NERC DTP Visualisation Workshop

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Contents

Introduction

This workshop will introduce you to using the `ggplot2` package in R to quickly and easily produce visualisations of (complex) data sets. This is part of a wider suite of packages known as the `tidyverse`, which I can thoroughly recommend.

Recommended reading

The following books are probably the most relevant to this workshop:

- R for Data Science by Hadley Wickham and Garrett Grolemund (2016), available online at http://r4ds.had.co.nz/;
- ggplot2 by Hadley Wickham (2009), available online at https://ggplot2-book.org/.

Structure of this workshop

R can be tricky to learn, so please feel free to e-mail me with questions at t.mckinley@exeter.ac.uk, though please make sure that you have thought through your question in advance. Most R problems can be solved with judicious use of Google and StackOverFlow…

In this workshop, R commands to be entered into the console are shown in grey boxes e.g.

```
seq(0, 1, length = 11)
```

and the corresponding outputs look like:

```
##  [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
```

Tasks

Task 1

All **tasks** will be denoted in panel boxes like this one. In the HTML version, all solutions can be toggled by hitting the **Show Solution** buttons. In the PDF version solutions are given in the Appendix and are linked via the **Show Solution** buttons.

Show: Solution on P37

Chapter 1

Visualisation using `ggplot2`

Note

A PDF handout for the slides for this part of the module can be found here. A PDF version of the slides (not in handout form) and a HTML version (which should be compatible with screen-readers) can also be found via the links here and here.

All required data files can be downloaded from here.

1.1 Introduction to `tidyverse`

Now that you're comfortable with R, and specifically with the concept of **`data.frame`** objects, we can begin to really start unlocking the power of R for analysing complex data sets. The ability to work with and visualise data frames is one of the key reasons why R is so popular among statisticians and data scientists. Although a vast amount can be achieved using base R functionality, one of R's other key strengths is the vast array of packages that it supports, which add a rich variety of additional functionality to R.

A suite of packages that are fast becoming *de rigueur* for performing myriad data science tasks is known as the **`tidyverse`**. These packages provide powerful functions for doing visualisation and manipulation of complex data sets. In this workshop we will introduce key **`tidyverse`** packages, and show how they can be used to efficiently process and visualise complex data sets.

`tidyverse` packages

The **`tidyverse`** is a suite of packages, including e.g. **`tidyr`**, **`dplyr`**, **`ggplot2`**, **`purrr`**, **`tibble`** and **`readr`**. Although these packages can each be installed and loaded separately, they are designed to work together, and as such will simply install and load the **`tidyverse`** directly, rather than worry too much about which functions belong to which packages.

As usual, if you want to install **`tidyverse`**, use:

```
install.packages("tidyverse")
```

and once installed, it can be loaded using:

```
library(tidyverse)
```

in the usual way. Let's start with a motivating example.

1.2 Gapminder

Professor Hans Rosling has made a name for himself in the field of data visualisation with his groundbreaking Gapminder project.

For a slightly longer presentation, his TED talk on global development has been watched over 11 million times. If you have 20 minutes, it can be found here, and is well worth a watch!

Info

Professor Rosling sadly passed away on 7th February 2017, aged 68. I hope you will find some time to explore the Gapminder website, and appreciate the immense contribution that he made to the world of public health and education. He presented a world-view based on facts and data. To this end he provided innovative and fascinating ways to explore and understand data, disseminated these findings with pathos and humour, and used this information to challenge many of our pre-conceptions about public health and the developing world. An obituary from the Guardian can be found here.

The Gapminder website provides really informative interactive visualisations for many fascinating data sets. In this practical we will explore how to use R to try to recreate something similar to the types of visualisation that Gapminder provides, and see how high-end R packages—such as `ggplot2`—have been developed that provide a systematic and flexible way to generate complex plots / visualisations. Our aim for this workshop is to emulate the plot in Figure 1.1.

1.3 Introduction to `ggplot2`

R has very powerful and flexible plotting capabilities, that can be used to produce high-quality, bespoke visualisations. The downside is that the syntax can be verbose, so for complex plots it can be time consuming

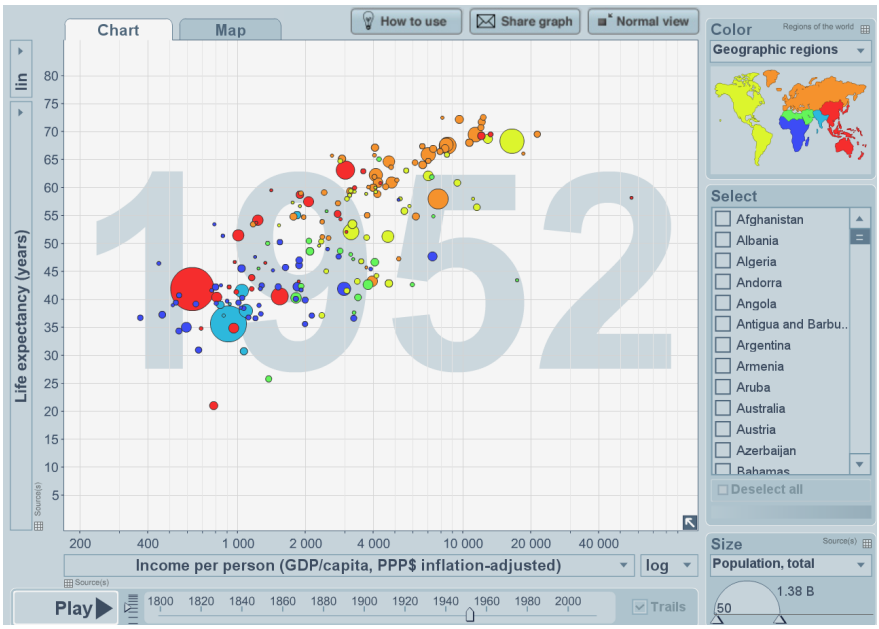


Figure 1.1: Life expectancy against GDP—screenshot from Gapminder project

to code up.

A general package that has been developed for visualisation of complex data sets is called `ggplot2`. This provides a wide variety of standard plot types and flexible customisation options, with a unifying syntax. In this part of the module, we will introduce `ggplot2` and illustrate its use on a range of real-world examples.

> **Note**
>
> We will not focus on using R's base graphics capabilities here, but will provide some comparison code for some of the examples (if you are interested) in order to show you how you can generate similar plots without `ggplot2`.

We will introduce some example code first, and then talk through it. First we load the `tidyverse` (of which `ggplot2` is included—you could just load `ggplot2` if you prefer).

```
library(tidyverse)
```

Let's begin by exploring the `iris` data set, which gives the measurements in centimeters of the variables sepal length and width, and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are *Iris setosa*, *versicolor*, and *virginica*. This data set is available as part of the base R package. Let's have a look at the data:

```
head(iris)
```

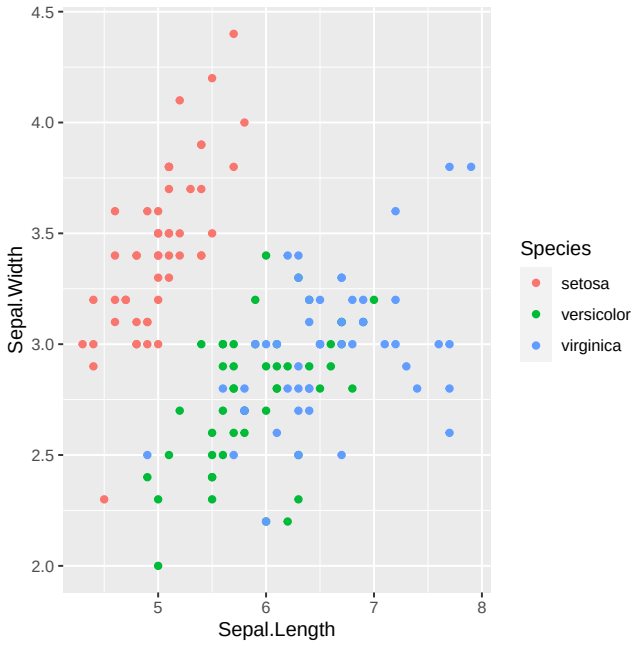
```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

You'll notice that the data is in **tidy** format. Specifically, a **tidy** data set is one in which:

- rows contain different **observations**;
- columns contain different **variables**;
- cells contain values.

We will discuss **tidy** data in more detail in a later section. For the time being, as a quick example, let's produce a plot of `Sepal.Width` against `Sepal.Length`, but with points coloured by `Species`:

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width, colour = Species))
```



Notice that we had to do little physical manipulation of the plot. We didn't have to choose how to position legends, or manually subset the data to plot the different points, or choose the colours; the package took care of all of these things.

Show: Analogous base R code on P47

Note

As usual, information can be found in the relevant help files, but a really useful resource for `ggplot2` is the Data Visualisation Cheat Sheet. Another fantastic resource, is the R Graphics Cookbook by Winston Chang, which has a free online version, or a physical book that you can buy.

So, how does it work? `ggplot2` is based on a book called the Grammar of Graphics by Leland Wilkinson—hence the name `gg-plot`! The ethos of `ggplot2` is that plots can be broken down into different **features**, most notably:

- **data**;
- **aesthetic mapping**;
- **geometric object**;

- **scales**;
- **faceting**;
- statistical transformations;
- coordinate system;
- position adjustments.

