G54DMA - Lab 5: Data Visualisation in R

Instructions

In this lab session, we will learn how to use basic R to visualise data. Additionally, we will learn to create more sophisticated and customizable graphs using one of the most popular R packages: ggplot2.

For a comprehensive reference manual on all things R, please refer to *An Introduction to R* by Venables et al., which can be found here:
https://cran.r-project.org/doc/manuals/r-release/R-intro.pdf

For a comprehensive reference manual on ggplot2, please refer to *ggplot2: Elegant Graphics for Data Analysis* by Hadley Wickham (2015)*,* which can be found in the Additional Resources section on Moodle.

I recommend you have them with you while you are working on these exercises.

Thorough the labs, we will be using *An Introduction to R* as a reference manual. Additionally, in this lab we will be using Hadley Wickham's *ggplot2: Elegant Graphics for Data Analysis* for section C. Chapters or sections of interest will be signalled with "***Reading:***" in the Instruction sheets.

Learning outcomes

After this lab session, you will be able to:

- **Create simple graphs to analyse your data using basic R.**
- **Create sophisticated graphs to analyse your data using the ggplot2 library.**
- **Choose appropriate visualisation methods for data analysis purposes.**

1. Simple graphs in R

R has many functions for graphs and plots, for example:

```
ir = iris #load iris dataset on a variable
pie(table(ir$Species)) #creates a piechart
pie(table(ir$Species), col=c("white","blue","red"))

plot(ir$Sepal.Length, ir$Sepal.Width, ylab="Sepal Width",
xlab="Sepal Length", main="Sepal Width vs Sepal Length") #creates a
scatterplot of sepal length vs sepal width

# You can also colour the points
plot(ir$Sepal.Length, ir$Sepal.Width, ylab="Sepal Width",
xlab="Sepal Length", main="Sepal Width vs Sepal Length", col =
"red") #All points will be red

plot(ir$Sepal.Length, ir$Sepal.Width, ylab="Sepal Width",
xlab="Sepal Length", main="Sepal Width vs Sepal Length", col =
ir$Species) # Points will be coloured according to ir$Species
```

The parameters *xlab* and *ylab* are used to name the axes. The parameter *main* is used to title your graph.

To study the distribution of your variables, you can use *hist()* to create histograms.

```
hist(ir$Sepal.Width) #creates a histogram for Sepal Width
hist(ir$Sepal.Width, breaks=15, col="red",
  main="Histogram of Sepal Width", xlab="Sepal Width")
```

The parameter *breaks* determines the number of bins/cells in the histogram, and it can be:

- a vector giving the breakpoints between histogram cells.
- a function to compute the vector of breakpoints.
- a single number giving the number of cells for the histogram.

```
hist(ir$Sepal.Width, breaks=seq(1,5,by=0.2), col="purple",
main="Histogram of Sepal Width", xlab="Sepal Width") # remember the
seq function?
```

You can also add extra lines, legends, text, etc. to plots.

```
  abline(v=mean(ir$Sepal.Width),col="red", lwd=3) #adds a mean line in
  red
  abline(v=median(ir$Sepal.Width),col="green", lwd=3) #adds a median
  line in green

  legend("topright",c("mean","median"),col=c("red","green"), pch=16)
  #created a legend for the graph
```

R also allows you to create boxplots, which can be a very useful for exploring data:

```
  boxplot(ir$Sepal.Length)
```

You can also easily plot multiple graphs on one window with the function *par()*:

```
par(mfrow=c(1,2)) ; # arranges graphs in rows (1 row, 2 columns)
boxplot(ir$Sepal.Length, las=3, main="Sepal length");
boxplot(ir$Sepal.Width, las=3, main="Sepal Width");
```

The *par()* function is very flexible. To learn more about its parameters, search for `??graphics::par` in RStudio.

Another form of plotting that can be very helpful for visualising complex data is *pairs()*, which returns scatterplots between all attributes passed as parameters.

```
  pairs(ir[,1:2])
  pairs(ir[,1:4], col=ir$Species)
```

Finally, the latest versions of R have introduced interactive 3-dimensional plotting capabilities:

```
  # You will have to install several packages
  install.packages("devtools")
  library(devtools)
  install_github("shinyRGL", "trestletech")
  install_github("rgl", "trestletech", "js-class")

  library(rgl)
  ?plot3d
  plot3d(ir$Sepal.Length, ir$Sepal.Width, ir$Petal.Length, type="s",
col=as.numeric(ir$Species))
```

You may not have permissions on the lab machines to install all of these libraries, but you can experiment on your own computer.

Reading: For more information about visualisation techniques, read chapter 12 of *An Introduction to R*.

2. Advanced graphs with *ggplot2*

As you practice more with the basic visualisation functions from the previous section, you will probably realise that, while useful, they are quite limited in terms of customisation and appearance. For more complex graphs, the *ggplot2* library is the best alternative.

In this lab, we are going to use the *iris* dataset and Harver's worshop on *ggplot2* as our main guide. You can find the tutorial here:

http://tutorials.iq.harvard.edu/R/Rgraphics/Rgraphics.html

The advantages of using ggplot2 are:

- consistent underlying grammar of graphs (i.e. all types of graphs follow the same rules and use the same functions) (Wilkinson, 2005)
- plot specification at a high level of abstraction
- very flexible
- theme system for polishing plot appearance
- mature and complete graphics system
- many users, active mailing list

That said, there are some things you cannot (or should not) do with *ggplot2*:

- 3-dimensional graphics (see the *rgl* package from the previous section)
- Graph-theory type graphs (nodes/edges layout; see the *igraph* package)
- Interactive graphics (see the *ggvis* package)

What Is The Grammar Of Graphics?

