

# Getting to plot in R

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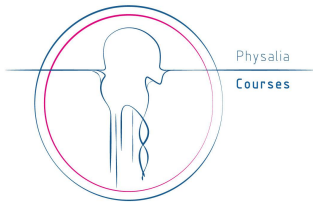
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# Plotting in R

- 1 Introduction
- 2 Plotting with traditional graphics
- 3 Plotting with `ggplot2`
- 4 Conclusion: traditional graphics vs. `ggplot2`

# Why plot in R?

- Powerful (large range of plot types)
- Fully customizable (make your own style)
- Practical (integrate your plots and your code together)

# Graphics paradigms in R

There are three dominant graphics paradigms in R:

- traditional graphics (based on `graphics`)
- `lattice` (based on `grid`)
- `ggplot2` (based on `grid`)

# Graphics paradigms in R

They are three dominant graphics paradigms in **R**:

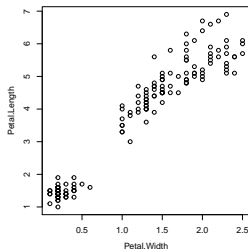
- traditional graphics (based on `graphics`)
- `lattice` (based on `grid`)
- `ggplot2` (based on `grid`)

Note:

- `graphics` and `grid` are part of any basic installation of **R**
- `lattice` is part of the so-called list of CRAN recommended packages
- `ggplot2` is part of the tidyverse universe (from RStudio)
- we will focus on traditional graphics and `ggplot2` (`lattice` is excellent but a bit more difficult)
- some other packages are sometimes useful too (e.g. `rgl`, `plotly`)

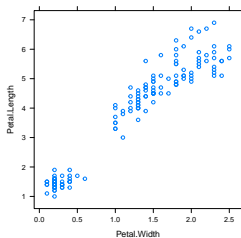
# An example (using default settings)

```
plot(Petal.Length ~ Petal.Width,
     data = iris)
```



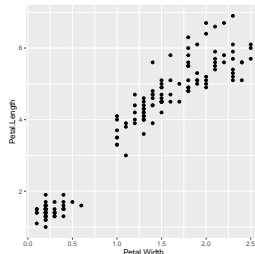
```
library(lattice)
```

```
xyplot(Petal.Length ~ Petal.Width,
       data = iris)
```



```
library(tidyverse) ## or ggplot2
```

```
ggplot(data = iris,
       aes(x = Petal.Width, y = Petal.Length)) +
  geom_point()
```



# How to learn on your own?

1. Check the examples readily available in **R**, e.g.

```
demo(graphics)
demo(image)
demo(persp)
demo(colors)
demo(plotmath)
demo(Hershey)

example(plot)
example(boxplot)
example(hist)
example(bartplot)

browseVignettes(package = "ggplot2")
```

# How to learn on your own?

## 2. Scroll the web:

(e.g. <http://www.r-graph-gallery.com/all-graphs/>)








The screenshot shows the homepage of 'THE R GRAPH GALLERY'. The header features an orange circular logo with a white line graph and the text 'THE R GRAPH GALLERY'. To the right is a navigation menu with links: HOME, GGLOT2, ALL GRAPHS (highlighted in red), BLOG, ABOUT, and PYTHON. Below the header is a large banner with a black background and purple circles of various sizes. A semi-transparent dark grey box in the bottom left of the banner contains the text 'ART FROM DATA'. Below the banner, the text 'ALL GRAPHS' is displayed. To the right of the main content area, there is a 'Share the Gallery!' section with social media icons for Facebook, Google+, Twitter, LinkedIn, and Email. At the bottom, there is a search bar with the placeholder text 'Type an R function, graph type, graph number...' and a 'Search ...' button. On the left side of the bottom section, there is a paragraph of text.

THE R GRAPH GALLERY

HOME GGLOT2 **ALL GRAPHS** BLOG ABOUT PYTHON

ART FROM DATA

ALL GRAPHS

Share the Gallery!     

Type an R function, graph type, graph number...

Search ...

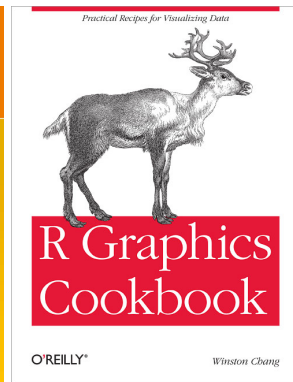
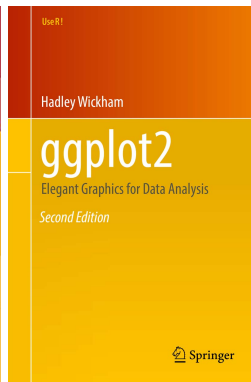
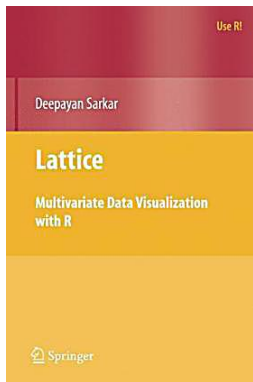
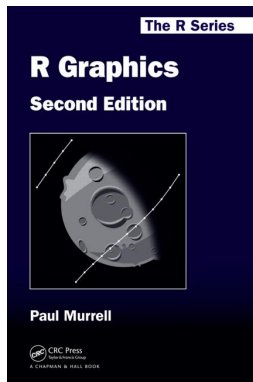
This page presents absolutely **every graphic** that is available on this website. It can be very practical if you are browsing and looking for inspiration. For graphics ordered by type, see the [Home page](#).

If you are looking for something in particular, please use the search tool below. It works even if you are looking for informations concerning an R graph function that is used in the website.



# How to learn on your own?

## 3. Read books:



# Plotting in R

1 Introduction

2 Plotting with traditional graphics

3 Plotting with `ggplot2`

4 Conclusion: traditional graphics vs. `ggplot2`

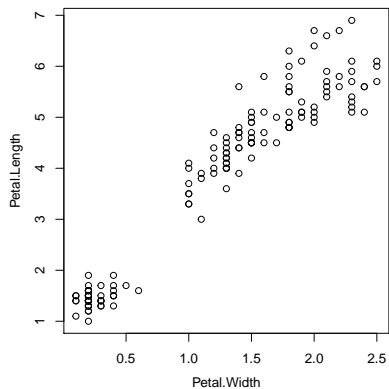
# Plotting in R

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- 4 Conclusion: traditional graphics vs. ggplot2

## Traditional graphics: scatter plots

In traditional graphics, use `plot()` to draw a scatter plot:

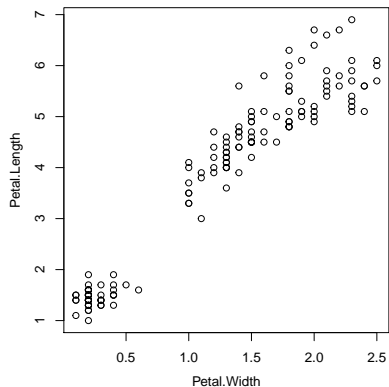
```
plot(Petal.Length ~ Petal.Width, data = iris)
```



## Traditional graphics: scatter plots

You can choose what type of scatter plot to display with argument `type`:

```
plot(Petal.Length ~ Petal.Width, data = iris, type = "p")
```

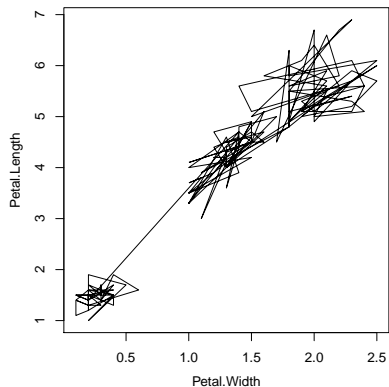


Note: see `"?plot.default"`.

## Traditional graphics: scatter plots

You can choose what type of scatter plot to display with argument `type`:

```
plot(Petal.Length ~ Petal.Width, data = iris, type = "l")
```

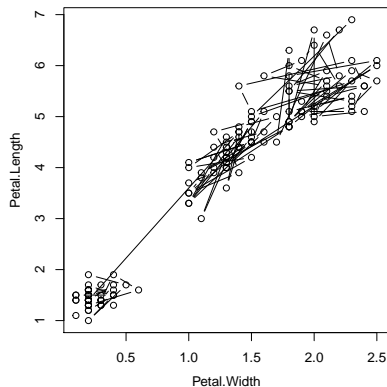


Note: it makes more sense when data are ordered...

## Traditional graphics: scatter plots

You can choose what type of scatter plot to display with argument `type`:

```
plot(Petal.Length ~ Petal.Width, data = iris, type = "b")
```

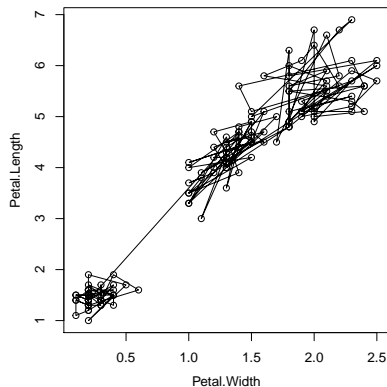


Note: it makes more sense when data are ordered...

## Traditional graphics: scatter plots

You can choose what type of scatter plot to display with argument `type`:

```
plot(Petal.Length ~ Petal.Width, data = iris, type = "o")
```



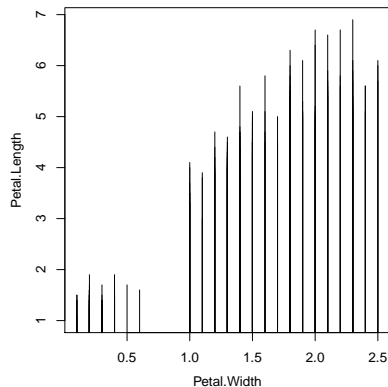
Note: it makes more sense when data are ordered...



## Traditional graphics: scatter plots

You can choose what type of scatter plot to display with argument `type`:

```
plot(Petal.Length ~ Petal.Width, data = iris, type = "h")
```

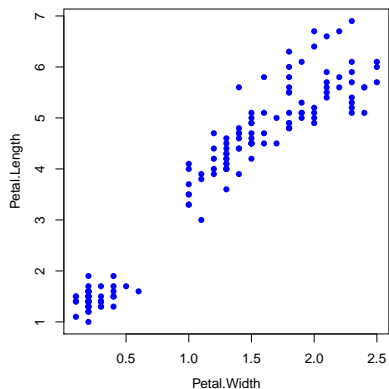


Note: it makes more sense when x-values are unique. . .

## Traditional graphics: scatter plots

You can change point shapes (pch) and colour (col):

```
plot(Petal.Length ~ Petal.Width, data = iris, pch = 16, col = "blue")
```

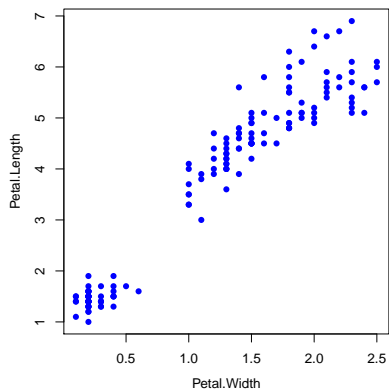


Note: you can use colour names.

## Traditional graphics: scatter plots

You can change point shapes (pch) and colour (col):

```
plot(Petal.Length ~ Petal.Width, data = iris, pch = 16, col = 4)
```

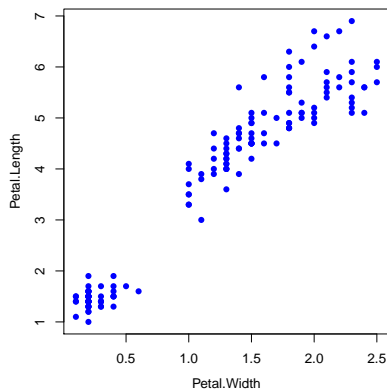


Note: you can use numbers to describe basic colours.