Perhaps the easiest way to explain some of these concepts is to work through our examples step-by-step. We will focus on the main components marked in **bold** above. Let's start with the scatterplot example first, and examine the first part of the code:

```
ggplot(iris)
```


This sets up the plot. The first argument to the `ggplot` function is the **data**, which here is the `iris` data set.

Important

Whereas base R graphics can plot various object types, `ggplot()` **requires** `data.frame` (or `tibble`[a]) objects. It is designed for plotting statistical data sets. Never fear, most R objects can be manipulated into `data.frames` for plotting if required. (See next session on **data wrangling** for more on this.)

[a] We will see `tibble` objects later on—just think of them as special `data.frames`.

Notice that only an **empty plot** has been drawn so far, there are no points present. This is because we haven't told `ggplot2` what type of plot we want. We do this by specifying a **geom**.

1.3.1 Geoms

A **geom** defines the type of plot we want. In this case we want a **scatterplot**, which can be defined by the `geom_point()` function. Geoms can be layered, allowing us to built up complex plots sequentially. Common geoms are:

- `geom_point()`

- `geom_line()`
- `geom_histogram()`
- `geom_density()`
- `geom_bar()`
- `geom_violin()`

Please see the Data Visualisation Cheat Sheet for more examples.

1.3.2 Aesthetics

The `aes(x = Sepal.Length, y = Sepal.Width, colour = Species)` part sets the **aesthetics**, which here are added as an argument to the `geom_point()` function. These define how the *data* are **mapped** onto the *visual aesthetics* of the plot. Here we are setting the `x` coordinates to be `Sepal.Length`, the `y` coordinates to be `Sepal.Width`, and the `colour` of the characters to be related to `Species`. In general, **aesthetics** include:

- position;
- colour (border or line colour);
- fill (inside colour);
- shape;
- linetype;
- size.

Note

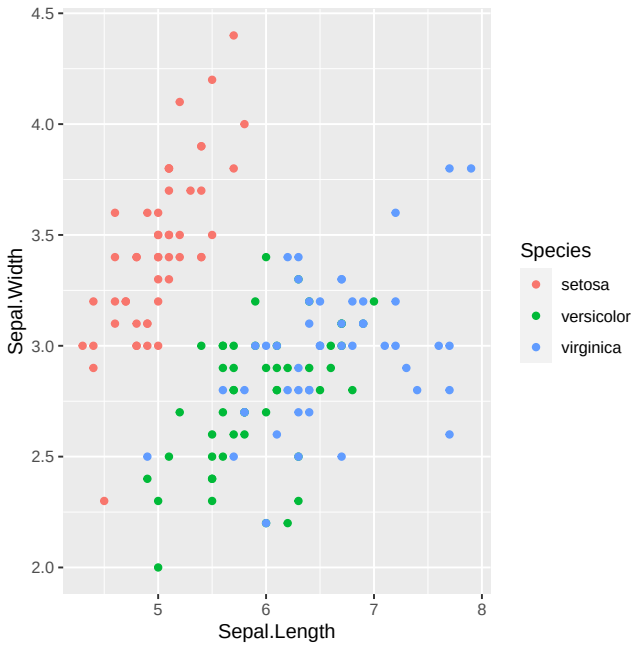
Notice that we did not have to use the `$` operator to extract columns. This makes `ggplot2` code a lot clearer. R knows to look for the `Sepal.Length` and `Sepal.Width` columns in the `iris` data, because we have told `ggplot()` which data set to operate on.

1.3.3 Building up plots

Note that `ggplot2` **builds** plots up by *adding* together components. There are lots of ways to do this. Here I have set up "global" options for the plot using the `ggplot()` function. I then **add** (`+`) to this the type of plot I want i.e. `+ geom_point(aes(x = Sepal.Length, y = Sepal.Width, colour = Species))` (in this case including the aesthetics in the `geom_*` call). The addition sign is important. If I want to split the function over multiple lines, make sure the `+` sign is at the **end** of each line, so R knows that the plot is not complete at the point.

Putting all this together we have:

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width, colour = Species))
```



Nice! With one tiny function we have added colours *and* legends. All neatly formatted to work together in one plot!

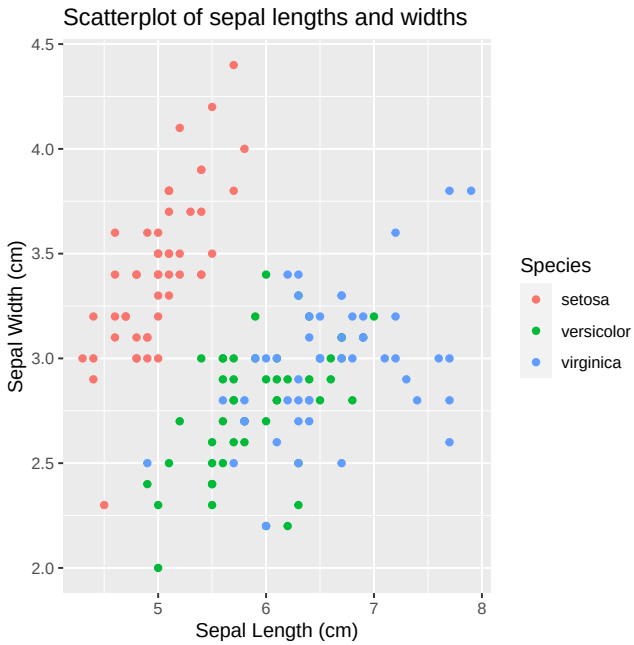
Important

Each type of `geom` accepts only a subset of all aesthetics. Information on these can be found in the help files for each `geom_*` type, or see also the Data Visualisation Cheat Sheet. Most of these are fairly obvious. For example, a scatterplot requires both `x` and `y` aesthetics as a minimum. A kernel density geom e.g. `geom_density()`, requires only an `x` aesthetic (we will come back to this shortly). Some aesthetics do not make sense for certain types of geom; for example, it makes sense that a `shape` aesthetic can be added to `geom_point()` but not to `geom_line()`. Conversely, adding a `linetype` aesthetic to `geom_line()` makes sense, but not to `geom_point()`.

1.3.4 Labels and titles

Labels and titles can be added fairly easily, using the `xlab()`, `ylab()` and `ggtitle()` functions, e.g.

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width, colour = Species)) +
    xlab("Sepal Length (cm)") + ylab("Sepal Width (cm)") +
    ggtitle("Scatterplot of sepal lengths and widths")
```



Task 2

Assume that we want to visualise the distribution of `Sepal.Length` values for each species, together on one plot. One way that we can do this is to use a kernel density plot (or alternatively a histogram) of the data. Produce a plot containing three density plots for `Sepal.Length`, stratified by `Species`. **Hint**: use the `geom_density()` geom, which requires an `x` aesthetic only, and set the `colour` aesthetic as before.

Show: Solution on P37

Show: Analogous base R code on P48

Task 3

Produce the same density plot, but replace the `colour` aesthetic with a `fill` aesthetic. What happens?

Show: Solution on P37

Task 4

Now add an `alpha` channel to this plot. An `alpha` channel controls the degree of opacity for the colours, where `alpha = 0` corresponds to complete transparency, and `alpha = 1` to complete opacity. Note that we **do not** want to map the `alpha` channel to an aesthetic here, rather we want all fill colours to be, say 50% transparent. We can therefore add an `alpha = 0.5` argument to the `geom_density()` function. What happens?

Show: Solution on P38

Task 5

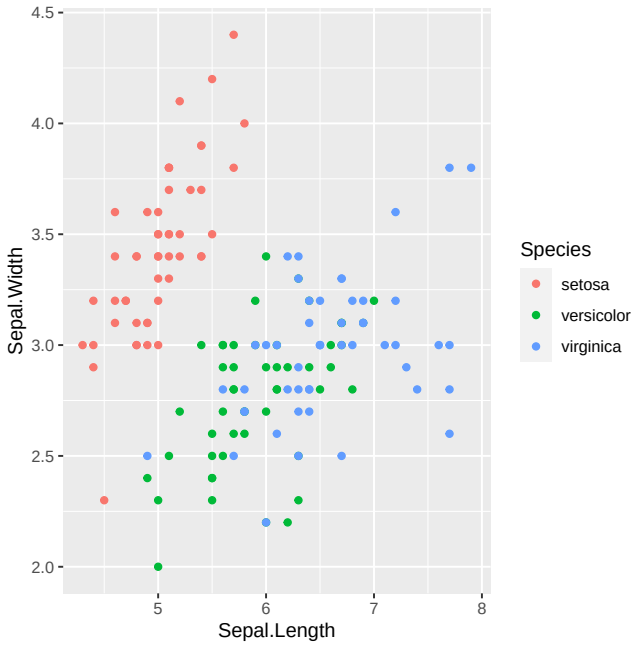
Tidy up the labels and add a plot title to produce a final plot.

Show: Solution on P39

1.3.5 Aside: aesthetics vs. generic options

As a quick aside, notice that when we set the `alpha` channel above, we did not set it as an aesthetic, rather we set it as a generic option which was applied to all components of the plot. Perhaps the easiest way to visualise this difference, is to consider different `colour` options. Take a look at these next pieces of code and try to understand the differences between them.

