colour
by species
     main = "Sepal vs Petal Length in Iris")      # plot
title

plot(iris$Sepal.Length, iris$Sepal.Width,         # x
variable, y variable
     col = iris$Species,                          # colour
by species
     main = "Sepal Length vs Width in Iris")      # plot
title
```




```
par(mfrow=c(1,1))     # sets the plot window back to normal

# OR

dev.off()      # But this will clear your plot history.
```

```
## null device
##           1
```

7. Saving a Plot

```
# png

png("Sepal vs Petal Length in Iris.png", width = 500,
height = 500, res = 72)

plot(iris$Sepal.Length, iris$Petal.Length,
     col = iris$Species,
     main = "Sepal vs Petal Length in Iris")

dev.off()
```

```
## pdf
##   2
```

```
# pdf

pdf("Sepal vs Petal Length in Iris.pdf")

plot(iris$Sepal.Length, iris$Petal.Length,
     col = iris$Species,
     main = "Sepal vs Petal Length in Iris")

dev.off()
```

```
## pdf
##   2
```