## Traditional graphics: scatter plots

You can change point shapes (pch) and colour (col):

```
plot(Petal.Length ~ Petal.Width, data = iris, pch = 16, col = "#0000FFFF")
```



```
rgb(red = 0, green = 0, blue = 255, alpha = 255, maxColorValue = 255)
```

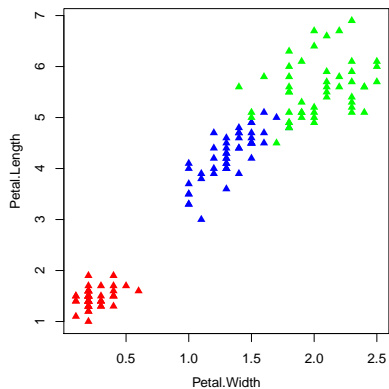
```
## [1] "#0000FFFF"
```

Note: you can have full control using hexadecimal!!

## Traditional graphics: scatter plots

You can change point shapes (pch) and colour (col):

```
palette(c("red", "blue", "green"))  
plot(Petal.Length ~ Petal.Width, data = iris, pch = 17, col = iris$Species)
```



Note: you can use a palette to match the levels of a factor.

## Traditional graphics: scatter plots

You can change point shapes (pch) and colour (col):

```
plot(rep(1, 25) ~ I(1:25), data = iris, pch = 1:25, col = rainbow(25))
```



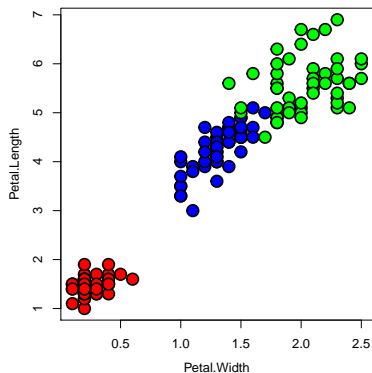
Note:

- there are 25 basic symbols (but other ways allow to use many more)
- check "?rainbow" for a list of different color palettes
- the `I()` allows for the creation of the vector before being interpreted by `plot()`

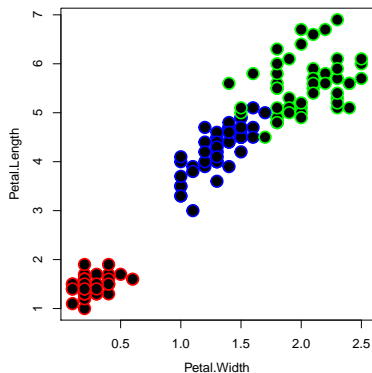
## Traditional graphics: scatter plots

For some point shapes you can set both an outline colour (col) and background colour (bg):

```
palette(c("red", "blue", "green"))  
plot(Petal.Length ~ Petal.Width, data = iris, cex = 2,  
      pch = 21, col = "black", bg = iris$Species, lwd = 2)
```



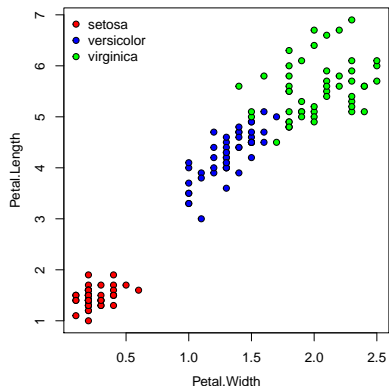
```
palette(c("red", "blue", "green"))  
plot(Petal.Length ~ Petal.Width, data = iris, cex = 2,  
      pch = 21, col = iris$Species, bg = "black", lwd = 2)
```



## Traditional graphics: scatter plots

You can add a legend to the plot:

```
palette(c("red", "blue", "green"))  
plot(Petal.Length ~ Petal.Width, data = iris, pch = 21, bg = iris$Species)  
legend(x = "topleft", legend = c("setosa", "versicolor", "virginica"), pch = 21, pt.bg = c("red", "blue", "green"), bty = "n")
```

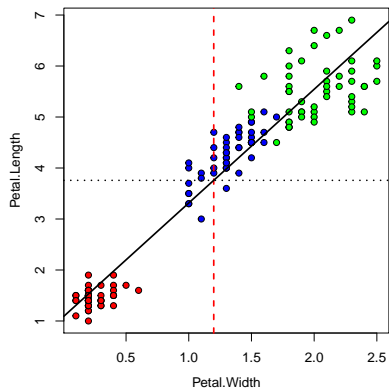




# Traditional graphics: scatter plots

You can add lines to the plot:

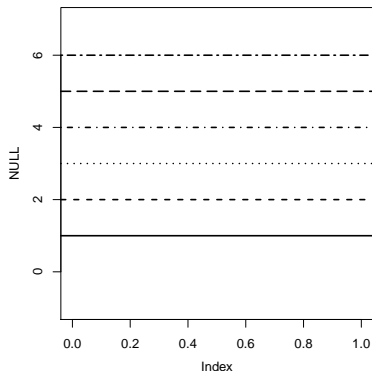
```
palette(c("red", "blue", "green"))  
plot(Petal.Length ~ Petal.Width, data = iris, pch = 21, bg = iris$Species)  
abline(v = mean(iris$Petal.Width), lty = 2, col = "red", lwd = 2)  
abline(h = mean(iris$Petal.Length), lty = 3, col = "black", lwd = 2)  
abline(a = 1.084, b = 2.23, lty = 1, lwd = 2)
```



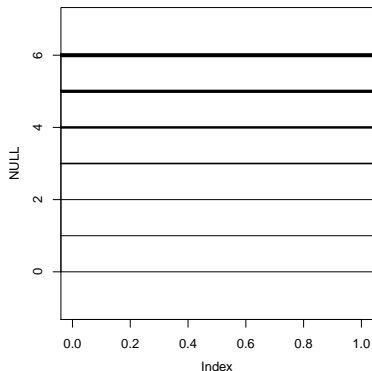
# Traditional graphics: scatter plots

You can add lines to the plot:

```
plot(NULL, xlim = c(0, 1), ylim = c(-1, 7))
abline(h = 0, lty = 0, lwd = 2)
abline(h = 1, lty = 1, lwd = 2)
abline(h = 2, lty = 2, lwd = 2)
abline(h = 3, lty = 3, lwd = 2)
abline(h = 4, lty = 4, lwd = 2)
abline(h = 5, lty = 5, lwd = 2)
abline(h = 6, lty = 6, lwd = 2)
```



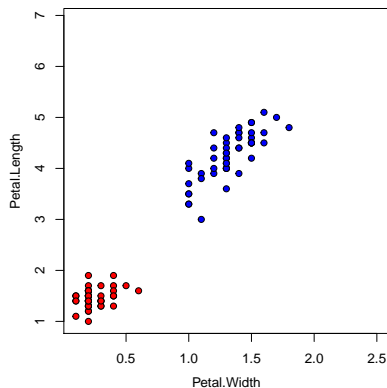
```
plot(NULL, xlim = c(0, 1), ylim = c(-1, 7))
abline(h = 0, lty = 1, lwd = 0.2)
abline(h = 1, lty = 1, lwd = 0.5)
abline(h = 2, lty = 1, lwd = 1)
abline(h = 3, lty = 1, lwd = 2)
abline(h = 4, lty = 1, lwd = 3)
abline(h = 5, lty = 1, lwd = 4)
abline(h = 6, lty = 1, lwd = 5)
```



## Traditional graphics: scatter plots

You can also add additional points to the plot:

```
versicolor <- subset(iris, Species == "versicolor")
setosa     <- subset(iris, Species == "setosa")
plot(Petal.Length ~ Petal.Width, data = versicolor, pch = 21, bg = "blue", xlim = range(iris$Petal.Width), ylim = range(iris$Petal.Length))
points(Petal.Length ~ Petal.Width, data = setosa, pch = 21, bg = "red")
```

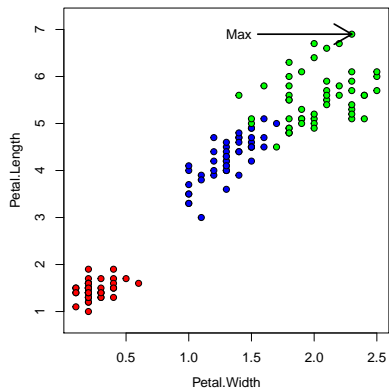


Note: You need to make sure the axis limits are the same!

# Traditional graphics: scatter plots

You can add text and arrows:

```
palette(c("red", "blue", "green"))
plot(Petal.Length ~ Petal.Width, data = iris, pch = 21, bg = iris$Species, ylim = c(0.8, 7.2))
max.value <- iris[iris$Petal.Length == max(iris$Petal.Length), ]
arrows(x0 = max.value$Petal.Width - 0.75, y0 = max.value$Petal.Length,
       x1 = max.value$Petal.Width, y1 = max.value$Petal.Length, lwd = 2)
text(x = max.value$Petal.Width - 0.9, y = max.value$Petal.Length, labels = "Max")
```

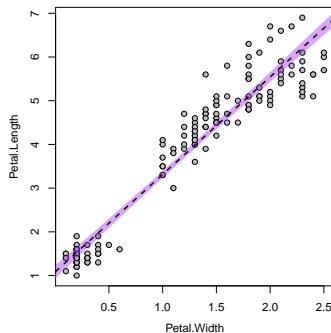


# Traditional graphics: scatter plots

Including an interval around a prediction line requires you to build a polygon:

```
test_mod <- lm(Petal.Length ~ Petal.Width, data = iris)
newdat    <- data.frame(Petal.Width = seq(0, 3, length.out = 100))
pred      <- predict(test_mod, newdata = newdat, interval = "confidence")
```

```
library(scales) ## for transparency
plot(Petal.Length ~ Petal.Width, data = iris, pch = 21, bg = "grey")
polygon(x = c(newdat$Petal.Width, rev(newdat$Petal.Width)),
       y = c(pred[, "lwr"], rev(pred[, "upr"])),
       col = alpha("purple", alpha = 0.4), ## alpha sets transparency!
       border = NA) ## removes black line around the polygon
abline(test_mod, lty = 2, lwd = 2)
```



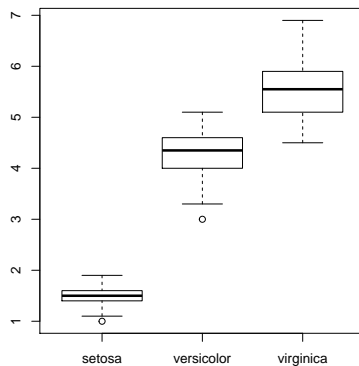
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## Traditional graphics: box plots

In traditional graphics, use `boxplot()` to draw a box plot:

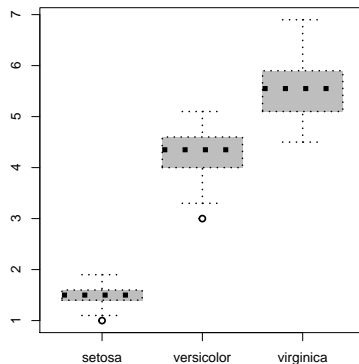
```
boxplot(Petal.Length ~ Species, data = iris)
```



## Traditional graphics: box plots

Many of the same changes made to scatter plots can be made here:

```
boxplot(Petal.Length ~ Species, data = iris, col = "grey", lwd = 2, lty = 3)
```