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width, colour = Species))
```



```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width), colour = "red")
```

Task 6

What happens if you try to run the following code?

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width), colour = Species)
```

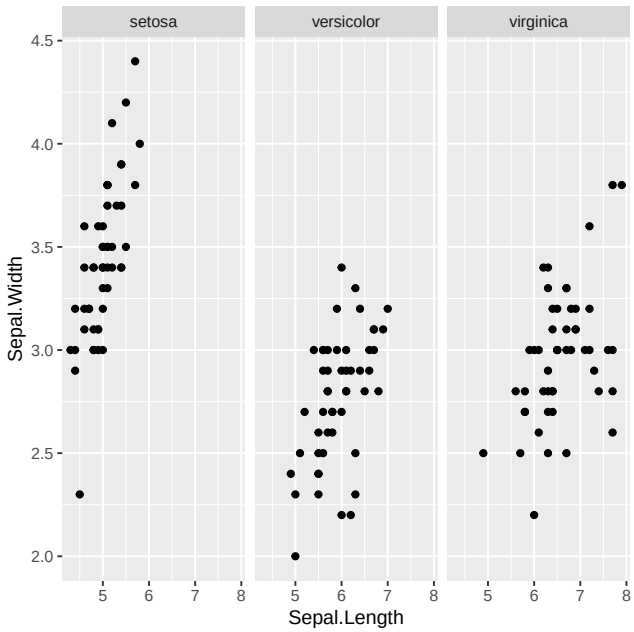
Why does this happen?

Show: Solution on P39

1.3.6 Faceting

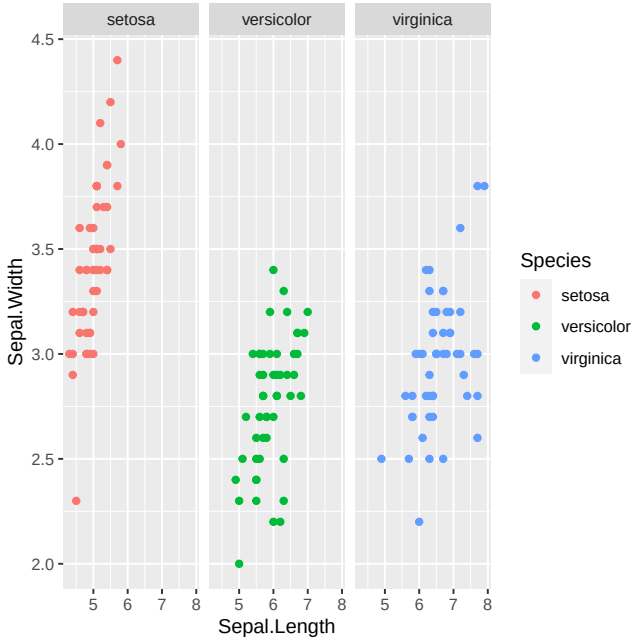
Another really useful feature of `ggplot` is the ability to use faceting to display sub-plots according to some grouping variable. For example, let's assume that we want to produce separate plots of sepal length vs. width for each of the three species of iris. We can do this using faceting:

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width)) +
    facet_wrap(~ Species)
```



Neat eh? Note that we can also use different aesthetics within the facets. For example, we could also add a `colour` aesthetic e.g.

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width, colour = Species)) +
    facet_wrap(~ Species)
```



This doesn't add anything more to the plot here since the colours are redundant. Later we will see a better example of this.

Note

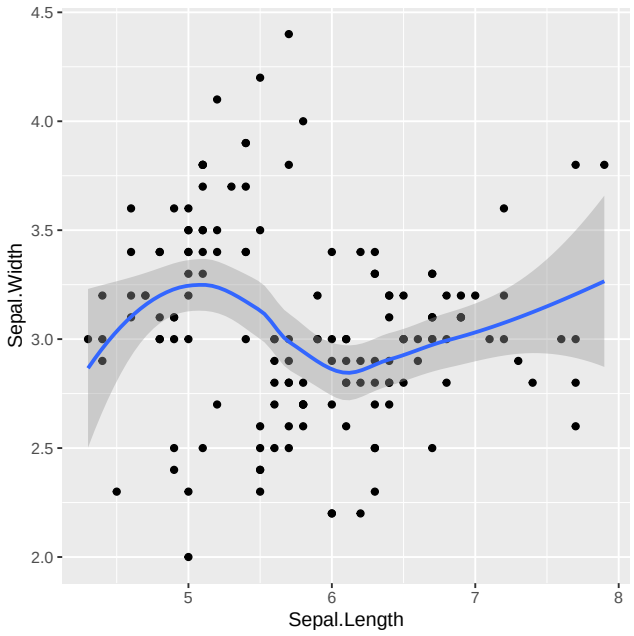
There is also a `facet_grid()` option that allows us to facet by more than one variable. Please see the Data Visualisation Cheat Sheet for more details.

1.3.7 Statistical transformations

Another feature of `ggplot2` is that we can layer transformations over the top of our raw data. For example, there is a `stat_smooth()` function that allows us to overlay a smoothed non-parametric line to a scatterplot. For example:

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width)) +
    stat_smooth(aes(x = Sepal.Length, y = Sepal.Width))
```

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

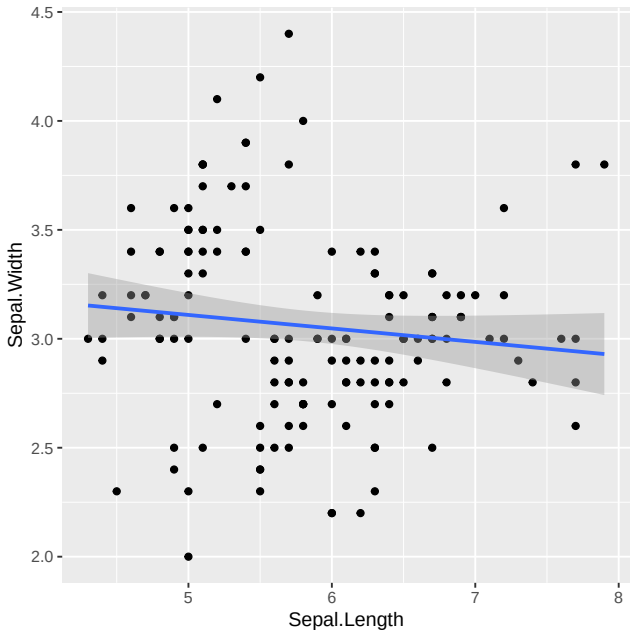


Notice that this has added a `loess` smoothed line to the plot[1]. We could instead add a linear line if we prefer, by setting a `method` argument to `stat_smooth` e.g.

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width)) +
    stat_smooth(aes(x = Sepal.Length, y = Sepal.Width), method = "lm")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

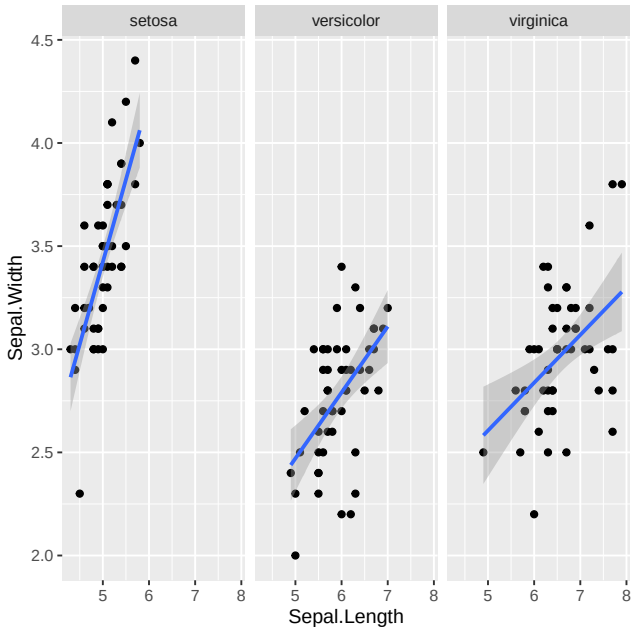
[1] just think of this as a smoothed line-of-best-fit through the data for the time being



With the addition of a single function we can now add different lines for each species:

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width)) +
    stat_smooth(aes(x = Sepal.Length, y = Sepal.Width), method = "lm") +
    facet_wrap(~ Species)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Aside

This is a neat example of Simpson's Paradox, which an apparent trend in the data disappears or reverses when the trend is explored in subsets of the data. (In this case the linear model suggested a negative correlation between sepal length and width when the species information was ignored, but a positive correlation within each species.)

1.3.8 Aside: "global" vs. "local" options

Notice that in the code below the `geom_point()` and `stat_smooth()` functions use the same aesthetics. In this case it is possible to add "global" aesthetics to a plot through the `ggplot2()` function, which can then be accessed by sub-functions. Hence the following two pieces of code are equivalent here.

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width)) +
    stat_smooth(aes(x = Sepal.Length, y = Sepal.Width), method = "lm") +
    facet_wrap(~ Species)
```

```
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width)) +
    geom_point() +
    stat_smooth(method = "lm") +
    facet_wrap(~ Species)
```

Mixtures of "global" and "local" aesthetics can be used where necessary, which is particularly useful when layering information from different data sets onto the same plot.

1.3.9 Scales

Scales control the details of how data values are translated to visual properties. These allow us to control translations from data to aesthetics. We will see some simple examples of these in due course.

Note

Some really useful colour palettes for categorical data in particular were designed by Cynthia Brewer and can be found through the colorbrewer website: https://colorbrewer2.org/. These provide a range of sequential, diverging and qualitative colour palettes, that can also be chosen to be colour-blind, print or photocopy friendly. `ggplot2` offers a `scales_*_brewer()` function that enables you to use these palettes for your own plots. More information can be found here.