The basic idea is that you will independently specify plot building blocks and combine them to create just about any kind of graphical display you want. All types of graphs will use the same building blocks. It is up to you to decide how to use them to create the graph you need. Building blocks of a graph include:

- data
- aesthetic mapping
- geometric object
- statistical transformations
- scales
- coordinate system
- position adjustments
- faceting

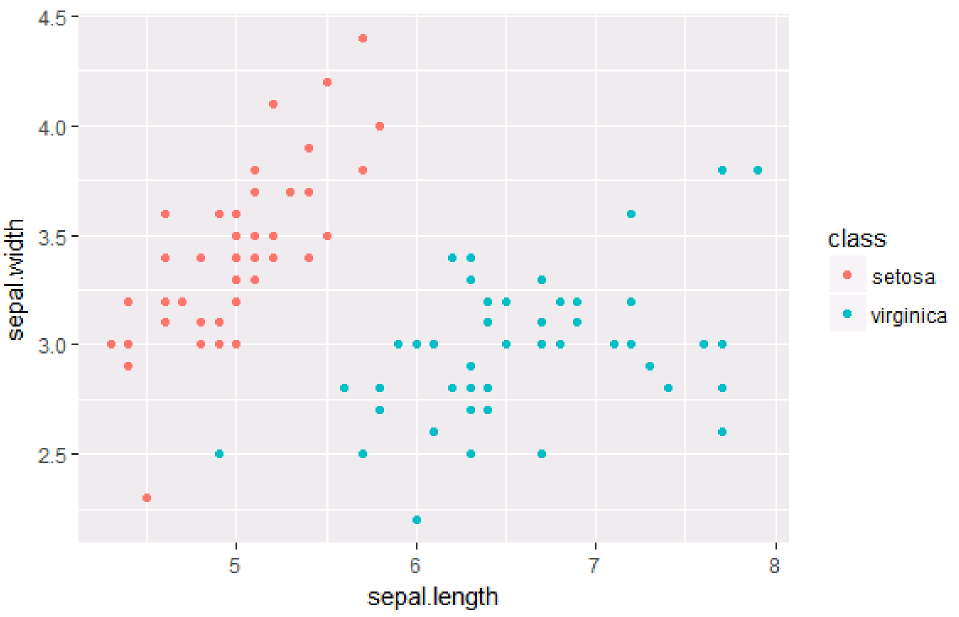
To do this, there are three major functions that you will use in ggplot2:

- ggplot() – for fine, granular control of graphs
- geom functions – to add points, lines, boxplots, etc. to the graph.
- ggsave() – to quickly save graphs

4.1 Plotting Function - ggplot():

ggplot is called with the data you want to show in the graph.
Let's see an example with a coloured scatter plot:

```
#initialization
ir = iris
names(ir) = c("sepal.length", "sepal.width",      "petal.length",
 "petal.width", "class")
names(ir) #Remember! We saw (Lab 4) as a way of changing names of
 fields for dataframes.

#visualisation
ggplot(subset(ir, class %in% c("setosa", "virginica"))) + geom_po
int(aes(x=sepal.length, y = sepal.width, color = class))
```



What is the purpose of the section in red? What happens if you change it to:

```
ggplot(ir) + geom_point(aes(x=sepal.length, y = sepal.width, colo
r = class))
```

The parameter inside *ggplot* will specify the default data of your graph. If the input is not a data.frame, it will be converted to one. If not specified, then data must be suppled in each layer added to the plot.

4.2 Geoms

Geometric objects are the actual marks we put on a plot. You can think of them as layers of data that can be shown in the graph. There are several types. The ones we will work with are:

- points (geom_point, for scatter plots, dot plots, etc)
- lines (geom_line, for time series, trend lines, etc)
- boxplot (geom_boxplot, for, well, boxplots!)

A plot must have at least one geom, but there is no upper limit. You can add a geom to a plot using the + operator

You can get a list of available geometric objects using the code below:

```
help.search("geom_", package = "ggplot2")
```

You can also simply type geom_<tab> in any good R IDE (such as Rstudio or ESS) to see a list of functions starting with geom_.

In *ggplot* land *aesthetic* means "something you can see". Examples include:

- position (i.e., on the x and y axes)
- color ("outside" color)
- fill ("inside" color)
- shape (of points)
- linetype
- size

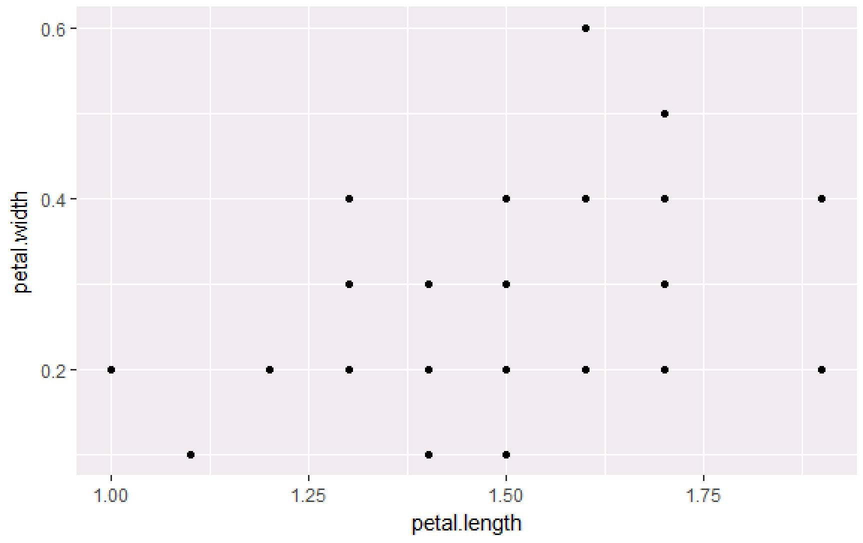
Each type of geom accepts only a subset of all aesthetics –refer to the geom help pages to see what mappings each geom accepts. Aesthetic mappings are set with the aes() function.