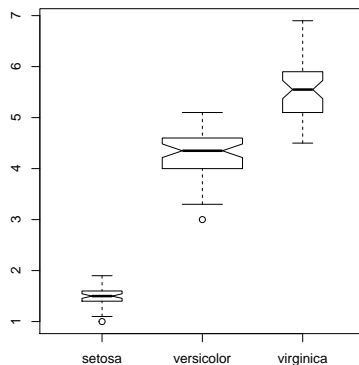




# Traditional graphics: box plots

There are also some boxplot specific arguments:

```
boxplot(Petal.Length ~ Species, data = iris, width = c(1, 2, 1), notch = TRUE)
```



# Traditional graphics: box plots

You can retrieve information by storing the output in an object:

```
my_boxcox <- boxplot(Petal.Length ~ Species, data = iris, plot = FALSE)
```

```
my_boxcox
## $stats
##      [,1] [,2] [,3]
## [1,]  1.1 3.30 4.50
## [2,]  1.4 4.00 5.10
## [3,]  1.5 4.35 5.55
## [4,]  1.6 4.60 5.90
## [5,]  1.9 5.10 6.90
##
## $n
## [1] 50 50 50
##
## $conf
##      [,1]      [,2]      [,3]
## [1,] 1.455311 4.215933 5.371243
## [2,] 1.544689 4.484067 5.728757
##
## $out
## [1] 1 3
##
## $group
## [1] 1 2
##
## $names
## [1] "setosa"      "versicolor" "virginica"
```

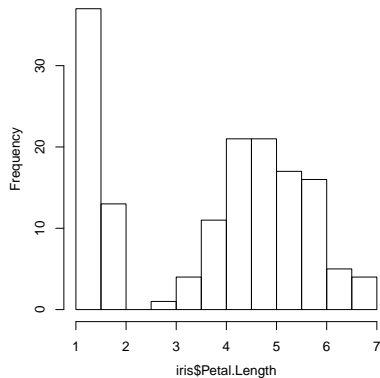
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## Traditional graphics: histograms

In traditional graphics, use `hist()` to draw an histogram:

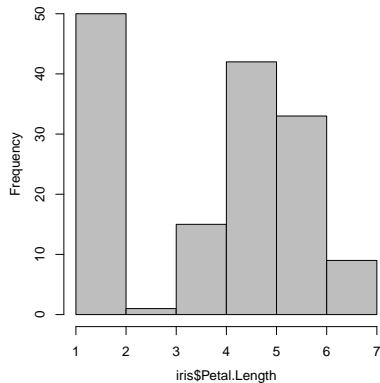
```
hist(iris$Petal.Length, main = "") ## main used here to remove the automatic title
```



## Traditional graphics: histograms

You can change the number and location of breaks between bins:

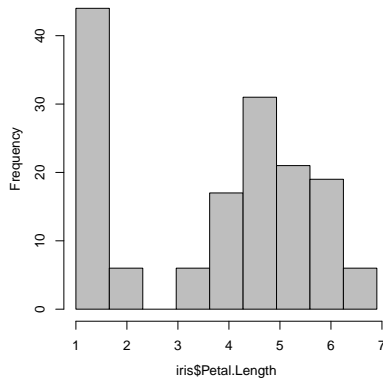
```
hist(iris$Petal.Length, main = "", breaks = 5, col = "grey")
```



## Traditional graphics: histograms

You can change the number and location of breaks between bins:

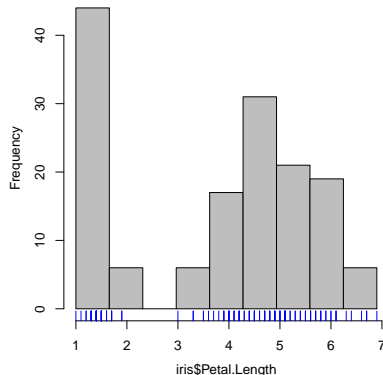
```
hist_breaks <- seq(min(iris$Petal.Length), max(iris$Petal.Length), length.out = 10)
hist(iris$Petal.Length, main = "", breaks = hist_breaks, col = "grey")
```



# Traditional graphics: histograms

You can change the number and location of breaks between bins:

```
hist_breaks <- seq(min(iris$Petal.Length), max(iris$Petal.Length), length.out = 10)
hist(iris$Petal.Length, main = "", breaks = hist_breaks, col = "grey")
rug(x = iris$Petal.Length, col = "blue")
```



Note: it never hurts to add a rug under an histogram!

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## Traditional graphics: bar plots

```
spp_means <- data.frame(Species = c("setosa", "versicolor", "virginica"),
                        mean = as.numeric(by(iris$Petal.Length, iris$Species, mean)),
                        SE = as.numeric(by(iris$Petal.Length, iris$Species, function(x)sd(x)/sqrt(length(x))))
                        )
```

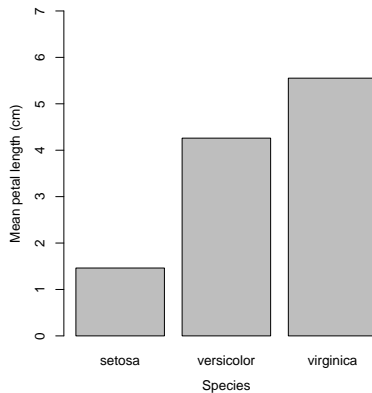
```
spp_means
```

```
##      Species mean      SE
## 1    setosa 1.462 0.02455980
## 2 versicolor 4.260 0.06645545
## 3  virginica 5.552 0.07804970
```

## Traditional graphics: bar plots

In traditional graphics, use `barplot()` to draw a bar plot:

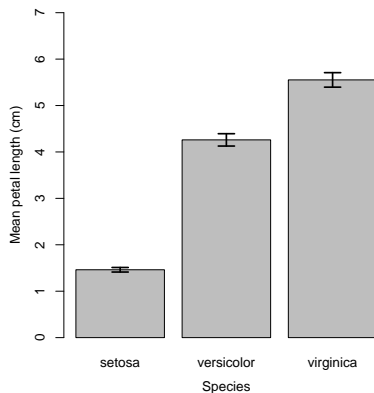
```
barplot(height = spp_means$mean, names.arg = spp_means$Species, ylim = c(0, 7),  
        xlab = "Species", ylab = "Mean petal length (cm)")
```



# Traditional graphics: bar plots

Adding error bars can be done with the arrows function:

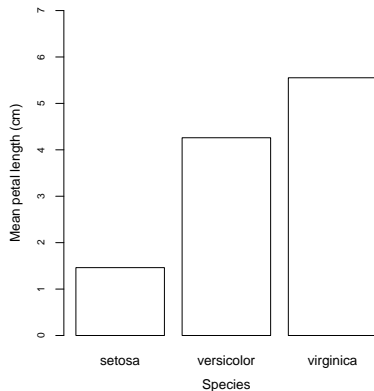
```
bar_locations <- barplot(height = spp_means$mean, names.arg = spp_means$Species, plot = FALSE)
barplot(height = spp_means$mean, names.arg = spp_means$Species, ylim = c(0, 7),
        xlab = "Species", ylab = "Mean petal length (cm)")
arrows(x0 = bar_locations[, 1], x1 = bar_locations[, 1],
       y0 = spp_means$mean - 2*spp_means$SE, y1 = spp_means$mean + 2*spp_means$SE,
       angle = 90, lwd = 2, code = 3, length = 0.1)
```



## Traditional graphics: bar plots

As before, there are similar arguments available:

```
barplot(height = spp_means$mean, names.arg = spp_means$Species, ylim = c(0, 7),  
        xlab = "Species", ylab = "Mean petal length (cm)",  
        col = "white", cex.axis = 0.75)
```



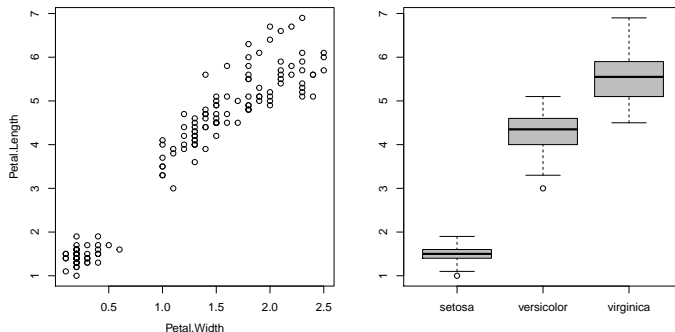
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## Combining plots

You can easily combine multiple traditional graphics using global parameters:

```
oldpar <- par(mfrow = c(1, 2))
plot(Petal.Length ~ Petal.Width, data = iris)
boxplot(Petal.Length ~ Species, data = iris, col = "grey")
```



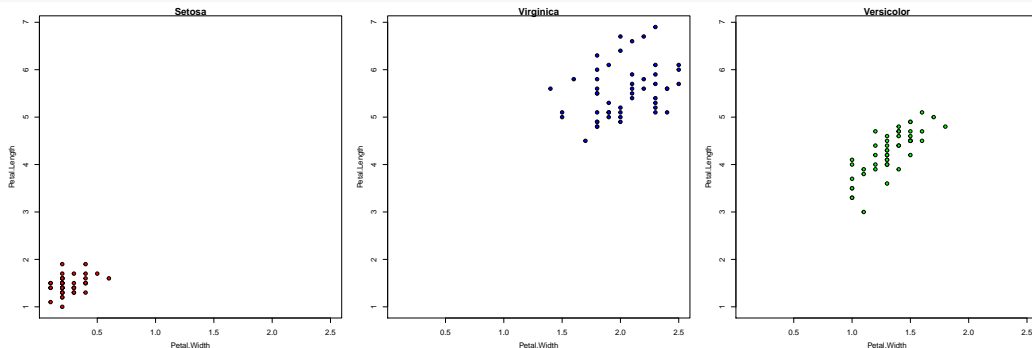
```
par(oldpar) ## restore default values
```

Note: if you want to combine graphics of different sizes it is a bit more complex (see `?layout`).