A set of colour palettes with similar properties that make them colour-blind and print friendly, but have better support for continuous colour scales are the viridis palettes. Information can be found here. The `viridis` package contains `ggplot2` bindings for these palettes, and more information on these can be found here.

1.4 A more complex example: Gapminder

Let's take these ideas and return to our Gapminder data. Datasets from the Gapminder project can be downloaded from https://www.gapminder.org/data. However, the particular data set required to replicate

Figure 1.1 is available in a package in R called (naturally) `gapminder`. If not already installed, then this can be installed in the usual way.

Firstly, load the package:

```
library(gapminder)
```

Have a quick look at the data, which are available as an object called `gapminder`:

```
gapminder
```

```
## # A tibble: 1,704 x 6
##    country     continent  year lifeExp      pop gdpPercap
##    <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
##  1 Afghanistan Asia       1952    28.8  8425333      779.
##  2 Afghanistan Asia       1957    30.3  9240934      821.
##  3 Afghanistan Asia       1962    32.0 10267083      853.
##  4 Afghanistan Asia       1967    34.0 11537966      836.
##  5 Afghanistan Asia       1972    36.1 13079460      740.
##  6 Afghanistan Asia       1977    38.4 14880372      786.
##  7 Afghanistan Asia       1982    39.9 12881816      978.
##  8 Afghanistan Asia       1987    40.8 13867957      852.
##  9 Afghanistan Asia       1992    41.7 16317921      649.
## 10 Afghanistan Asia       1997    41.8 22227415      635.
## # i 1,694 more rows
```

Here we can see that the data set consists of 1704 rows and 6 columns, and contains information on country, continent, life expectancy, population size, GDP (per capita) and year.

Note

Any R aficionados amongst you might notice the slightly strange `print` behaviour of the `gapminder` object. If we try to `print` a `data.frame` object to the screen, then it usually prints the whole object. Here it's printed an attenuated version of the object. This is because the `gapminder` data set is saved as a `tibble` object, rather than a standard `data.frame`.

`tibble` objects are simply enhanced data frames, which are generally easier to examine. For example, they force R to display only the data that fits onscreen. They also add some information about the class of each column. In fact, the `tibble` package—loaded as part of the `tidyverse`—introduces the `as_tibble()` function to convert ordinary `data.frame` objects to `tibble` objects, in case you want to use this functionality in future. Please see the Data Import Cheat Sheet for more information.

Note also that `tibble` objects seem to make a distinction between integers (`<int>`) and doubles (`<dbl>`), instead of just using `numeric`. R makes no such distinction in practice, and so you can think of either of these as simply `numeric` types.

We'll use `tibbles` more generally in the later data wrangling session.

Let's just clarify the data:

- **`country`**: country of interest (`factor`);
- **`continent`**: continent country can be found in (`factor`);
- **`year`**: year corresponding to data (in increments of 5 years) (`numeric`);
- **`lifeExp`**: life expectancy at birth (in years) (`numeric`);
- **`pop`**: population size (`numeric`);
- **`gdpPercap`**: GDP per capita, in dollars, by Purchasing Power Parities and adjusted for inflation (`numeric`).

1.4.1 GDP against life expectancy

Let's think about Figure 1.1 and try to map the various aesthetics in the plot to our data set. We have:

Table 1.1: Aesthetics for gapminder plot

Aesthetic	Variable
x	gdpPercap
y	lifeExp
colour	continent
size	pop

Task 7

Using `ggplot2`, produce a scatterplot that uses the aesthetics in Table 1.1 for just the year 1952.

Show: Solution on P40

Notice how rich this plot is already. One thing to note is that in Figure 1.1 the x-axis is plotted on the $\log_{10}$ scale. There are two ways in which we can handle this: either by transforming the `gdpPercap` variable directly, or by using an appropriate `scales_*` function. Here we want to apply a $\log_{10}$ transformation to the `x` aesthetic.

Task 8

1. Redo the previous plot but with the aesthetic `x = log10(gdpPercap)`.
2. Redo the previous plot with the aesthetic `x = gdpPercap` but with an additional `scale_x_log10()` layer.

How do these plots differ?

Show: Solution on P40

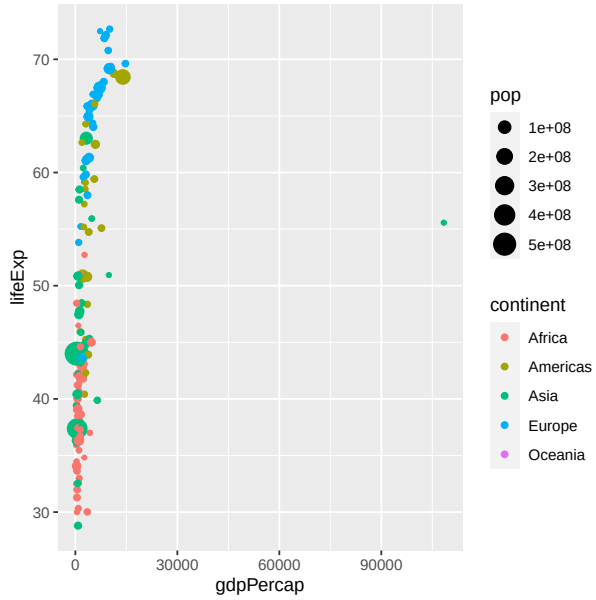
Important

`ggplot2` also allows you to save the plot as an object, which can be updated at a later date or used within other functions. For example,

```
p <- ggplot(gapminder[gapminder$year == 1952, ],
       aes(x = gdpPercap, y = lifeExp, size = pop, colour = continent)) +
   geom_point()
```

creates an object called `p` that contains the plot information. This will not be plotted until the object is **printed** to the screen e.g.

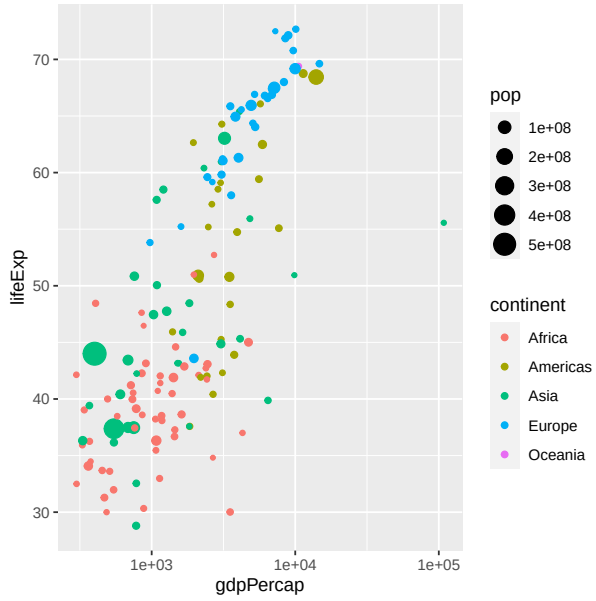
```
p
```



Note: If using `ggplot` inside functions you may have to explicitly use the `print()` function (e.g. `print(p)`).

This can be useful if we want to add things to an existing plot at a later stage without having to rewrite the entire plot. For example, to set the scales on plot `p` we can do:

```
p <- p + scale_x_log10()
p
```

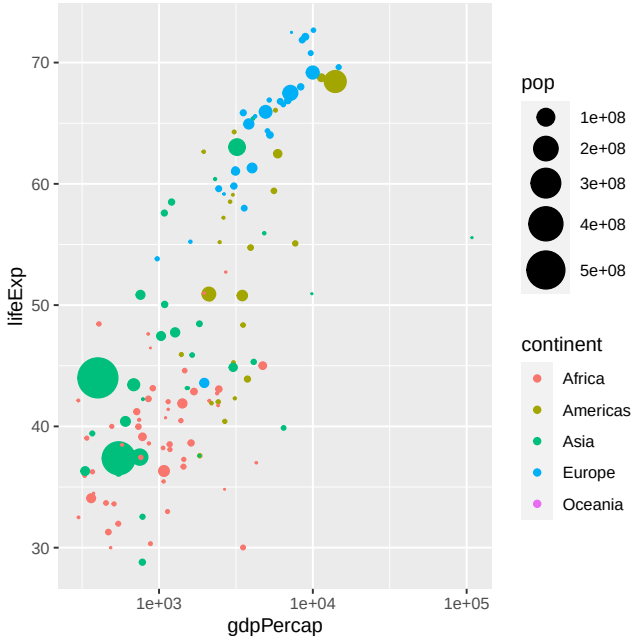


`ggplot2` has lots of built in transformations e.g. `"log"`, `"exp"`, `"sqrt"`, `"log10"` and so on. Or you can define your own. Notice that we have not transformed the data, we have merely told `ggplot()` on what scale to plot it. This sorts out the axis tick labelling automatically.