Let's look at each type of geom separately.

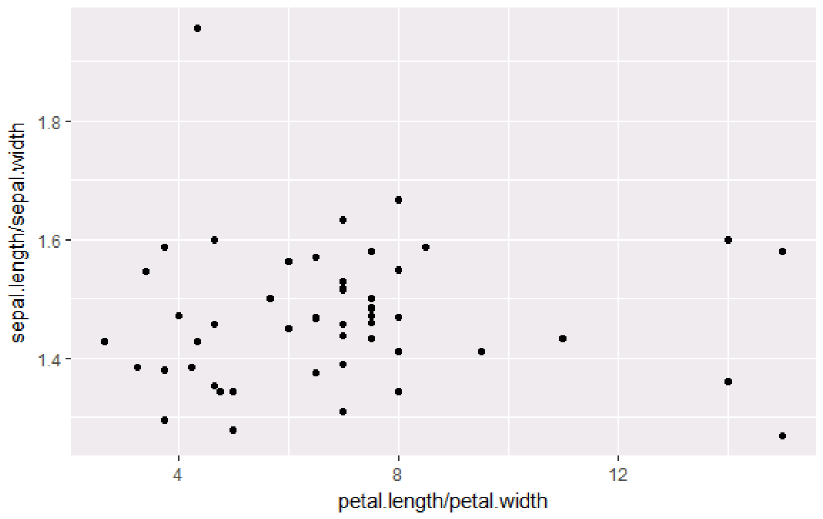
4.2.1 Points (Scatterplot)

Now that we know about geometric objects and aesthetic mapping, we can make a *ggplot*. geom_point requires mappings for *x* and *y*, all others are optional.

```
ir_set = subset(ir, class %in% c("setosa")) # grab only setosa
plants
ggplot(ir_set, aes(x=petal.length, y=petal.width)) + geom_point()
#this graph plots Petal length vs Petal width, but only for
setosa plants.
```



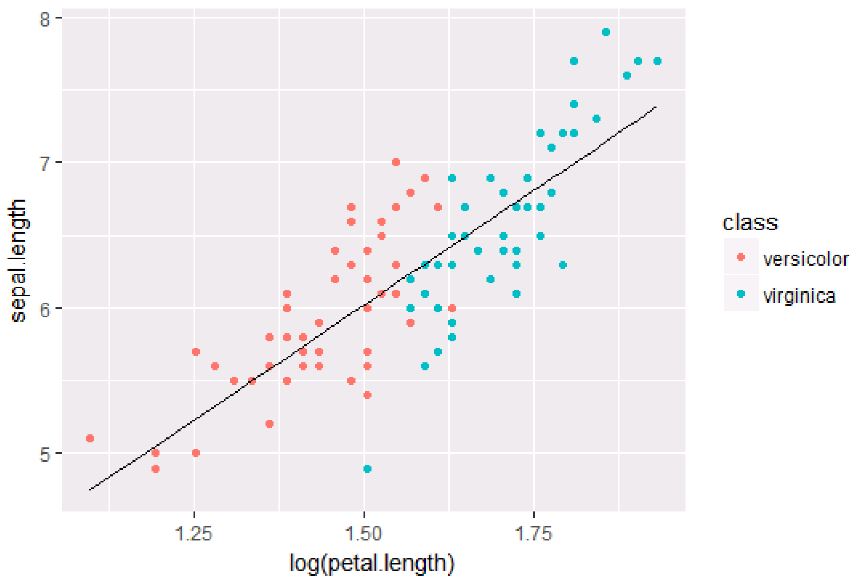
```
ggplot(ir_set, aes(x=petal.length/petal.width,
y=sepal.length/sepal.width)) + geom_point() # we can change the
data displayed in the aes function, too.
```



4.2.2 Lines (Prediction Line)

A plot constructed with ggplot can have more than one geom. In that case the mappings established in the ggplot() call are plot defaults that can be added to or overridden. Our plot could use a regression line:

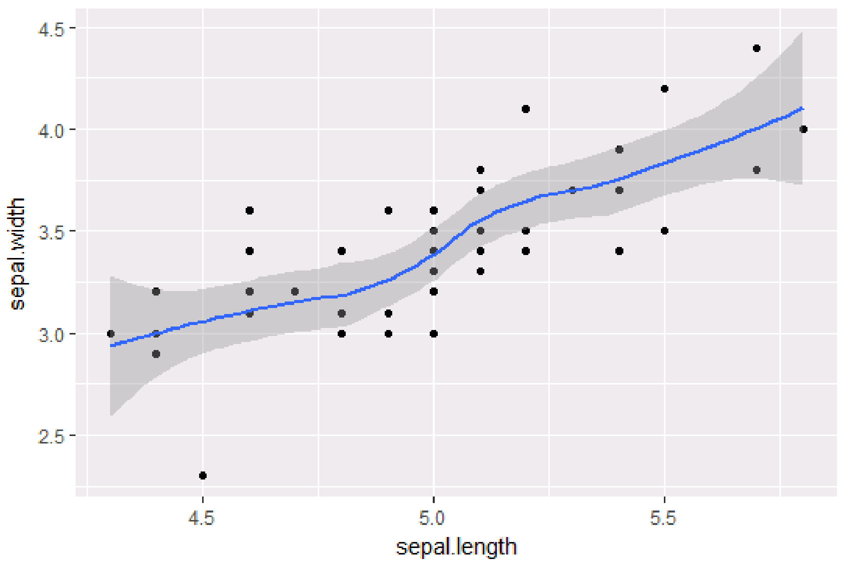
```
ir_versi = subset(ir, class %in% c("versicolor","virginica"))

ir_versi$pred.SL = predict(lm(sepal.length ~ log(petal.length),
data= ir_versi))

ggplot(ir_versi, aes(x = log(petal.length), y = sepal.length)) +
geom_point(aes(color = class)) + geom_line(aes(y = pred.SL))
```



Smoothers

Not all geometric objects are simple shapes –the smooth geom includes a line and a ribbon.

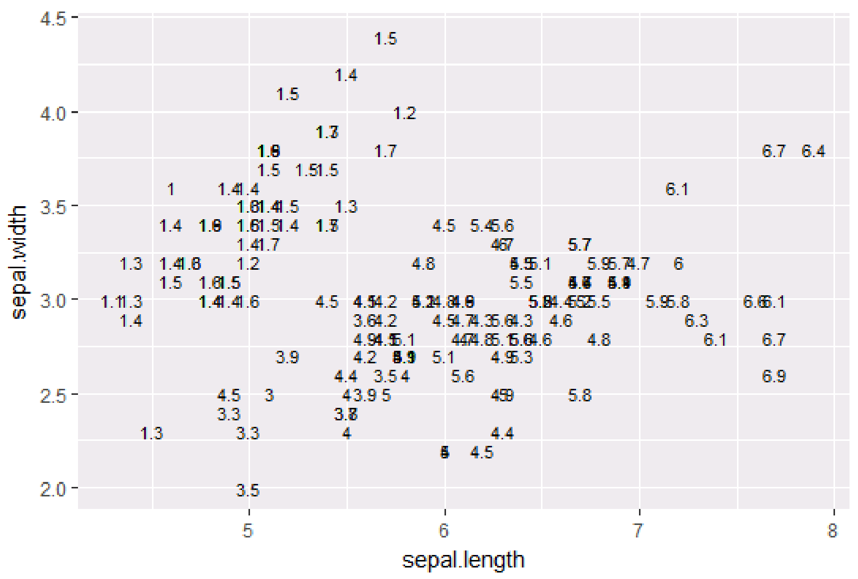
```
ir_set = subset(ir, class %in% c("setosa"))
ggplot(ir_set, aes(x=sepal.length, y=sepal.width)) + geom_point()
+ geom_smooth()
```



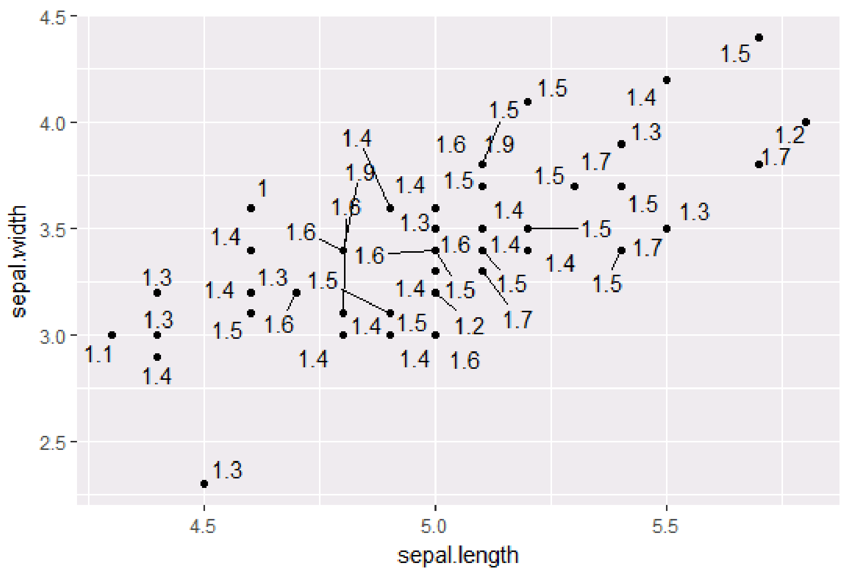
4.2.3 Text (Label Points)

Each geom accepts a particular set of mappings. For example geom_text() accepts a labels mapping.

```
ggplot(ir, aes(x=sepal.length, y=sepal.width)) +
geom_text(aes(label=petal.length), size=3)
```