# Facetting

This can be used to created 'facet' plots:

```
oldpar <- par(mfrow = c(1, 3))
split_data <- split(iris, iris$Species)
plot(Petal.Length ~ Petal.Width, data = split_data$setosa, main = "Setosa", pch = 21,
     bg = "red", col = "black", xlim = range(iris$Petal.Width), ylim = range(iris$Petal.Length))
plot(Petal.Length ~ Petal.Width, data = split_data$virginica, main = "Virginica", pch = 21,
     bg = "blue", col = "black", xlim = range(iris$Petal.Width), ylim = range(iris$Petal.Length))
plot(Petal.Length ~ Petal.Width, data = split_data$versicolor, main = "Versicolor", pch = 21,
     bg = "green", col = "black", xlim = range(iris$Petal.Width), ylim = range(iris$Petal.Length))
```

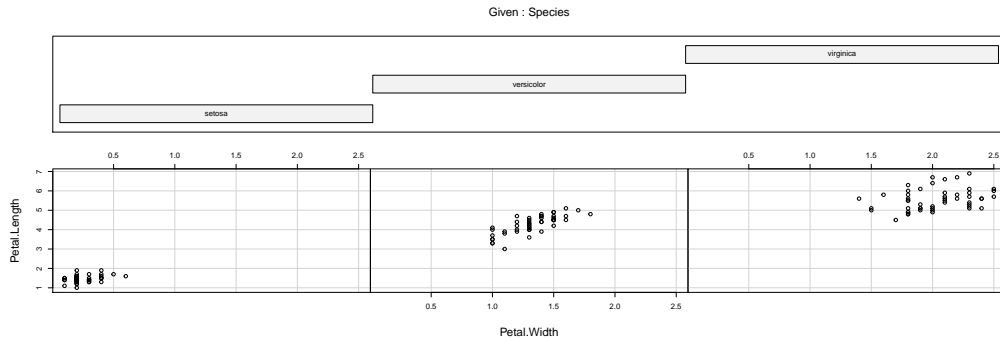


```
par(oldpar) ## restore default values
```

# Facetting

Note: there is also an easier function for that:

```
coplot(Petal.Length ~ Petal.Width | Species, data = iris, rows = 1)
```

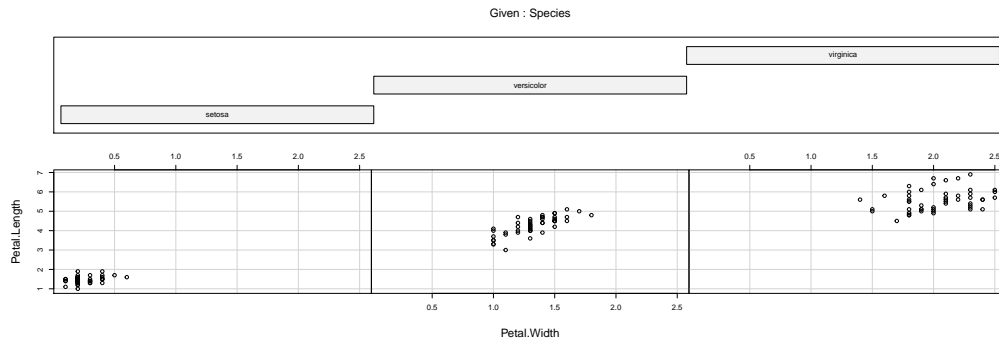




# Facetting

Note: there is also an easier function for that:

```
coplot(Petal.Length ~ Petal.Width | Species, data = iris, rows = 1)
```

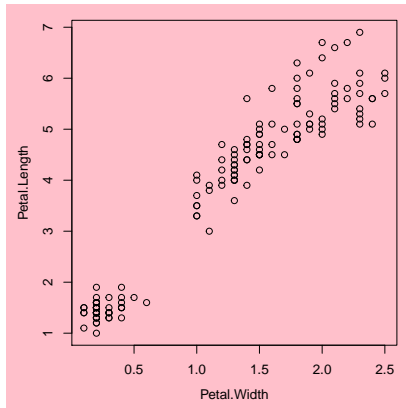


Challenge: have a look at the relationship between the happiness and the price of present using the dataset Surprise.

# Background

Global parameters can also be used to change the background colour:

```
oldpar <- par(bg = "pink")  
plot(Petal.Length ~ Petal.Width, data = iris)
```



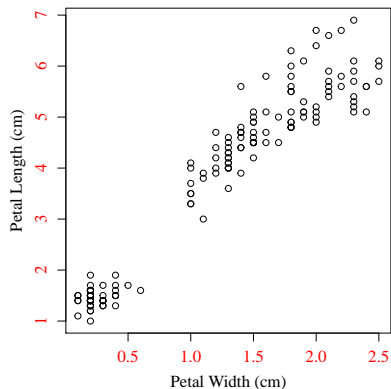
```
par(oldpar) ## restore default values
```

Note: you can also plot a background image but you need to use specific packages for that.

# Modifying typefaces

Global parameters can also be used to change the typeface:

```
oldpar <- par(family = "serif")
plot(Petal.Length ~ Petal.Width, data = iris,
     xlab = "Petal Width (cm)", ylab = "Petal Length (cm)",
     cex.lab = 1.25, cex.axis = 1.25, col.axis = "red")
```

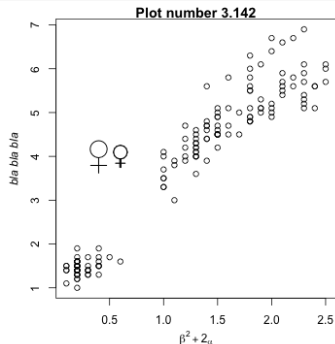


```
par(oldpar) ## restore default values
```

## Special characters

You can use weird characters:

```
foo <- round(pi, 3)
plot(Petal.Length ~ Petal.Width, data = iris,
     xlab = expression(beta^2 + 2[alpha]), ylab = expression(paste(italic("bla bla bla"))),
     main = paste("Plot number", foo))
text(0.4, 4, "\u2640", cex = 3) ## requires font with unicode installed (try it!)
text(0.6, 4, "\\VE", vfont = c("serif", "plain"), cex = 3)
```

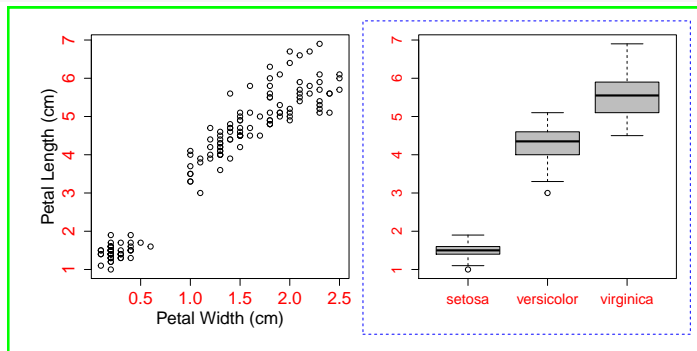


Note: unicode characters are nice but source of problems. How to make it work depends on both the OS, graphical device and typefaces installed on your computer.

# Plot margins

Global parameters can also be used to change individual plot margins (**blue**) and outer margins (**green**):

```
oldpar <- par(mfrow = c(1, 2), mar = c(4, 4, 1, 1), oma = c(1.5, 2, 1, 1))
plot(Petal.Length ~ Petal.Width, data = iris,
     xlab = "Petal Width (cm)", ylab = "Petal Length (cm)",
     cex.lab = 1.5, cex.axis = 1.5, col.axis = "red")
boxplot(Petal.Length ~ Species, data = iris, col = "grey",
        cex.lab = 0.75, cex.axis = 1.25, col.axis = "red")
box('figure', col = 'blue', lty = "dashed")
box('outer', col = 'green', lwd = 5)
```

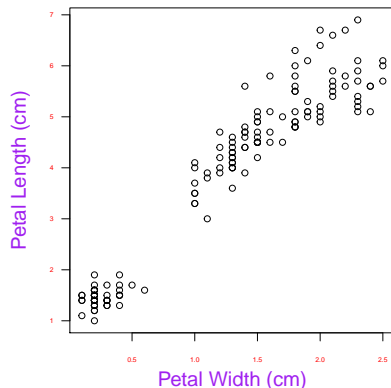


```
par(oldpar) ## restore default values
```

## Change axes

You can change the size, colour and orientation of the axis labels and text easily:

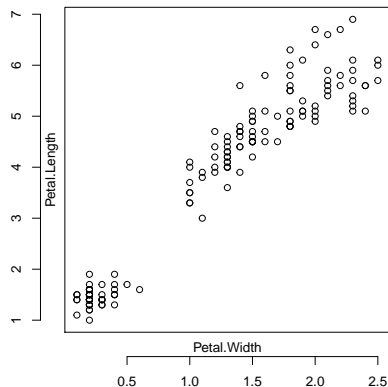
```
plot(Petal.Length ~ Petal.Width, data = iris,  
     xlab = "Petal Width (cm)", ylab = "Petal Length (cm)",  
     cex.lab = 1.5, cex.axis = 0.5, col.axis = "red", col.lab = "purple", las = 1)
```



# Change axes

You can change the position of the axes:

```
oldpar <- par(mgp = c(0.4, 2, 1.5))  
plot(Petal.Length ~ Petal.Width, data = iris)
```



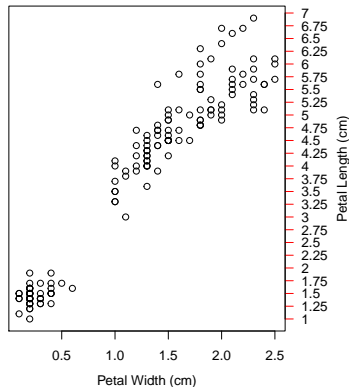
```
par(oldpar) ## restore default values
```

Note: check `?par` for a huge list of the things you can easily change!

# Change axes

You can change the axes themselves:

```
oldpar <- par(mar = c(4, 4, 1, 4))
plot(Petal.Length ~ Petal.Width, data = iris, axes = FALSE,
     xlab = "Petal Width (cm)", ylab = "")
axis(side = 1)
axis(side = 4, at = seq(1, 7, 0.25), labels = seq(1, 7, 0.25), col.ticks = "red", las = 1)
mtext("Petal Length (cm)", side = 4, line = 3)
box()
```



```
par(oldpar) ## restore default values
```



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# Traditional graphics: exporting

```
?pdf ?jpeg ?tiff ?bmp ?postscript
```

```
pdf("base_plot.pdf", width = 15, height = 5)  
plot(Petal.Length ~ Petal.Width, data = iris)  
dev.off()
```

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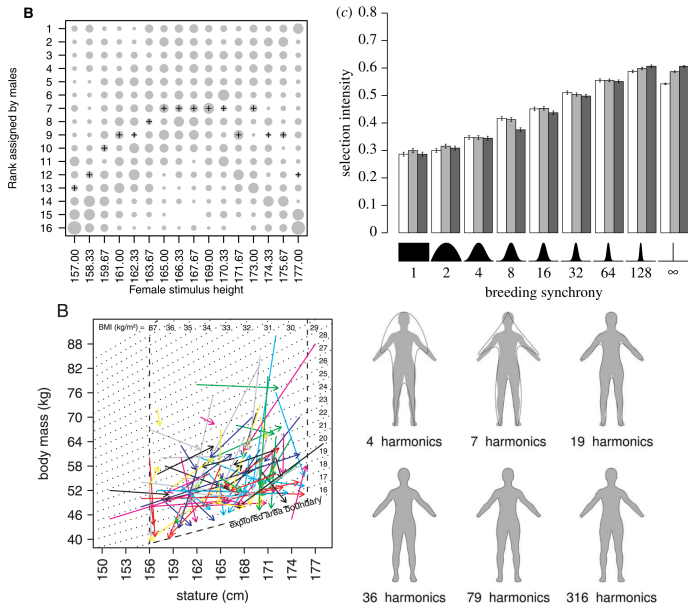
# Challenge

Run the examples of the following traditional plot functions:

- `plot.ecdf()`
- `curve()`
- `pie()`
- `cdplot()`
- `image()`
- `contour()`
- `persp()`
- `dotchart()`
- `mosaicplot()`
- `stars()`
- `matplot()`
- `pairs()`
- `sunflowerplot()`

Note: there are a few other ones, but they do not seem very interesting...

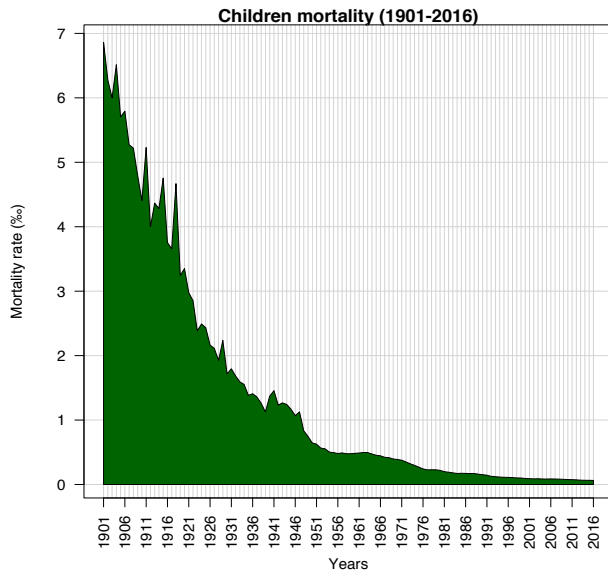
# You can create home-made R graphics too



# Challenge

Use the datasets called `population_UK` and `deaths_UK` to compute yearly mortality rates for individuals below 15 yrs only and make a really nice plot of the outcome!