We can also scale other aesthetics. For example, although the relative areas of the points are scaled nicely,

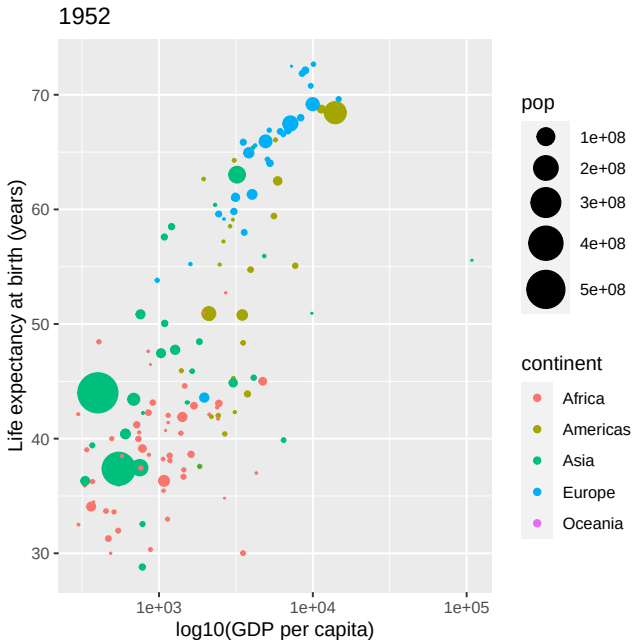
we probably want the largest points to be slightly larger. Hence we can scale the area of the maximum point by using the `scale_size_area()` function:

```
p <- p + scale_size_area(max_size = 10)
p
```



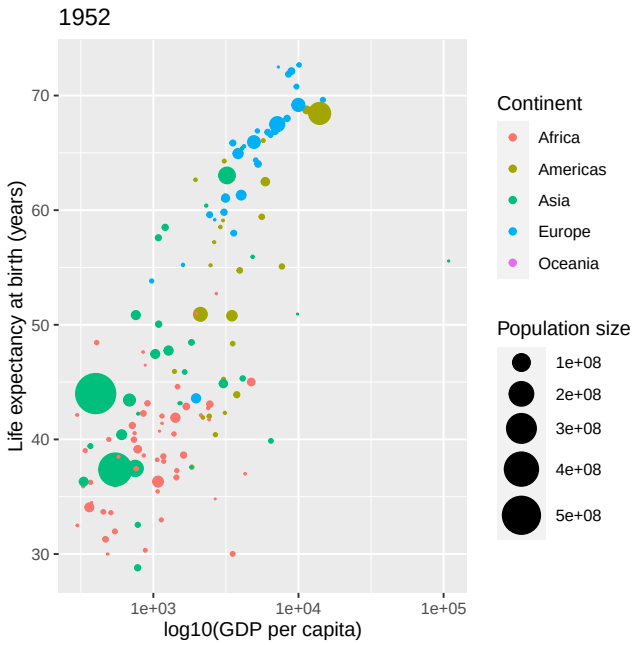
Again, labels and titles can be added fairly easily, using the `xlab()`, `ylab()` and `ggtitle()` functions:

```
p <- p + xlab("log10(GDP per capita)") +
    ylab("Life expectancy at birth (years)") +
    ggtitle("1952")
p
```



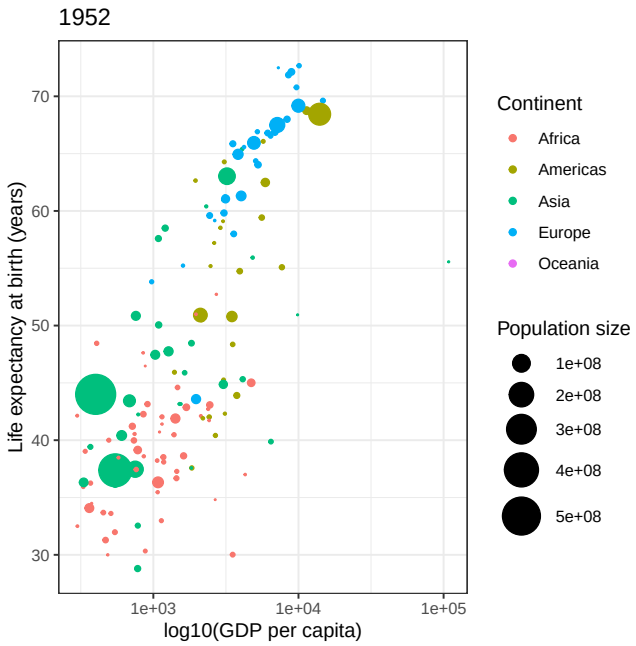
Changing the legend titles can also be done using the `labs()` option. Notice that the legends map to the aesthetics, so there is a `colour` legend that maps to the colour aesthetic, and a `size` legend that maps to the size aesthetic.)

```
p <- p + labs(colour = "Continent", size = "Population size")
p
```



Not bad. Finally notice that by default `ggplot2` uses a light-grey background. This seems to prove somewhat divisive. There is a solid theory behind choosing this as the default, since it provides clarity without having too much contrast. However, some people don't like it, and so there are options to turn this off (using `theme()`). In this case we can simply turn this off using `theme_bw()` (a black-and-white theme).

```
p <- p + theme_bw()
p
```



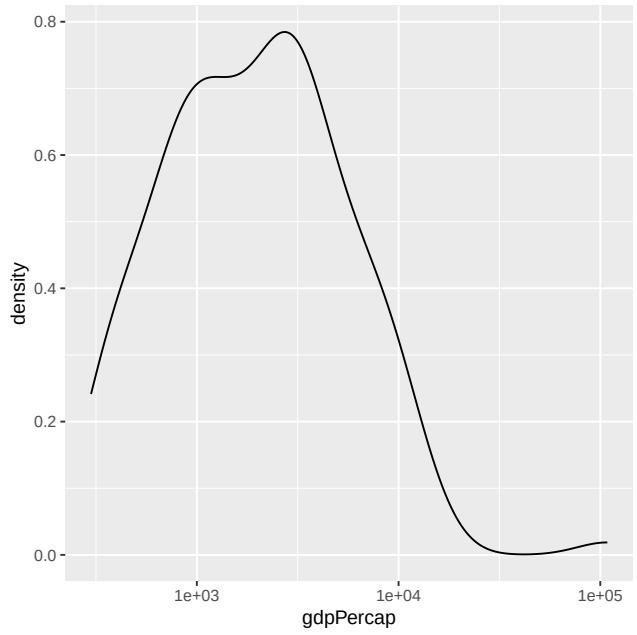
There are many, many possible options with `ggplot2`. Far too many to cover here. We can only really get a flavour of what can be achieved. I have often found Google to be invaluable for learning `ggplot2`.

Let's have a look at a couple of other examples.

1.4.2 GDP per continent

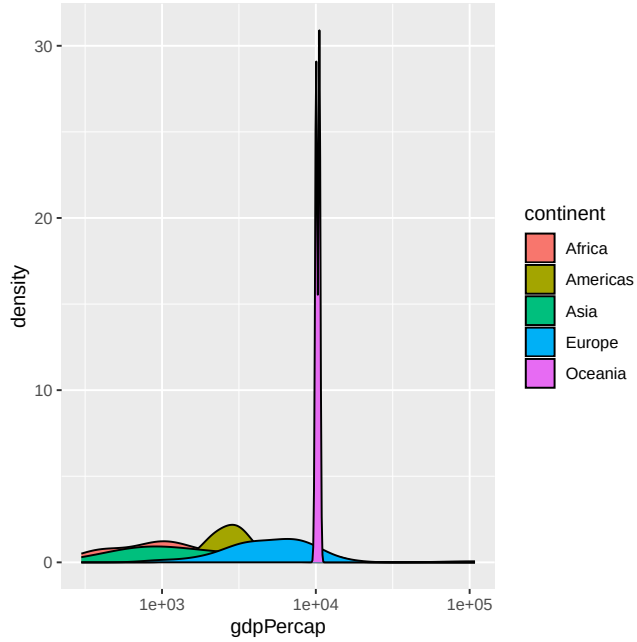
Another chart that Professor Rosling used in an associated TED talk was a stacked density plot. This is a smoothed version of a **histogram**. Let's start by looking at the distribution of GPD values across all countries in 1952. This can be done with the `geom_density()` geom as in the earlier example, which requires only an `x` aesthetic—see `?geom_density`—since it calculates the density on the y-axis automatically from the data once we have chosen an appropriate bandwidth.

```
ggplot(gapminder[gapminder$year == 1952, ],
       aes(x = gdpPercap)) +
    geom_density() +
    scale_x_log10()
```



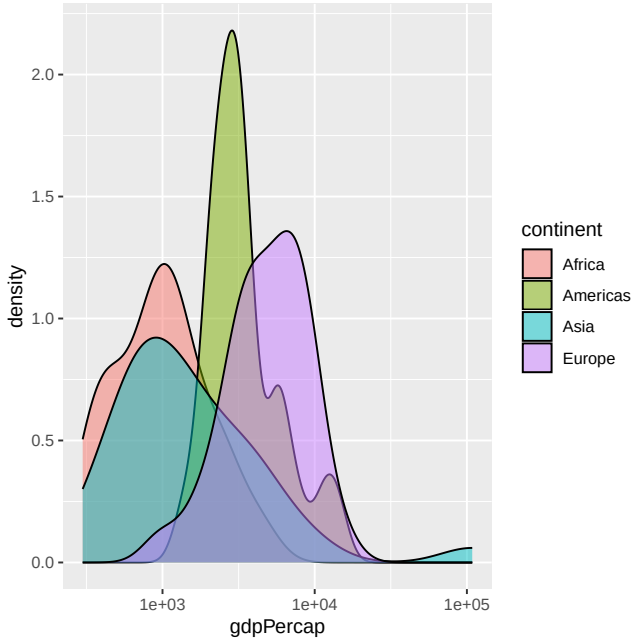
This simple plot is producing a density plot of the distribution of GDP across **all countries** in 1952. How do split this by continent? Well, there are various ways. One way would be to set the `fill` aesthetic to map to the `continent` variable:

```
ggplot(gapminder[gapminder$year == 1952, ],
       aes(x = gdpPercap, fill = continent)) +
    geom_density() +
    scale_x_log10()
```



This produces an **overlapped** density plot by default. (The patterns are quite difficult to see here, due to the `Oceania` data, so for the purposes of exposition only we're going to remove `Oceania` from the subsequent plots.)

```
## remove Oceania (for exposition purposes only)
gapminderNoOc <- gapminder[gapminder$continent != "Oceania", ]

## produce overlapped density plot
ggplot(gapminderNoOc[gapminderNoOc$year == 1952, ],
       aes(x = gdpPercap, fill = continent)) +
    geom_density(alpha = 0.5) +
    scale_x_log10()
```



This is an informative plot. We can see that African countries tend to have lower GDP per capita than the Americas for example; with Asia and Africa the poorest continents in the 1950s in terms of GDP.