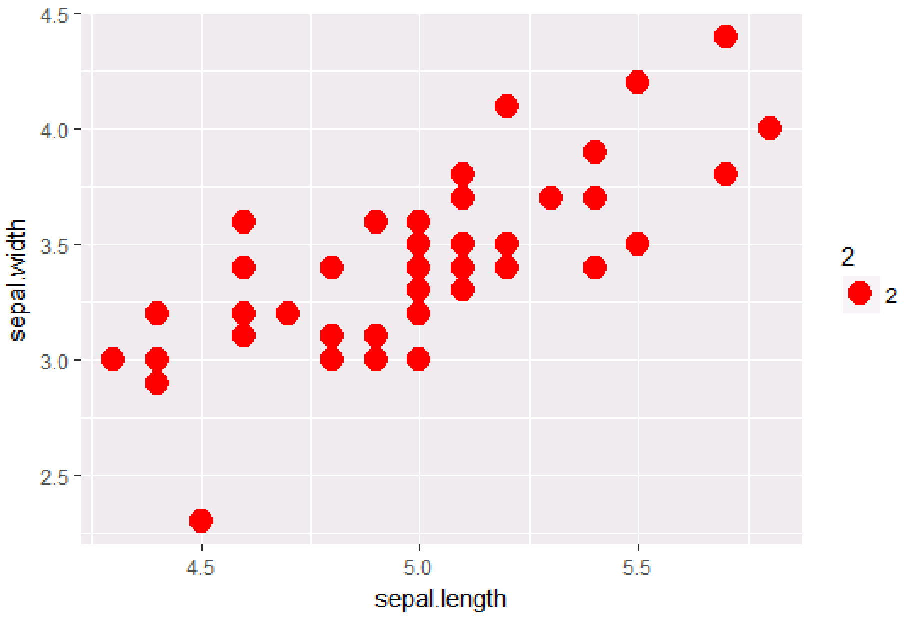
```
p1 = ggplot(ir_set, aes(x=sepal.length, y=sepal.width))
install.packages("ggrepel")
library("ggrepel")
p1 + geom_point() + geom_text_repel(aes(label=petal.length),
force = 3)
```



4.3 Aesthetic Mapping VS Assignment

Note that variables are mapped to aesthetics with the aes() function, while fixed aesthetics are set outside the aes() call. This sometimes leads to confusion, as in this example:

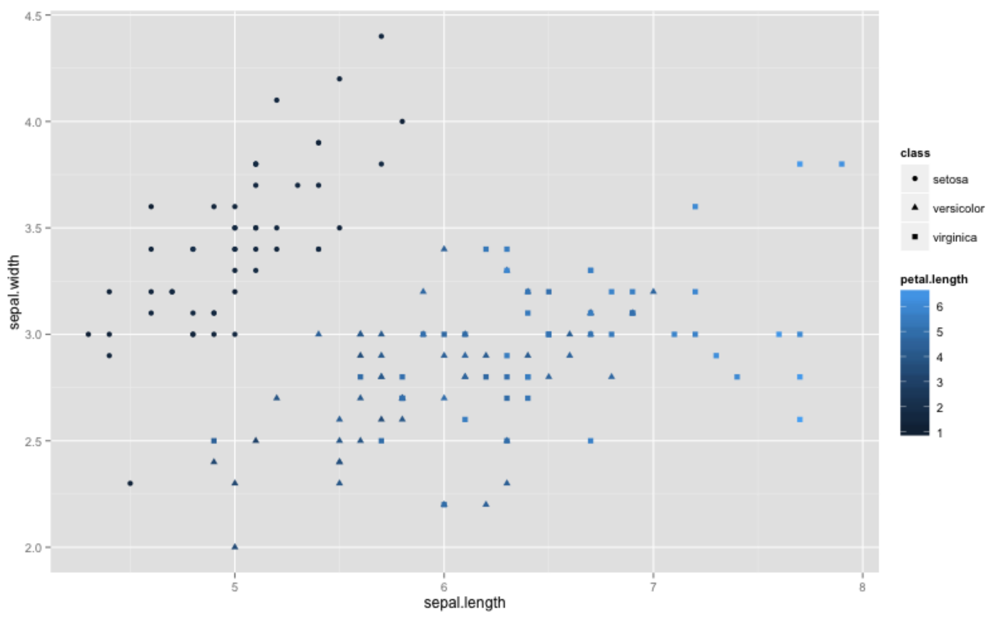
```
p1 +
geom_point(aes(size = 2), #incorrect! 2 is not a variable
color="red") # this is fine -- all points red
```



4.3.1 Mapping Variables to Other Aesthetics

Other aesthetics are mapped in the same way as x and y in the previous example.

```
ggplot(ir, aes(x=sepal.length, y=sepal.width)) +
geom_point(aes(color=petal.length, shape = class))
```



4.4 Statistical Transformations

Some plot types (such as scatterplots) do not require transformations–each point is plotted at x and y coordinates equal to the original value. Other plots, such as boxplots, histograms, prediction lines etc. require statistical transformations. For example:

- for a boxplot the y values must be transformed to the median and 1.5(IQR)
- for a smoother boxplot the y values must be transformed into predicted values

Each geom has a default statistic, but these can be changed.

4.5 Controlling Aesthetic Mapping: Scales

Aesthetic mapping (i.e., with aes()) only says that a variable should be mapped to an aesthetic. It doesn't say *how* that should happen. For example, when mapping a variable to *shape* with aes(shape = x) you don't say *what* shapes should be used. Similarly, aes(color = z) doesn't say *what* colours should be used. Describing what colours/shapes/sizes etc. to use is done by modifying the corresponding *scale*.