# Possible solution



# Possible solution

```

deaths_UK %>%
  filter(Age_cat %in% levels(Age_cat)[1:3]) %>%
  group_by(Year) %>%
  summarize(tot_Deaths = sum(Deaths)) -> deaths_processed

population_UK %>%
  group_by(Year) %>%
  summarize(tot_Pop = sum(Pop)) -> pop_processed

full_join(deaths_processed, pop_processed) %>%
  mutate(rel_Deaths = 1000*tot_Deaths/tot_Pop) -> data_processed

par(mgp = c(3.2, 1, 0), mar = c(5, 5, 1, 1))

plot(rel_Deaths ~ Year, data = data_processed, col = NULL, axes = FALSE,
     ylab = "Mortality rate (\u2030)", xlab = "Years",
     main = paste0("Children mortality (", min(data_processed$Year), "-", max(data_processed$Year), ")"))

abline(v = seq(min(data_processed$Year), max(data_processed$Year), by = 1), col = "lightgrey", lwd = 0.5)
abline(h = 0:ceiling(max(data_processed$rel_Deaths)), col = "lightgrey", lwd = 0.5)

polygon(x = c(data_processed$Year, rev(x = data_processed$Year)),
       y = c(data_processed$rel_Deaths, rep(x = 0, times = nrow(data_processed))),
       col = "darkgreen")

axis(side = 1, at = seq(min(data_processed$Year), max(data_processed$Year), by = 5), las = 2)
axis(side = 2, las = 1)
box()

```



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## ggplot2: introduction

ggplot (defunct) and ggplot2 were both created by Hadley Wickham (now chief Scientist at Rstudio) during his PhD: <http://had.co.nz/thesis/practical-tools-hadley-wickham.pdf>

## ggplot2: introduction

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The idea was to create a grammar of graphics for R.

It is inspired from the seminal Leland Wilkson's book **The Grammar of Graphics**: *"This book [...] presents a unique foundation for producing almost every quantitative graphic found in scientific journals, newspapers, statistical packages, and data visualization systems."*

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In Wickham's words:

*"The grammar of graphics is an answer to a question: what is a statistical graphic? [...] In brief, the grammar tells us that a statistical graphic is a mapping from data to aesthetic attributes (colour, shape, size) of geometric objects (points, lines, bars). The plot may also contain statistical transformations of the data and is drawn on a specific coordinate system. Facetting can be used to generate the same plot for different subsets of the dataset. It is the combination of these independent components that make up a graphic."* (Wickham ggplot2 book)

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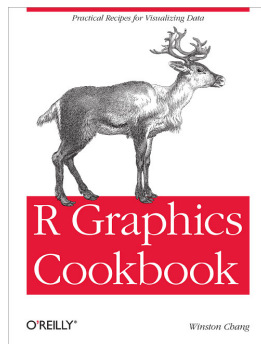
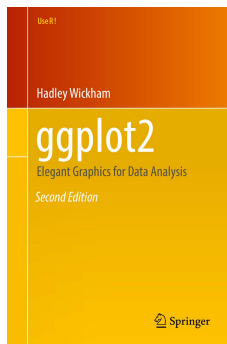
In Wickham's words:

*"The grammar of graphics is an answer to a question: what is a statistical graphic? [...] In brief, the grammar tells us that a statistical graphic is a mapping from data to aesthetic attributes (colour, shape, size) of geometric objects (points, lines, bars). The plot may also contain statistical transformations of the data and is drawn on a specific coordinate system. Facetting can be used to generate the same plot for different subsets of the dataset. It is the combination of these independent components that make up a graphic."* (Wickham ggplot2 book)

In plain english, that means that the graphics are build by considering building blocs or layers. The originality is that the user directly handles different functions corresponding to each layer and can combine them freely.

# How to learn ggplot2 on your own?

- forum: <https://community.rstudio.com>
- reference: <http://ggplot2.tidyverse.org/reference/>
- the RStudio cheatsheet
- the books:

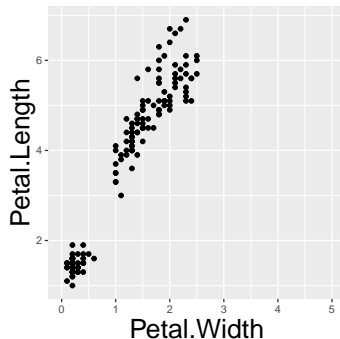


Note: Wickham's books (or their sources) are free and open source!

## ggplot2: introduction

Overall structure of a ggplot2 call:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length)) + ## we specify the source of data and map the variables  
  geom_point() + ## we use a function that specifies the type of plot (e.g. scatterplot, histogram). A geom_* function is always required!  
  scale_x_continuous(limits = c(0, 5)) + ## we can fiddle with the scale_* functions to adjust the axes, colouration etc.  
  theme(axis.title = element_text(size = 22)) # we can use one of the theme_* functions to change things like legends, font size etc.
```



Note: to better understand, execute the code progressively adding one command at a time!



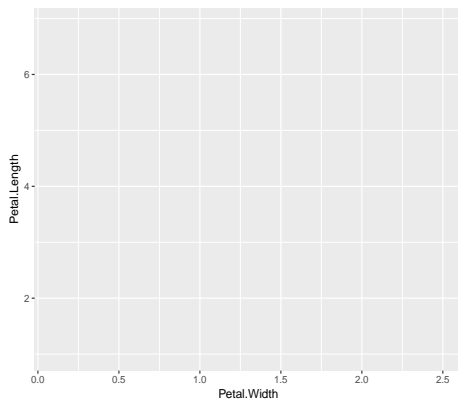
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## ggplot2: scatter plots

We start by preparing the data:

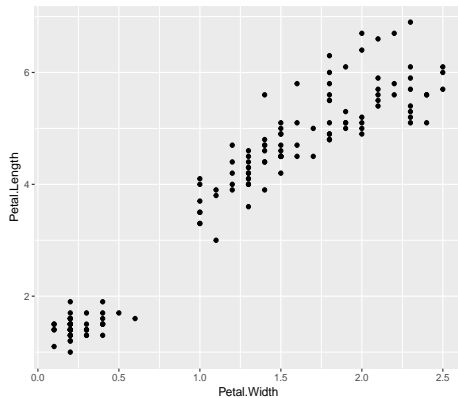
```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length))
```



## ggplot2: scatter plots

We add points on the empty plot:

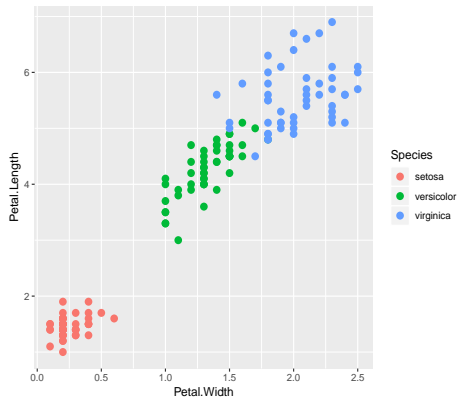
```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length)) + geom_point()
```



## ggplot2: scatter plots

You can change point shapes `shape` (= `pch` in traditional graphics) and `colour` (= `col` in traditional graphics):

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, colour = Species)) +  
  geom_point(shape = 16, size = 3)
```

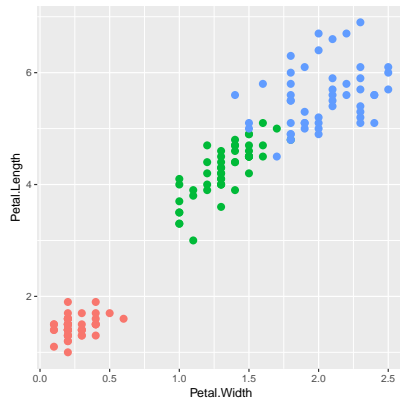


Note: everytime we want to create a connection between the data and some elements of the plot, we use the same function: `aes()`!

## ggplot2: scatter plots

In ggplot the legend is included by default but you can remove it:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, colour = Species)) +  
  geom_point(shape = 16, size = 3) +  
  theme(legend.position = "none")
```



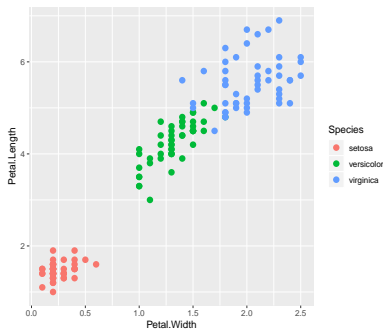
## ggplot2: scatter plots

The aesthetic function in ggplot is a powerful tool for changing plot aesthetics.

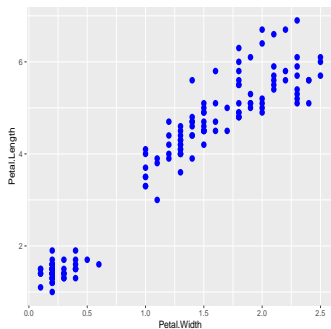
If you specify an aesthetic argument inside `aes()`, it will give each point a different aesthetic based on its value.

If you specify the same aesthetic argument outside `aes()`, it will give all data points the same aesthetic:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length,  
                                colour = Species)) +  
  geom_point(shape = 16, size = 3)
```



```
ggplot(data = iris,  
       mapping = aes(x = Petal.Width, y = Petal.Length)) +  
  geom_point(colour = "blue", shape = 16, size = 3)
```

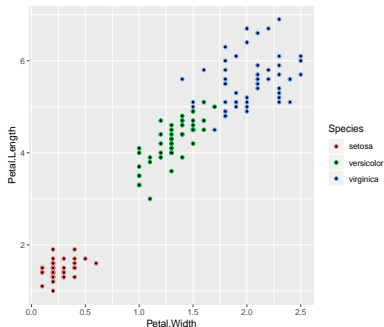


Note: we have used `aes()` to apply colours but it can be used to make other changes (see later).