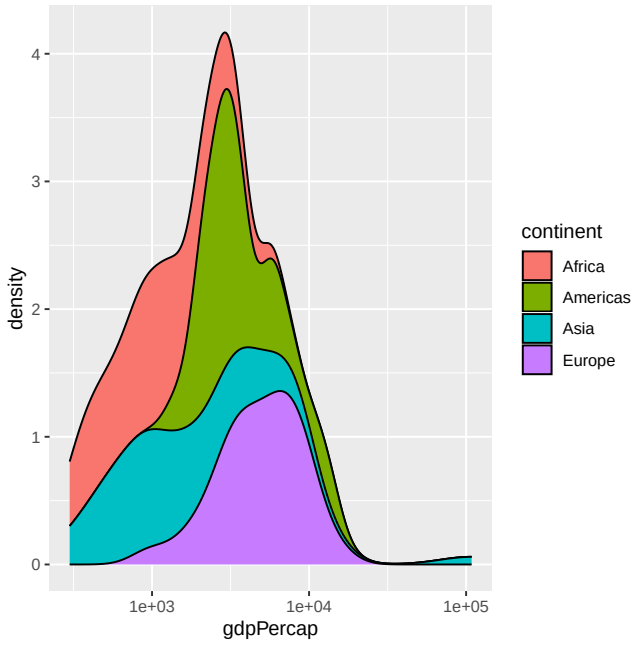
Question 9

What does the `Oceania` density plot tell us about the range of GDPs in the Oceania continent?

1.4.2.1 Positions

Professor Rosling uses a **stacked** density plot, rather than overlapping density plots. We can use a `position = "stack"` argument to the geom to force the stacking.

```
## produce stacked density plot
ggplot(gapminderNoOc[gapminderNoOc$year == 1952, ],
       aes(x = gdpPercap, fill = continent)) +
    geom_density(position = "stack") +
    scale_x_log10()
```



Histograms and barplots have equivalent `position = "dodge"` and `position = "stack"` commands. By default histograms use the latter. The former is not very useful for histograms, but very useful for barplots with multiple discrete groupings.

Task 10

Try tidying up the axis and legend titles on these plots.

Show: Solution on P42

Task 11

Write a function in R that takes a `data` and a `year` argument and plots a stacked density plot for a given year. Use this to plot the data for 1952, 1982, 1992 and 2002. (Remember that if you want to plot a `ggplot2` figure from inside a function, you will have to call `print()` explicitly.)

Show: Solution on P42

Task 12

Produce a density plot of `log10(gdpPercap)` faceted by `continent`, for the year 1952.

Show: Solution on P44

Task 13

Now generate a series of stacked density plots, with colours corresponding to different continents, but faceted by different years, to see how the relative distributions change over time.

Show: Solution on P45

1.5 Saving plots

To save plots you can use the `ggsave()` function. This allows you to write out your file to a range of formats, and specify size, resolution etc. as required e.g.

```
## produce lovely plot
p <- ggplot(gapminderNoOc,
       aes(x = gdpPercap, fill = continent)) +
    geom_density(position = "stack") +
    scale_x_log10() +
    facet_wrap(~year)

## save plot as PDF
ggsave("myplot.pdf", p)
```

Take a look at the help file `?ggsave` for more details.

1.6 Additional task

Let's look at some data from an experiment exploring the effect of sexual activity on lifespan of male fruitflies, described in Partridge and Farquhar (1981).

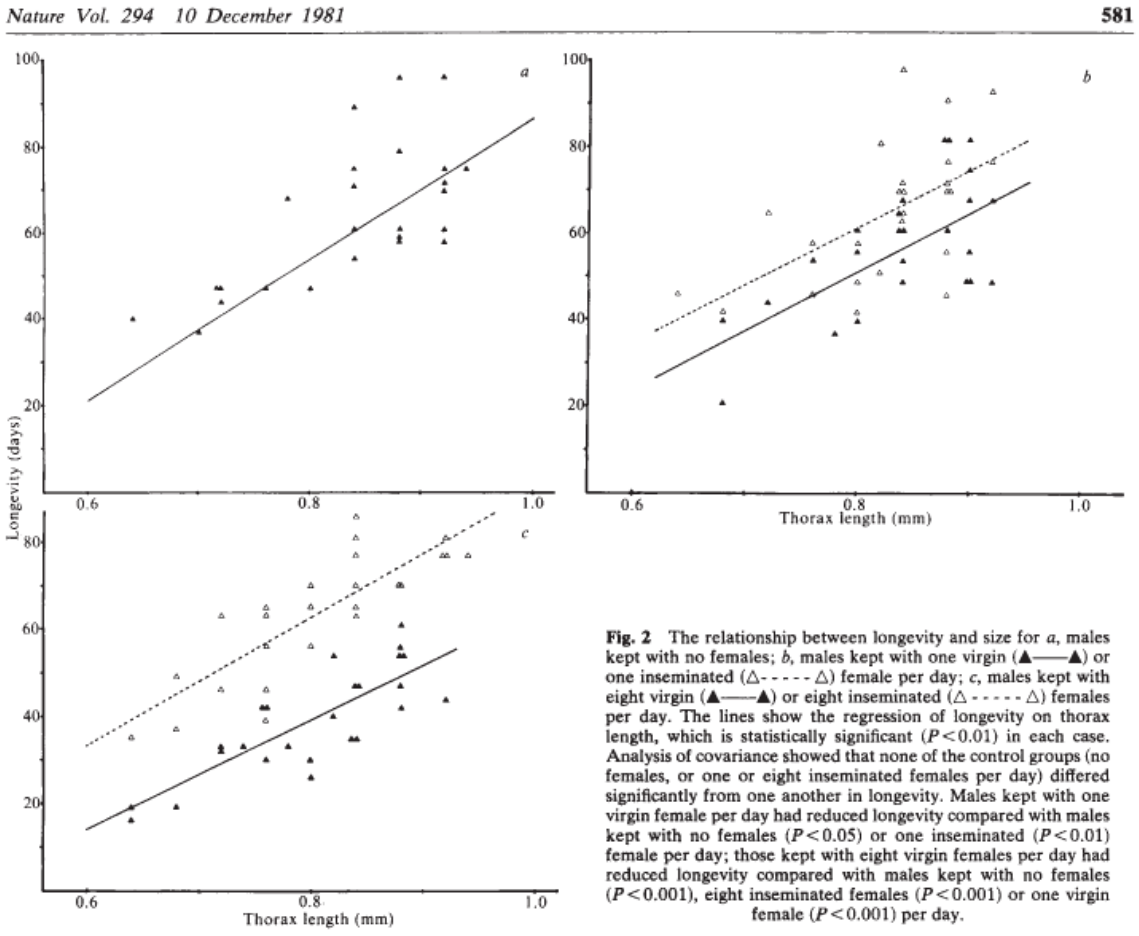
> *A cost of increased reproduction in terms of reduced longevity has been shown for female fruitflies, but not for males. We have data from an experiment that used a factorial design to assess whether increased sexual activity affected the lifespan of male fruitflies.*
>
> *The flies used were an outbred stock. Sexual activity was manipulated by supplying individual males with one or eight receptive virgin females per day. The longevity of these males was compared with that of two control types. The first control consisted of two sets of individual males kept with one or eight newly inseminated females. Newly inseminated females will not usually re-mate for at least two days, and thus served as a control for any effect of competition with the male for food or space. The second control was a set of individual males kept with no females. There were 25 males in each of the five groups, which were treated identically in number of anaesthetisations (using CO_2) and provision of fresh food medium.*
>
> The data should have the following columns:
>
> - **id**: a ID for each fly in each group (1–25).
> - **partners**: number of companions (0, 1 or 8).
> - **type**: type of companion (inseminated female; virgin female; not applicable (when 'partners = 0')).
> - **longevity**: lifespan, in days.
> - **thorax**: length of thorax, in mm.
>
> Source: Partridge and Farquhar (1981)

Task 14

The file `ff.rds` contains the data from this experiment. Download this data set to your working directory, read it into R using the command:

```
ff <- readRDS("ff.rds")
```

and use `ggplot2` to reproduce something similar to the plot below:



Show: Solution on P46

1.7 Additional functionality: going beyond static plots

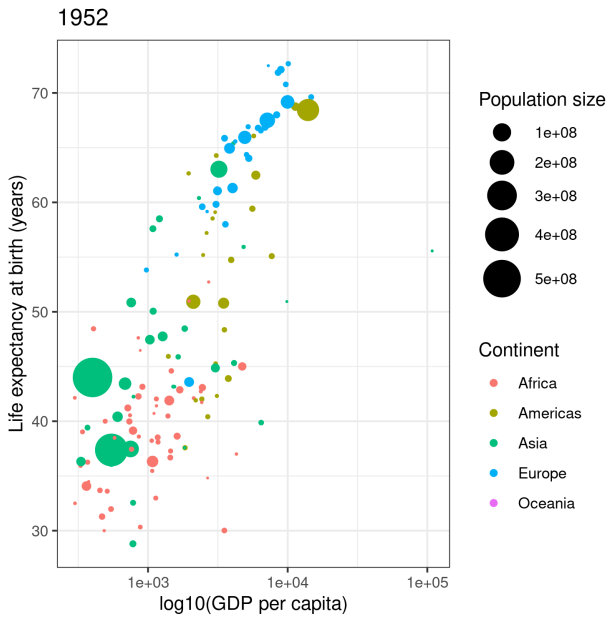
There has been a whole ecosystem of packages that have evolved from the core `tidyverse`. One such package is `gganimate`, which, as the name suggests, allows one to turn `ggplot2` plots into animations.