In ggplot2 scales include:

- position
- colour and fill
- size
- shape
- line type

Scales are modified with a series of functions using a scale_<aesthetic>_<type> naming scheme. Try typing scale_<tab> to see a list of scale modification functions.

4.5.1 Common Scale Arguments

The following arguments are common to most scales in ggplot2:

name

the first argument gives the axis or legend title

limits

the minimum and maximum of the scale

breaks

the points along the scale where labels should appear

labels

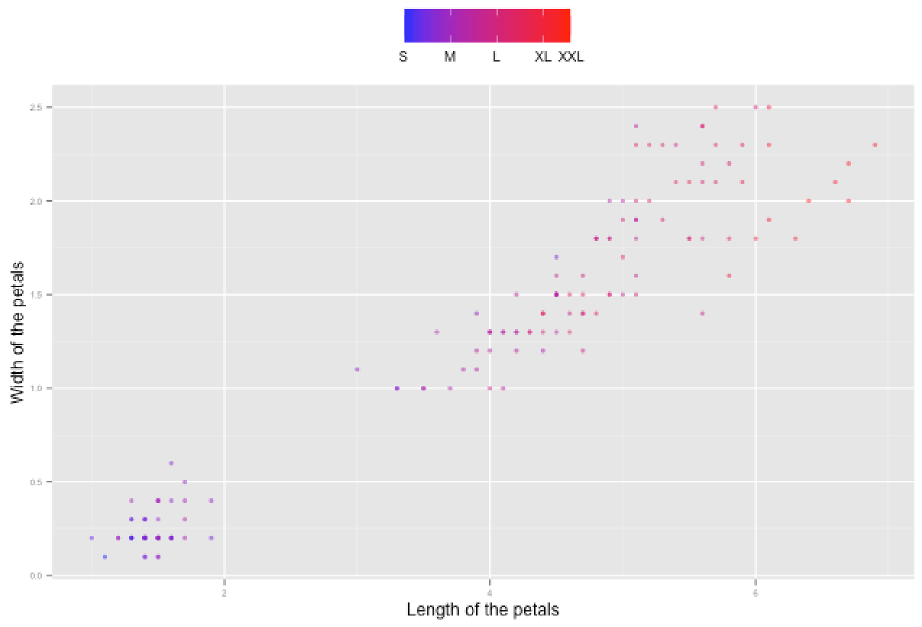
the labels that appear at each break

Specific scale functions may have additional arguments. For example, the scale_color_continuous function has arguments low and high for setting the colours at the low and high end of the scale.

4.5.2 Scale Modification Examples

Start by constructing a dotplot showing the distribution of home values by Length and Width of the petals.

```
p1 = ggplot(ir, aes(x=petal.length, y=petal.width)) +
theme(legend.position = "top", axis.text=element_text(size = 6))

p1 + geom_point(aes(color=sepal.length), alpha = 0.5, size = 1.5) +
scale_x_continuous(name="Length of the petals") +
scale_y_continuous(name="Width of the petals") +
scale_color_continuous(name="", breaks = c(4.3,5.3,6.3,7.3,7.9),
labels = c("S", "M", "L","XL","XXL"), low = "blue", high = "red")
```



ggplot2 has a wide variety of color scales. Note that in RStudio you can type scale_ followed by TAB to get the whole list of available scales.

4.6 Faceting

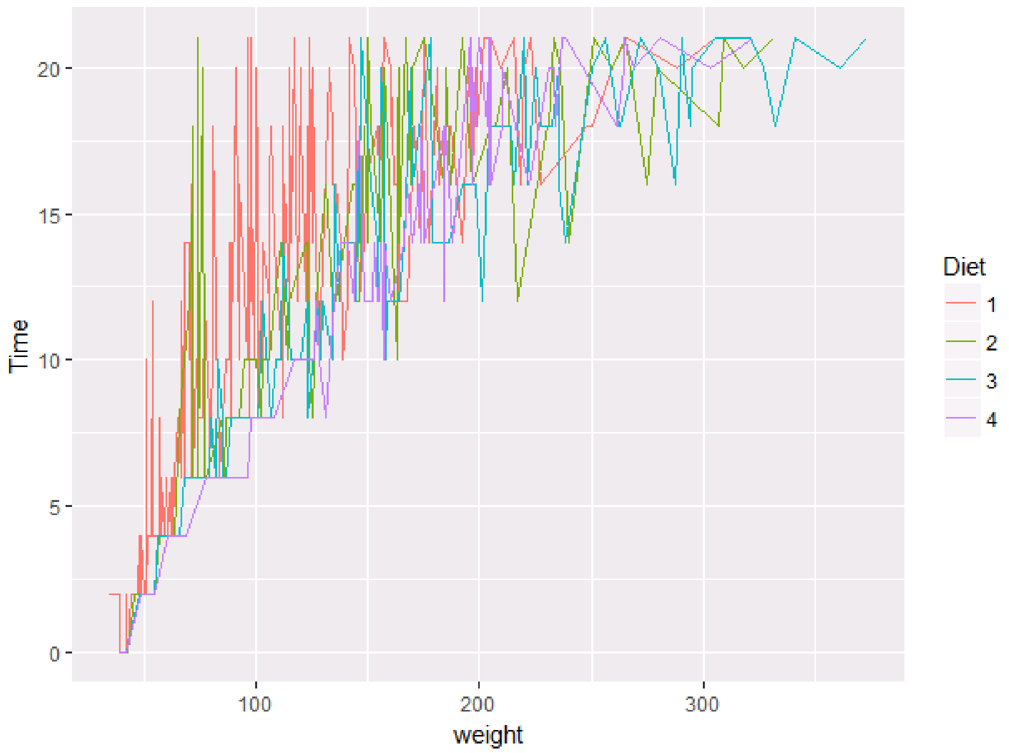
- Faceting is ggplot2 parlance for **small multiples**
- The idea is to create separate graphs for subsets of data
- ggplot2 offers two functions for creating small multiples:
  1. facet_wrap(): define subsets as the levels of a single grouping variable