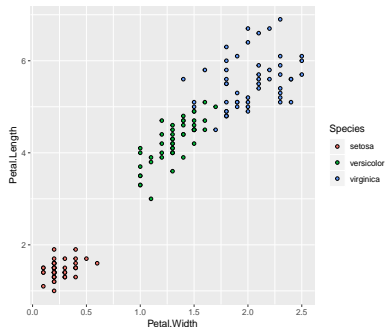
## ggplot2: scatter plots

Again, for many elements you can set both an outline colour (= col for traditional graphics) and background fill colour (= bg for traditional graphics):

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length,
                                   colour = Species)) +
  geom_point(fill = "black", shape = 21)
```



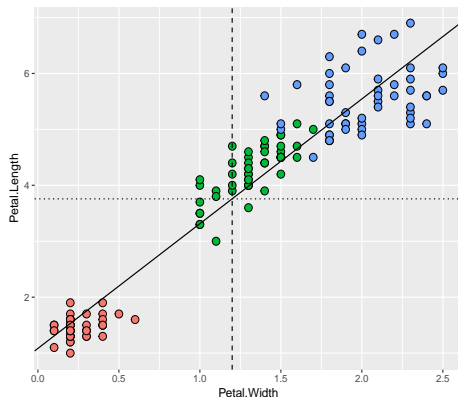
```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length,
                                   fill = Species)) +
  geom_point(colour = "black", shape = 21)
```



## ggplot2: scatter plots

You can also add lines to the plot:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, fill = Species)) +  
  geom_point(shape = 21, size = 3) +  
  theme(legend.position = "none") +  
  geom_hline(mapping = aes(yintercept = mean(Petal.Length)), lty = 3) +  
  geom_vline(mapping = aes(xintercept = mean(Petal.Width)), lty = 2) +  
  geom_abline(intercept = 1.084, slope = 2.23, lty = 1)
```

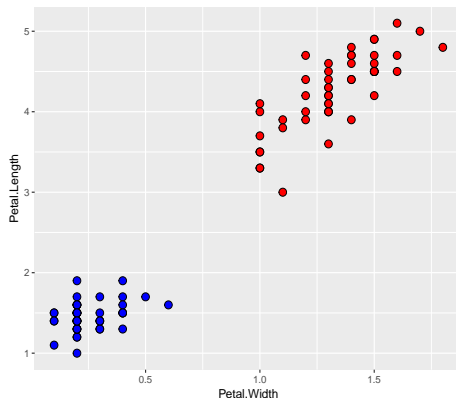




## ggplot2: scatter plots

You can add extra points to the plot by using two `geom_point` layers:

```
versicolor <- subset(x = iris, Species == "versicolor")
setosa      <- subset(x = iris, Species == "setosa")
ggplot() +
  geom_point(data = versicolor, mapping = aes(x = Petal.Width, y = Petal.Length), fill = "red", shape = 21, size = 3) +
  geom_point(data = setosa, mapping = aes(x = Petal.Width, y = Petal.Length), fill = "blue", shape = 21, size = 3)
```



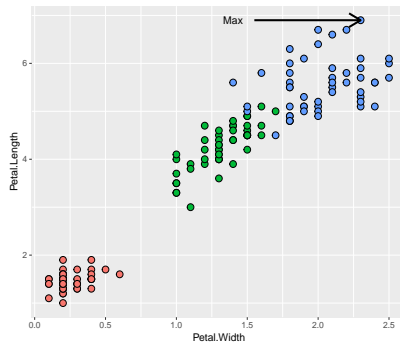
Note 1: unlike traditional plots, ggplot will automatically adjust the axes limits.

Note 2: if needed you can define the `aes()` in the geoms!!

# Traditional graphics: scatter plots

You can add text and arrows:

```
max.value <- iris[iris$Petal.Length == max(iris$Petal.Length), ]
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, fill = Species)) +
  geom_point(shape = 21, size = 3) +
  theme(legend.position = "none") +
  geom_segment(data = max.value, aes(x = Petal.Width - 0.75,
                                     xend = Petal.Width,
                                     y = Petal.Length,
                                     yend = Petal.Length),
              size = 1, arrow = arrow(length = unit(0.5, "cm"))) +
  geom_text(data = max.value, mapping = aes(x = Petal.Width - 0.9,
                                             y = Petal.Length, label = "Max"))
```

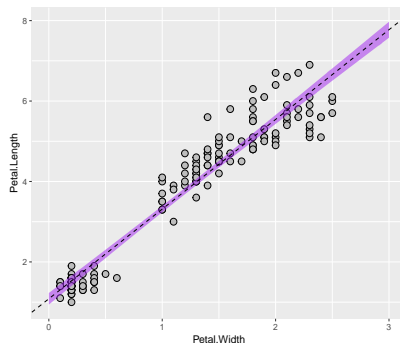


## ggplot2: scatter plots

In ggplot, confidence intervals can be added with specialised function `geom_ribbon()`:

```
test_mod <- lm(Petal.Length ~ Petal.Width, data = iris)
newdat    <- data.frame(Petal.Width = seq(0, 3, length.out = 100))
pred      <- predict(object = test_mod, newdata = newdat, interval = "confidence")

ggplot() +
  geom_point(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length), fill = "grey", shape = 21, size = 3) +
  geom_ribbon(data = cbind(newdat, pred), mapping = aes(x = Petal.Width, ymin = lwr, ymax = upr), fill = "purple", alpha = 0.5) +
  geom_abline(intercept = coef(test_mod)[1], slope = coef(test_mod)[2], lty = 2)
```

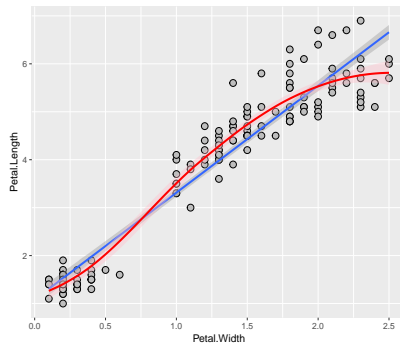


Note: because we are building the plot with two different datasets (i.e. `iris` & `newdat`), we specify the data and `aes()` separately in each line of the ggplot code.

## ggplot2: scatter plots

In ggplot, you can also do basic statistics directly:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length)) +  
  geom_point(fill = "grey", shape = 21, size = 3) +  
  geom_smooth(method = "lm") +  
  geom_smooth(method = "loess", fill = "pink", colour = "red")
```



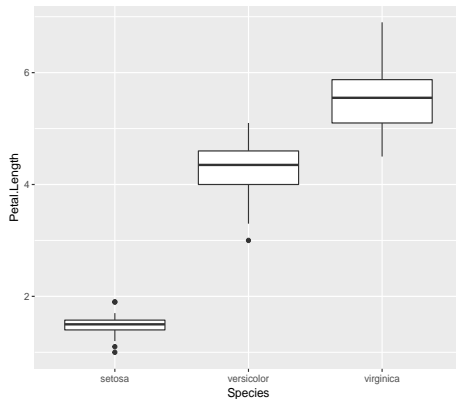
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## ggplot2: box plots

In ggplot, use `geom_boxplot()` to draw a box plot:

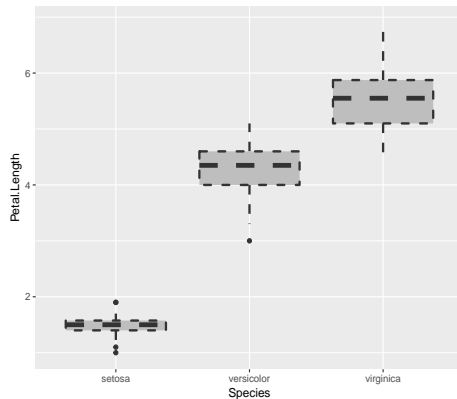
```
ggplot(data = iris, mapping = aes(x = Species, y = Petal.Length)) +  
  geom_boxplot()
```



## ggplot2: box plots

Many of the same changes made to scatter plots can be made here:

```
ggplot(data = iris, mapping = aes(x = Species, y = Petal.Length)) +  
  geom_boxplot(fill = "grey", size = 1, lty = 2)
```



# Plotting in R

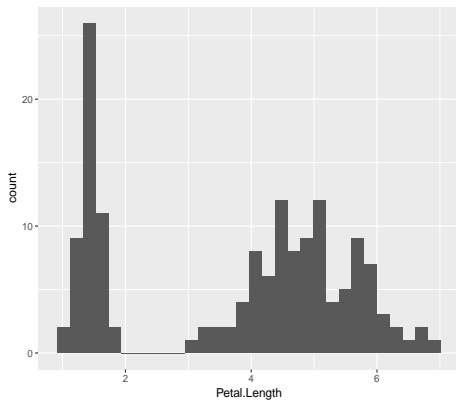
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## ggplot2: histograms

In ggplot, use `geom_histogram()` to draw an histogram:

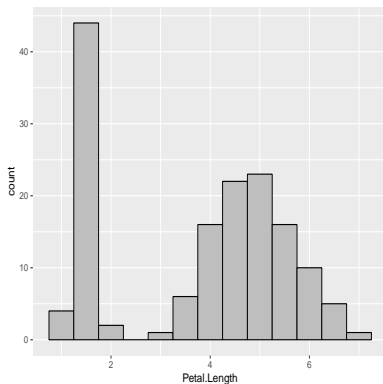
```
ggplot(data = iris, mapping = aes(x = Petal.Length)) +  
  geom_histogram()  
  
## 'stat_bin()' using 'bins = 30'. Pick better value with  
## 'binwidth'.
```



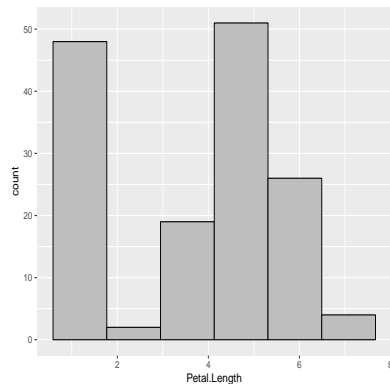
# ggplot2: histograms

You can change the width of bins with `binwidth` or their number with `bins`:

```
ggplot(data = iris, mapping = aes(x = Petal.Length)) +  
  geom_histogram(binwidth = 0.5, colour = "black", fill = "grey")
```



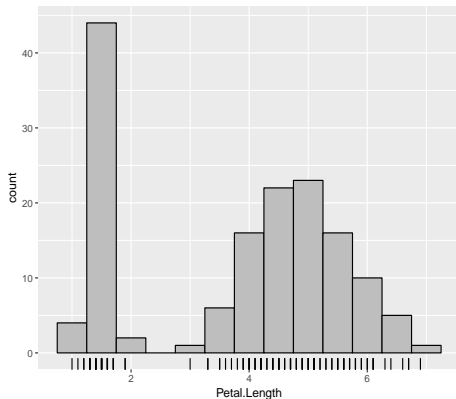
```
ggplot(data = iris, mapping = aes(x = Petal.Length)) +  
  geom_histogram(bins = 6, colour = "black", fill = "grey")
```



## ggplot2: histograms

Add a rug below the histogram with `geom_rug`:

```
ggplot(data = iris, mapping = aes(x = Petal.Length)) +  
  geom_histogram(binwidth = 0.5, colour = "black", fill = "grey") +  
  geom_rug()
```



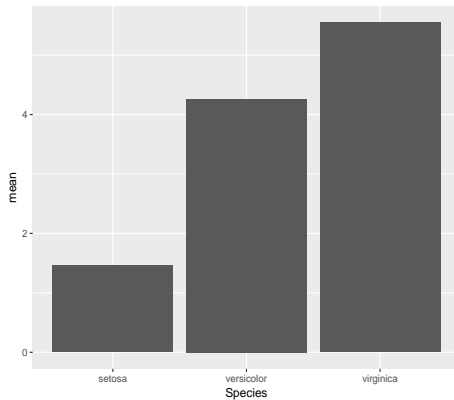
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## ggplot2: bar plots

In ggplot, use `geom_col()` to draw a bar plot:

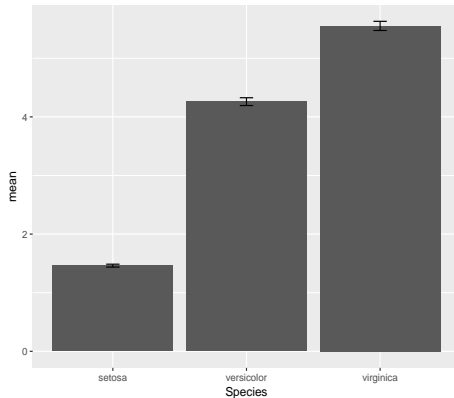
```
ggplot(data = spp_means, mapping = aes(x = Species, y = mean)) +  
  geom_col()
```



## ggplot2: bar plots

Adding error bars in ggplot is much easier than in traditional graphics:

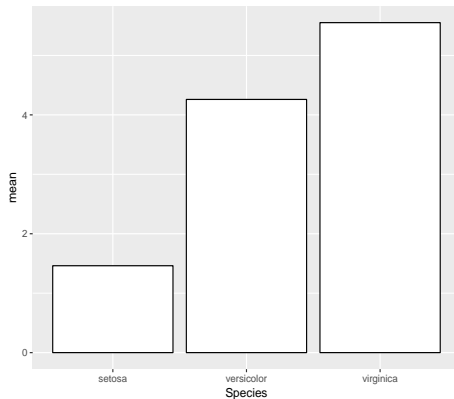
```
ggplot(data = spp_means, mapping = aes(x = Species, y = mean)) +  
  geom_col() +  
  geom_errorbar(aes(ymin = mean - SE, ymax = mean + SE), width = 0.1)
```



## ggplot2: bar plots

As before, modifications are straightforward:

```
ggplot(data = spp_means, mapping = aes(x = Species, y = mean)) +  
  geom_col(fill = "white", colour = "black")
```



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# Introduction to aesthetics

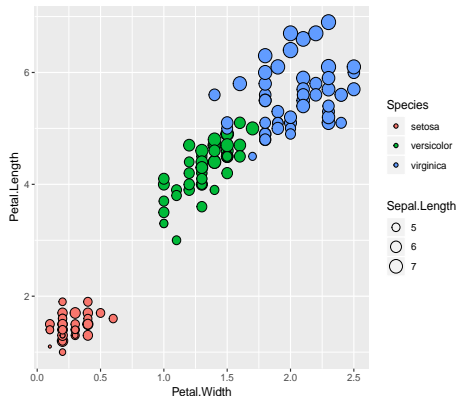
In ggplot, you can change aesthetics in individual segments of the code (`aes()`) or you can change information for the whole plot using themes (`theme()`).

## Using the aesthetic function more

We'll start by looking back at `aes()`.

We can use it to change multiple aesthetics of a plot:

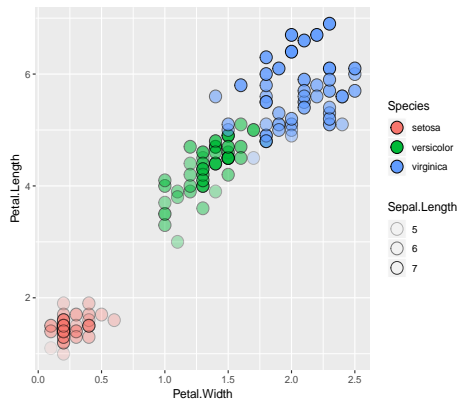
```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, fill = Species, size = Sepal.Length)) +  
  geom_point(shape = 21)
```



## Using the aesthetic function more

Here we change the transparency:

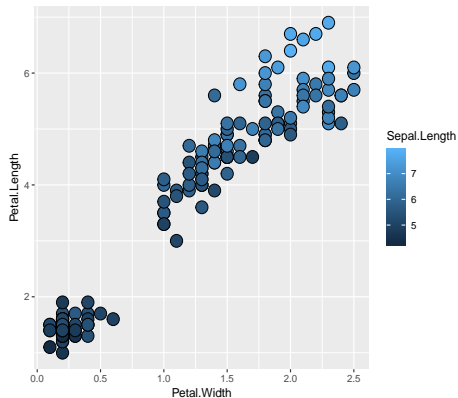
```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, fill = Species, alpha = Sepal.Length)) +  
  geom_point(shape = 21, size = 5)
```



## Using the aesthetic argument more

Applying aesthetics to continuous variables will be different to categorical variables:

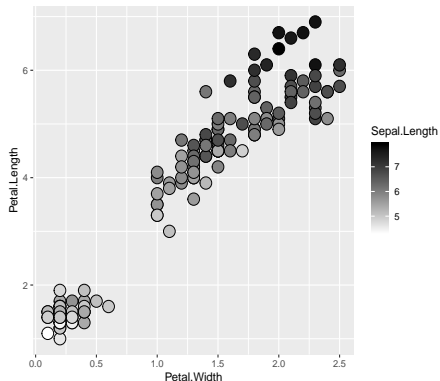
```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, fill = Sepal.Length)) +  
  geom_point(shape = 21, size = 5)
```



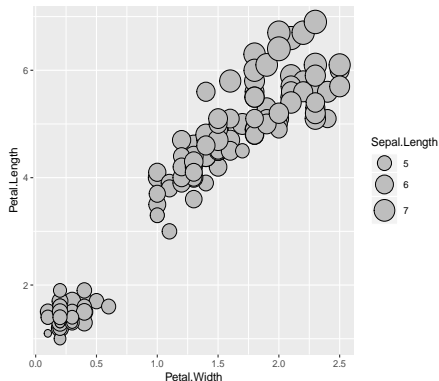
## Using the aesthetic argument more

You can indicate values for a third dimension in different ways:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length,
                                  fill = Sepal.Length)) +
  geom_point(shape = 21, size = 5) +
  scale_fill_continuous(low = "white", high = "black")
```



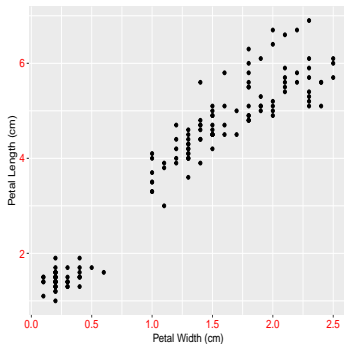
```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length,
                                  size = Sepal.Length)) +
  geom_point(shape = 21, fill = "grey") +
  scale_size_continuous(range = c(3, 10))
```



## Change text

You can change size and colour of axis text easily:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  labs(x = "Petal Width (cm)", y = "Petal Length (cm)") +
  theme(axis.text = element_text(size = 12, colour = "red"), axis.title = element_text(size = 12))
```



Note: the text size uses different measurement units than traditional graphics.

# Combining plots

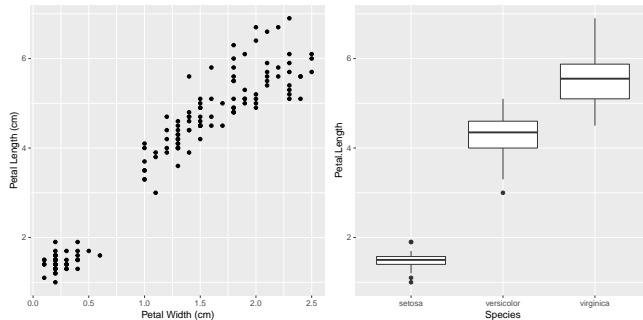
Combining plots is less straightforward in ggplot2...

You need to use an additional package:

```
scatter <- ggplot(iris, mapping = aes(x = Petal.Width, y = Petal.Length)) + geom_point() +
  labs(x = "Petal Width (cm)", y = "Petal Length (cm)")

box <- ggplot(iris, mapping = aes(x = Species, y = Petal.Length)) + geom_boxplot()

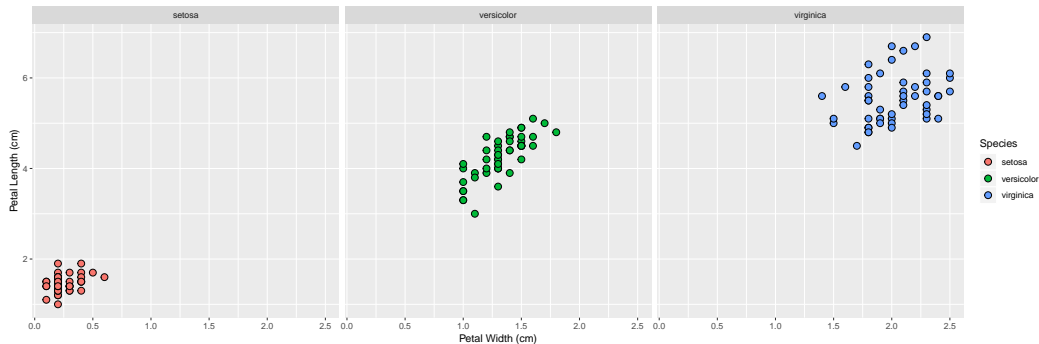
library(gridExtra)
grid.arrange(scatter, box, nrow = 1)
```



# Faceting

Although combining multiple plots is cumbersome, there is an inbuilt function to create facets:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, fill = Species)) +
  geom_point(shape = 21, colour = "black", size = 3) +
  labs(x = "Petal Width (cm)", y = "Petal Length (cm)") +
  facet_wrap(~ Species)
```

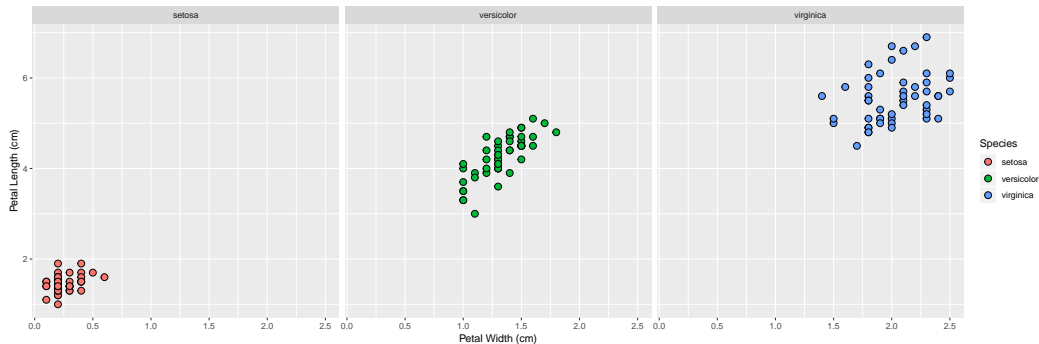




# Faceting

Although combining multiple plots is cumbersome, there is an inbuilt function to create facets:

```
ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length, fill = Species)) +  
  geom_point(shape = 21, colour = "black", size = 3) +  
  labs(x = "Petal Width (cm)", y = "Petal Length (cm)") +  
  facet_wrap(~ Species)
```



Challenge: have a second look at the relationship between the happiness and the price of present using the dataset Surprise.