The website for the package can be found here. We will not give a full demonstration here, but instead show how we can produce an animation similar to that of Professor Rosling's, with the addition of two more lines of code.

> **Note**
>
> You will have to view these plots on the HTML notes to interact with them since PDF documents will only include static plots.

Firstly, you will need to install `gganimate`, and you might also have to install the `gifski` and `av` packages in order to write out the animation into a `.gif` or other video file. Then:

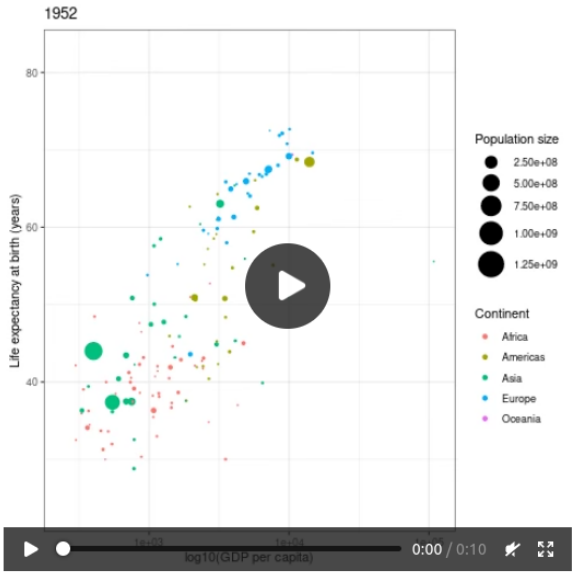
```
## load library
library(gganimate)

## produce plot (ignoring year)
p <- ggplot(gapminder,
    aes(x = gdpPercap, y = lifeExp, size = pop, colour = continent)) +
    geom_point() +
    scale_x_log10() +
    scale_size_area(max_size = 10) +
    xlab("log10(GDP per capita)") +
    ylab("Life expectancy at birth (years)") +
    labs(colour = "Continent", size = "Population size") +
    theme_bw()

## turn into animation, using year to guide transitions
p <- p + transition_time(year) +
    ggtitle("{frame_time}")
p
```



Neat eh? To save animations, once can use the `anim_save()`, similarly to the `ggsave()` function we saw earlier.

```
## save as gif (renders to gif by default)
anim_save("gapminder.gif", p)
```

```
## save to mp4 (needs new renderer argument)
anim_save("gapminder.mp4", animate(p, renderer = av_renderer()))
```

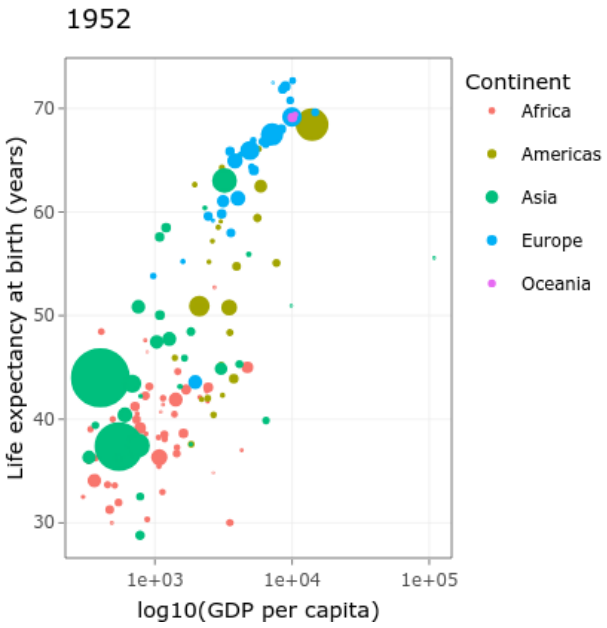


Take a look at the `gganimate` website for more examples and ideas.

Another useful package is `plotly`, which allows you to generate interactive plots from data (if you are viewing the HTML note, then try interacting with the plot below). There is even a useful `ggplotly()` function to automatically turn `ggplot2` figures into `plotly` figures.

```
## load library
library(plotly)

## produce plot from 1952
p <- ggplot(filter(gapminder, year == 1952),
    aes(x = gdpPercap, y = lifeExp, size = pop, colour = continent)) +
    geom_point() +
    scale_x_log10() +
    scale_size_area(max_size = 10) +
    xlab("log10(GDP per capita)") +
    ylab("Life expectancy at birth (years)") +
    guides(size = "none") +
    labs(colour = "Continent") +
    ggtitle("1952") +
    theme_bw()
```

```
ggplotly(p, width = 420, height = 420)
```



Note

`plotly` is much more flexible than just converting `ggplot2` figures, and is not restricted to R (you can also use it as a standalone package, or through e.g. Python, Julia or MatLab as well)—see https://plotly.com/graphing-libraries/ for more details. It is also being actively developed, which is why it still has a few teething problems, such as an inability to handle multiple legends currently, which is why I had to turn the `size` legend off using the function `guides(size = "none")` in the above code. Hopefully future updates will fix this, but it gives you an idea about what's possible.

Another awesome package is `shiny`, which enables you to create **interactive webpages** directly from R. We will not cover `shiny` in this module, but please take a look at the gallery for lots of ideas and examples in case you are interested.

Part I

Appendix

Answers

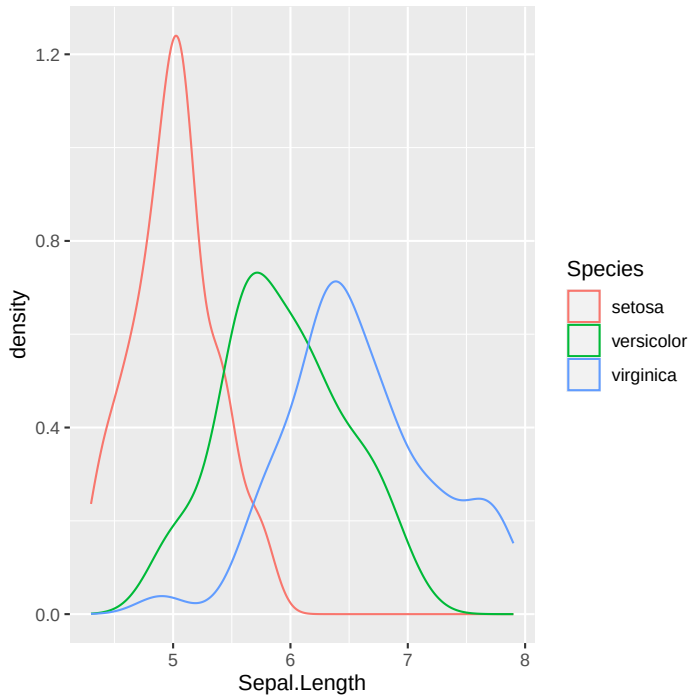
Solution 1

The answer is, of course, 42.

Return to task on P5

Solution 2

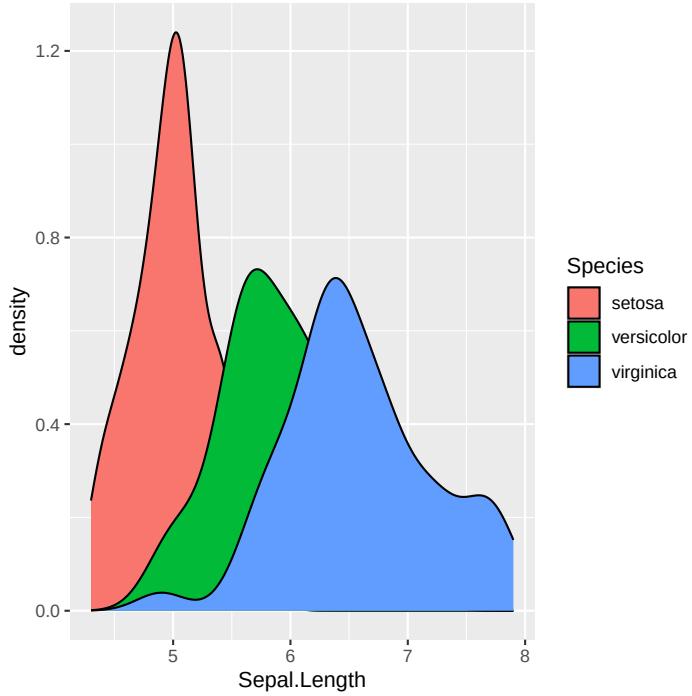
```
ggplot(iris) +
    geom_density(aes(x = Sepal.Length, colour = Species))
```