2. facet_grid(): define subsets as the crossing of two grouping variables

- Facilitates comparison among plots, not just of geoms within a plot

What is the trend in petal length in each class? Start by using a technique we already know – map the class to color.
Let's try this with a different dataset from R: ChickWeight. Let's try to find the trend of each the weight in terms of diet:

```
cw=ChickWeight

p <- ggplot(cw, aes(x = weight , y = Time))
p + geom_line(aes(color = Diet))
```

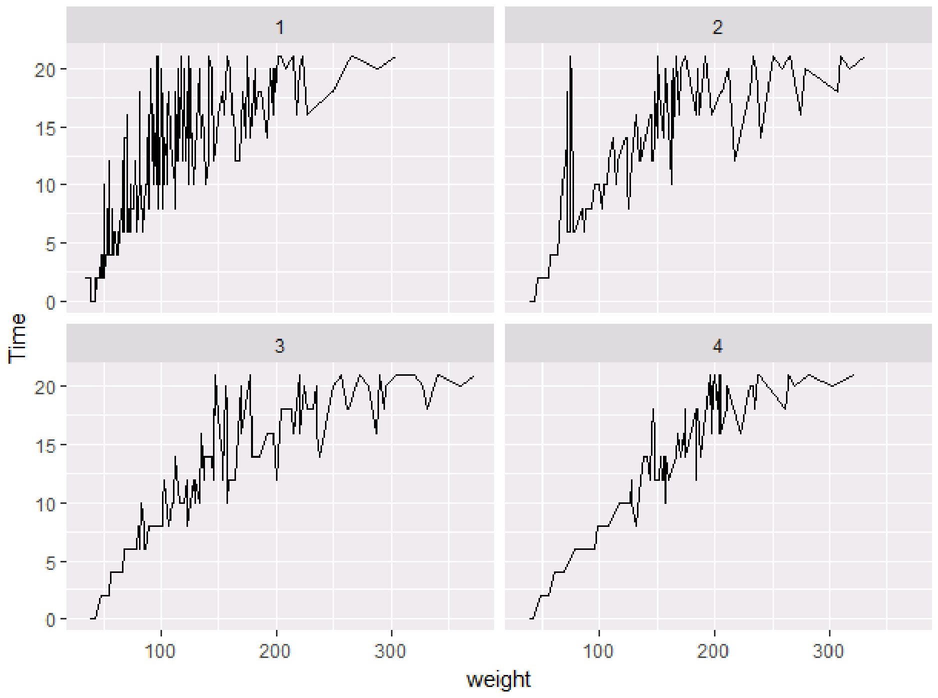


There are two problems here: there are too many lines to distinguish each one by colour, and the lines obscure one another.

Faceting to the rescue!

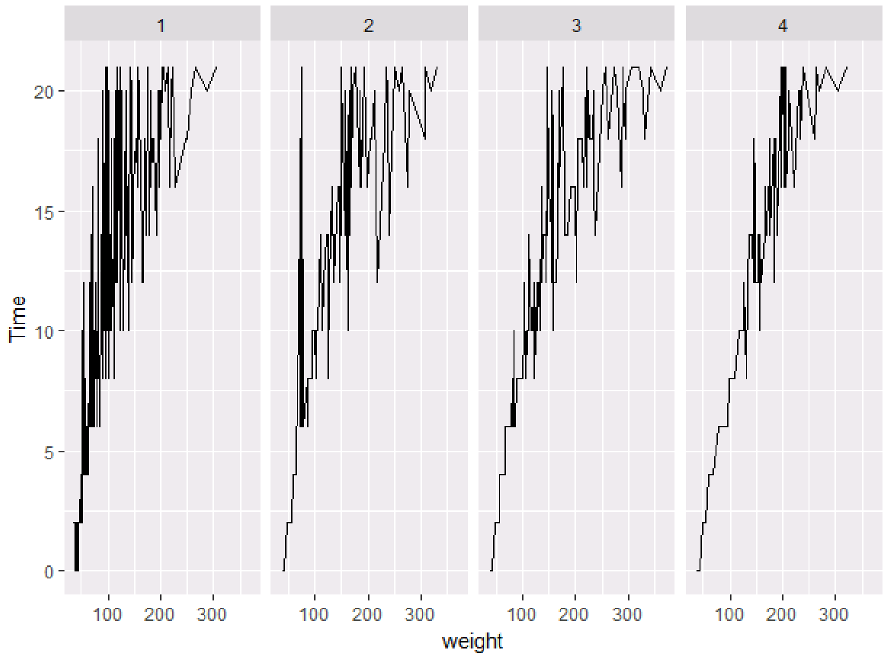
We can remedy the deficiencies of the previous plot by faceting by state rather than mapping Diet to colour.

```
p + geom_line()+facet_wrap(~Diet)
```



There is also a facet_grid() function for faceting in two dimensions.

```
p5 = p + geom_line() + facet_grid (~Diet)
```