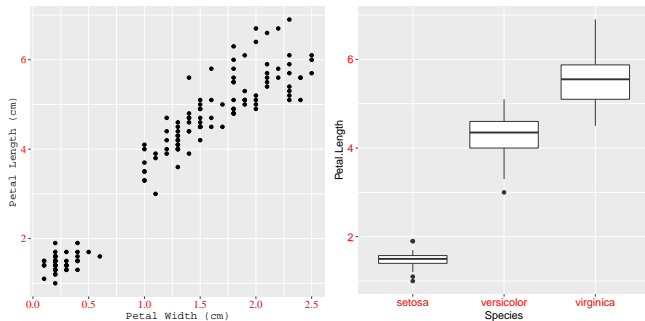
# Modifying typefaces

Unlike traditional graphics, in ggplot2 you can easily change the typeface of individual elements in theme:

```
scatter <- ggplot(data = iris, mapping = aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  labs(x = "Petal Width (cm)", y = "Petal Length (cm)") +
  theme(axis.text = element_text(size = 12, colour = "red", family = "serif"), axis.title = element_text(size = 12, family = "mono"))

box <- ggplot(iris, mapping = aes(x = Species, y = Petal.Length)) +
  geom_boxplot() +
  theme(axis.text = element_text(size = 12, colour = "red", family = "sans"), axis.title = element_text(size = 12, family = "sans"))

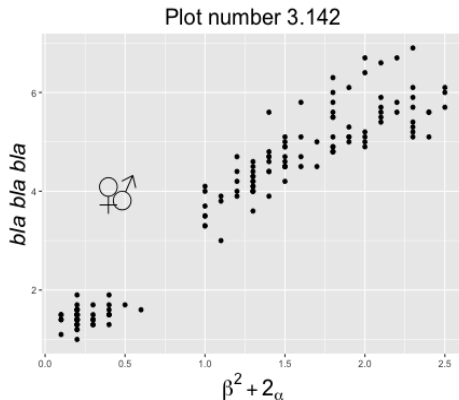
grid.arrange(scatter, box, nrow = 1)
```



# Special characters

You can use weird characters:

```
foo <- round(pi, 3)
ggplot(iris, mapping = aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  labs(x = expression(beta^2 + 2[alpha]), y = expression(paste(italic("bla bla bla"))), title = paste("Plot number", foo)) +
  annotate("text", x = c(0.4, 0.5), y = c(4, 4), label = c("\u2640", "\u2642"), size = 12) + ## requires font with unicode installed!
  theme(plot.title = element_text(hjust = 0.5, size = 20),
        axis.title = element_text(size = 20))
```



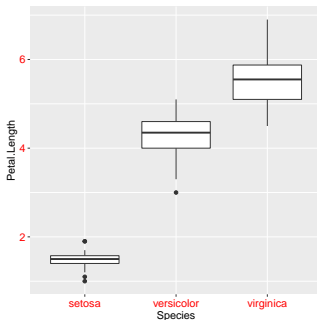
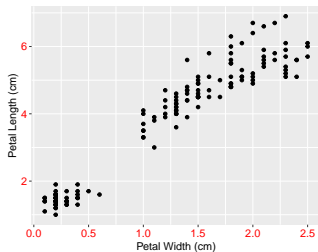
# Plot margins

Plot margins are also controlled in theme of each plot individually:

```
scatter <- ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  labs(x = "Petal Width (cm)", y = "Petal Length (cm)") +
  theme(axis.text = element_text(size = 12, colour = "red"),
        axis.title = element_text(size = 12),
        plot.margin = unit(c(30, 4, 1, 1), "mm"))

box <- ggplot(iris, aes(x = Species, y = Petal.Length)) +
  geom_boxplot() +
  theme(axis.text = element_text(size = 12, colour = "red"),
        axis.title = element_text(size = 12))

grid.arrange(scatter, box, nrow = 1)
```



# Preset themes

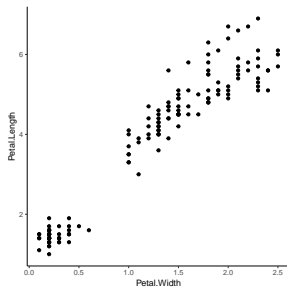
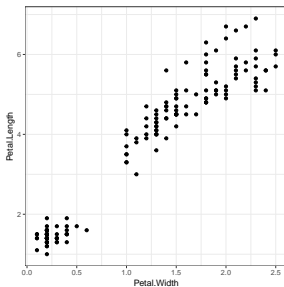
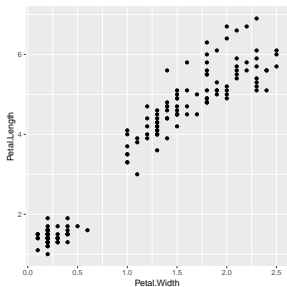
ggplot2 also has a number of preset themes that you can use:

```
grey <- ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  theme_grey()

bw <- ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  theme_bw()

classic <- ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  theme_classic()

grid.arrange(grey, bw, classic, nrow = 1)
```

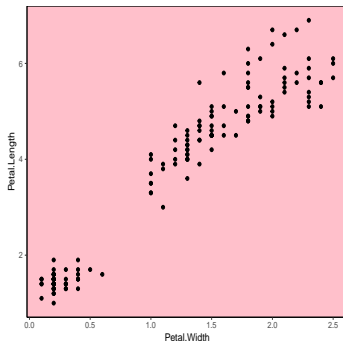


## Preset themes

You can create your own theme once for all!

```
theme_pink <- theme_classic() %+replace% theme(panel.background = element_rect(fill = "pink"))

ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length)) +
  geom_point() +
  theme_pink
```



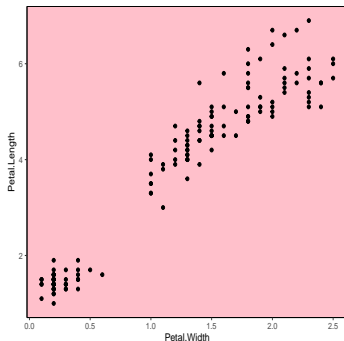
Note: check `?theme` for the list of options that can be changed.

# Preset themes

You can set a theme for all plots with `theme_set`

```
theme_old <- theme_set(theme_pink)
```

```
ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length)) +  
  geom_point()
```



```
theme_set(theme_old) ## restore original theme
```

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## ggplot2: Exporting

?ggsave

```
classic <- ggplot(iris, aes(x = Petal.Width, y = Petal.Length)) +  
  geom_point() +  
  theme_classic()  
  
ggsave("ggplot.pdf", plot = classic, width = 15, height = 5)
```

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## There are other geom out there!

There are a few other plot types in ggplot2 that are worth looking at (check the cheatsheet!):

- `geom_violin()`, `geom_area()`, `geom_smooth()`, `geom_density()`

## There are other geom out there!

There are a few other plot types in ggplot2 that are worth looking at (check the cheatsheet!):

- `geom_violin()`, `geom_area()`, `geom_smooth()`, `geom_density()`

But the true force of having developed something as modular as ggplot2 is that there are many more packages each week providing ggplot2 extensions!

A few random examples of ggplot2 extensions:

- `ggforce` (for extra geoms to draw circles, pie charts, fancy violin plots, ...)
- `ggExtra` (for marginal distribution)
- `ggthemes` (for extra themes, including `theme_excel()`!! :-/)
- `ggmap` (for maps)
- `ggson` (for adding a scale bar and north arrow to maps)
- `ggrepel` (for adding labels to plots)
- `ggalt` (for creating cluster plots)
- `cowplot` (for creating nested figures)

Note: see also <http://www.ggplot2-exts.org/gallery/> (but the list is incomplete).

## A random example: ggmap

```
library(ggmap)

map_us <- get_map(location = c(lon = 13.349342, lat = 52.500033), source = "google", maptype = "satellite", zoom = 20)

## Warning in download.file(url, destfile = tmp, quiet = !messaging, mode = "wb"): cannot open URL
## 'http://maps.googleapis.com/maps/api/staticmap?center=52.500033,13.349342&zoom=20&size=640x640&scale=2&maptype=satellite&language=en-EN&sensor=
## HTTP status was '403 Forbidden'
## Error in download.file(url, destfile = tmp, quiet = !messaging, mode = "wb"): cannot open URL
## 'http://maps.googleapis.com/maps/api/staticmap?center=52.500033,13.349342&zoom=20&size=640x640&scale=2&maptype=satellite&language=en-EN&sensor=
ggmap(map_us, extent = "panel") +
  geom_point(mapping = aes(x = 13.349342, y = 52.500033), colour = "white", size = 60, shape = 21) +
  geom_text(mapping = aes(x = 13.349342, y = 52.500033), label = "ALEX IS\n HERE", colour = "white", size = 8) +
  labs(x = "longitude", y = "latitude")

## Error in ggmap(map_us, extent = "panel"): object 'map_us' not found
```

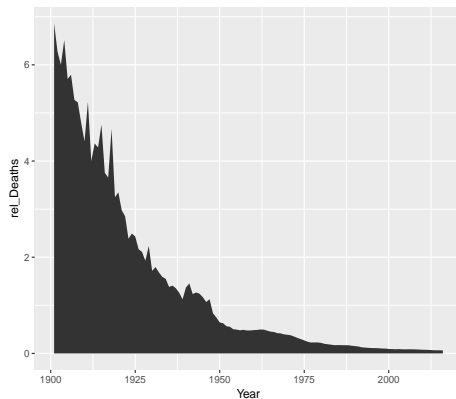
Note: this package does not seem very well maintained. . .

# Challenge

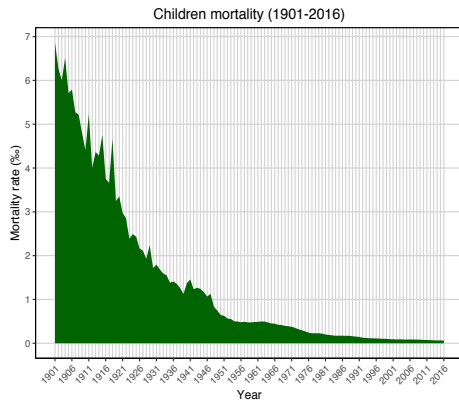
Use the datasets called `population_UK` and `deaths_UK` to compute yearly mortality rates for individuals below 15 yrs only and make a nice plot of the outcome using `ggplot2`!

# Simple solution

```
ggplot(data = data_processed, mapping = aes(y = rel_Deaths, x = Year)) +  
  geom_area()
```



## More complex solution





## More complex solution

```
ggplot(data = data_processed, mapping = aes(y = rel_Deaths, x = Year)) +
  geom_area(fill = "darkgreen") +
  ylab("Mortality rate (\u2030)") +
  labs(title = paste0("Children mortality (", min(data_processed$Year), "-", max(data_processed$Year), ")")) +
  scale_x_continuous(breaks = seq(min(data_processed$Year), max(data_processed$Year), by = 5),
    minor_breaks = min(data_processed$Year):max(data_processed$Year)) +
  scale_y_continuous(breaks = 0:ceiling(max(data_processed$Year)),
    minor_breaks = NULL) +
  theme_classic() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
    plot.title = element_text(hjust = 0.5),
    panel.grid.minor = element_line(colour = "lightgrey"),
    panel.grid.major = element_line(colour = "lightgrey"),
    panel.border = element_rect(colour = "black", fill = NA))
```

## Challenge

Use the datasets called `population_UK` and `deaths_UK` to compute yearly mortality rates for individuals of each age class and make a quick plot of the outcome using `ggplot2`!

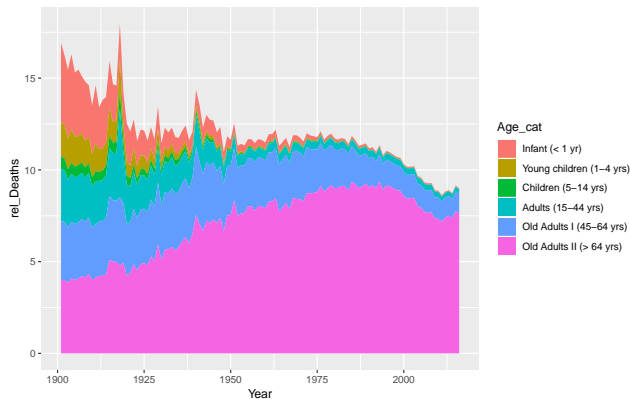
## Possible solution

```

deaths_UK %>% group_by(Year, Age_cat) %>% summarize(tot_Deaths = sum(Deaths)) -> deaths_processed_all
population_UK %>% group_by(Year) %>% summarize(tot_Pop = sum(Pop)) -> pop_processed## as before
full_join(deaths_processed_all, pop_processed) %>% mutate(rel_Deaths = 1000*tot_Deaths/tot_Pop) -> data_processed_all

## Joining, by = "Year"
ggplot(data = data_processed_all, mapping = aes(y = rel_Deaths, x = Year, fill = Age_cat)) +
  geom_area()

```



# Plotting in R

- 1 Introduction
- 2 Plotting with traditional graphics
- 3 Plotting with `ggplot2`
- 4 Conclusion: traditional graphics vs. `ggplot2`

# Which plotting tool should you use?

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- arguments often differ between functions
- help files useful
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- uniform grammar
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→ It may be useful to know both!?