4.7 Themes

The ggplot2 theme system handles non-data plot elements such as:

- Axis labels
- Plot background

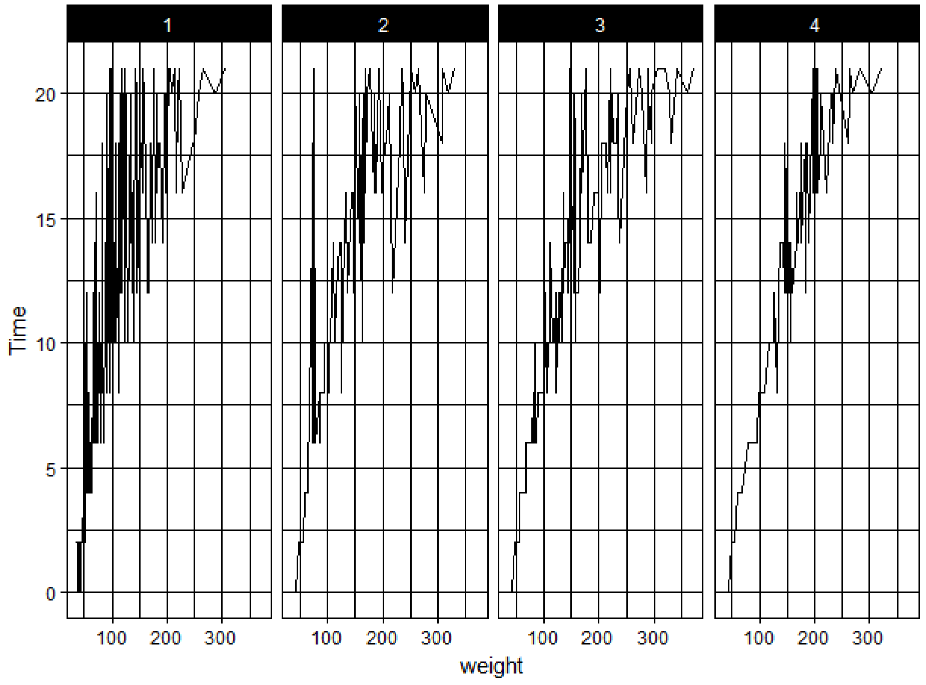
- Facet label backround
- Legend appearance

Built-in themes include:

- theme_gray() (default)
- theme_bw()
- theme_classc()

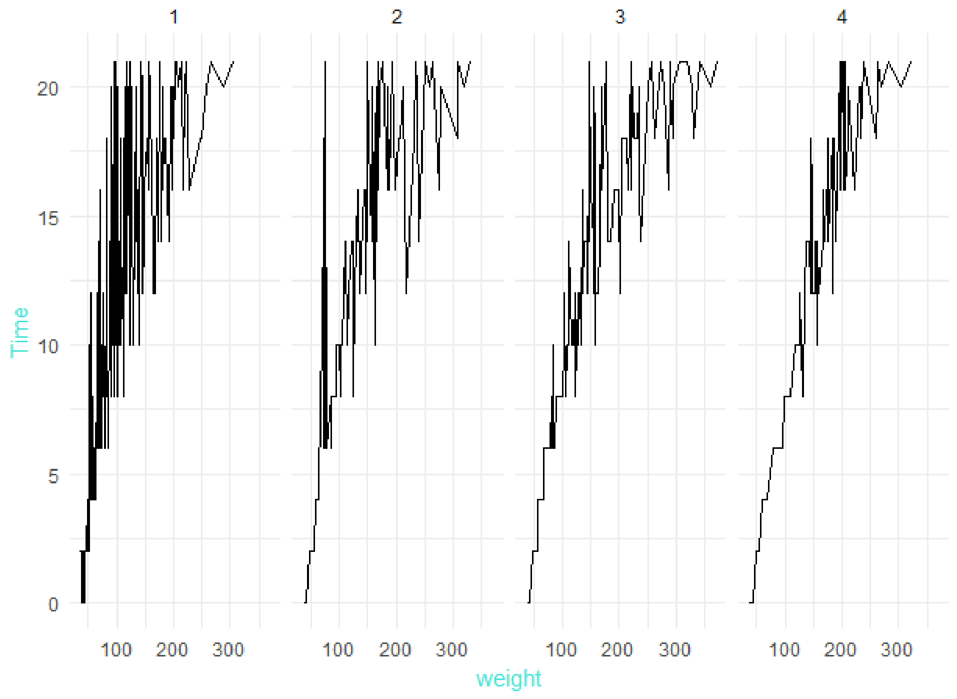
For example:

```
p5 + theme_linedraw()
```



Specific theme elements can be overridden using theme(). For example:

```
p5 + theme_minimal() + theme(text = element_text(color = "turquoise"))
```



All theme options are documented in ?theme. You can create new themes, as in the following example:

```
theme_new <- theme_bw() +
  theme(plot.background = element_rect(size = 1, color = "blue", fill
= "black"),
        text=element_text(size = 12, family = "Serif", color =
"ivory"),
        axis.text.y = element_text(colour = "purple"),
        axis.text.x = element_text(colour = "red"),
        panel.background = element_rect(fill = "pink"),
        strip.background = element_rect(fill = muted("orange")))

p5 + theme_new
```

Reading: For more information about *ggplot2*, read chapters 1 to 5 of *ggplot2: Elegant Graphics for Data Analysis*.