Return to task on P14

Solution 3

```
ggplot(iris) +
    geom_density(aes(x = Sepal.Length, fill = Species))
```

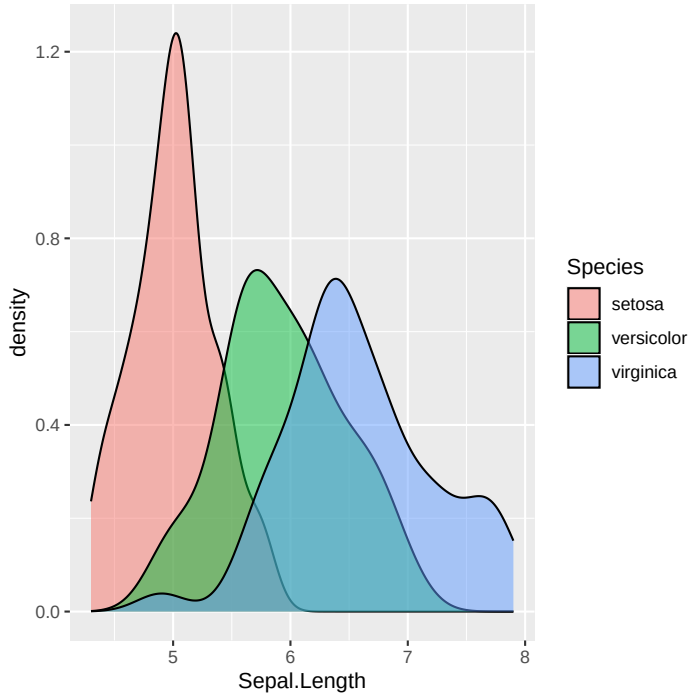


We can see that now we have produced filled density plots. However, since these overlap each other, it is difficult to see the full shapes of these distributions.

Return to task on P14

Solution 4

```
ggplot(iris) +
    geom_density(aes(x = Sepal.Length, fill = Species), alpha = 0.5)
```

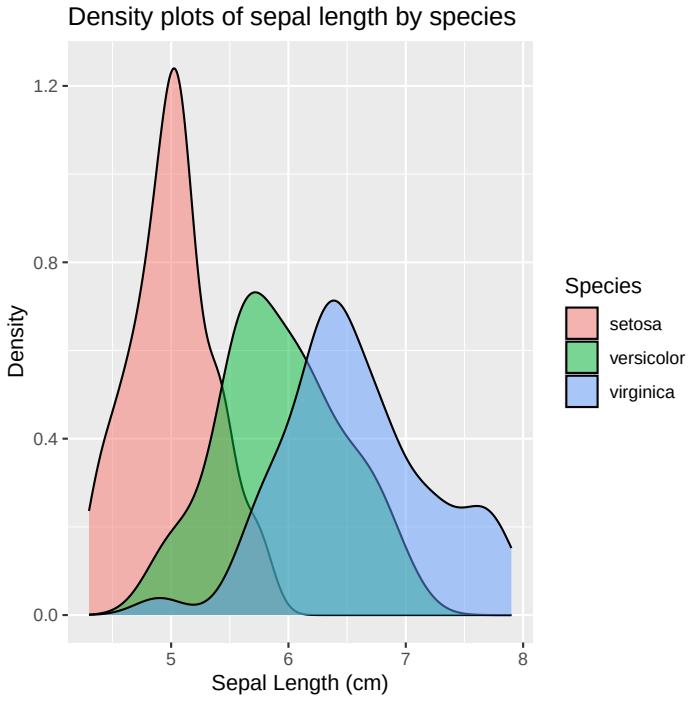


Now we can better see the shapes of these distributions.

Return to task on P14

Solution 5

```
ggplot(iris) +
    geom_density(aes(x = Sepal.Length, fill = Species), alpha = 0.5) +
    xlab("Sepal Length (cm)") + ylab("Density") +
    ggtitle("Density plots of sepal length by species")
```



Return to task on P15

Solution 6

In this case you get an error:

```
ggplot(iris) +
    geom_point(aes(x = Sepal.Length, y = Sepal.Width), colour = Species)
```

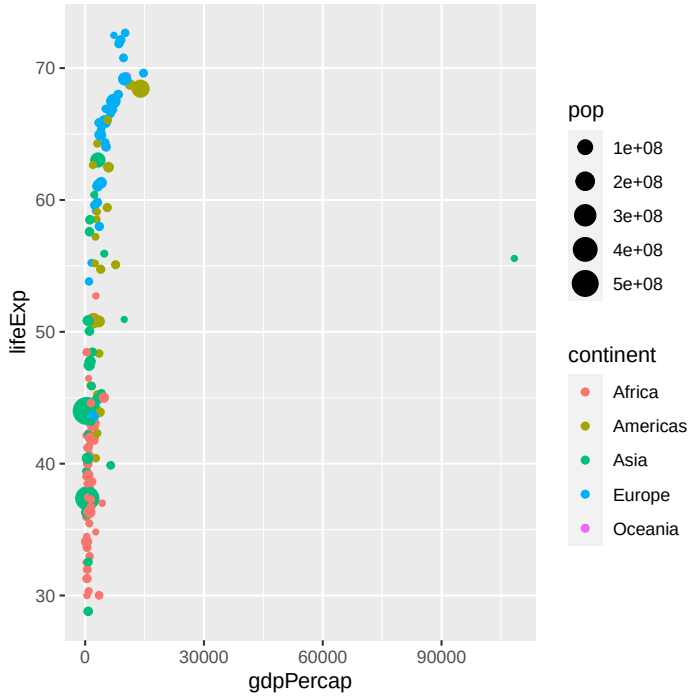
```
## Error in list2(na.rm = na.rm, ...): object 'Species' not found
```

This is because you are trying to set a generic `colour` using a vector object `Species`. Since the `colour` option is not part of the aesthetics, `ggplot()` does not know where to find `Species`.

Return to task on P16

Solution 7

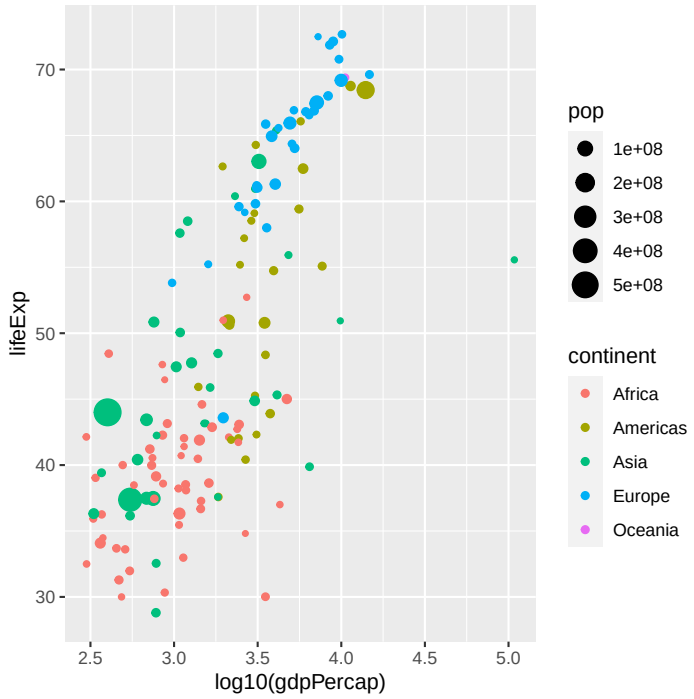
```
ggplot(gapminder[gapminder$year == 1952, ],
       aes(x = gdpPercap, y = lifeExp, size = pop, colour = continent)) +
    geom_point()
```



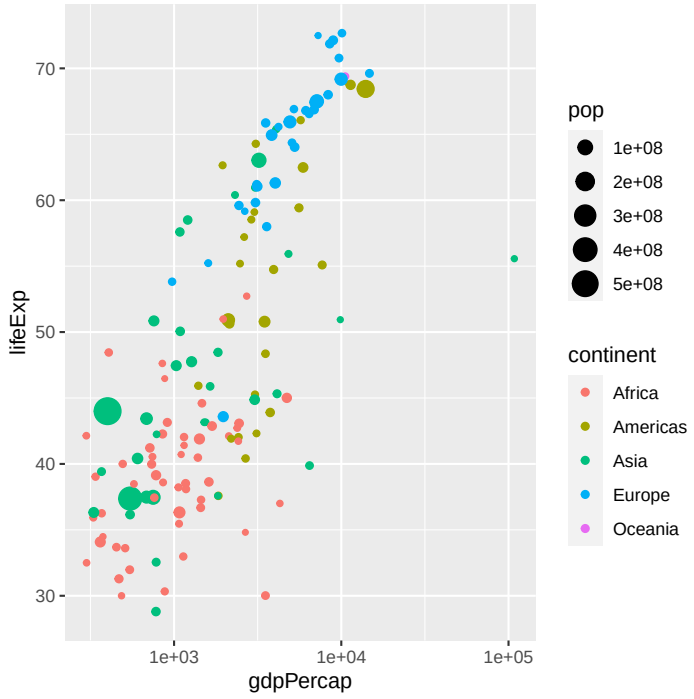
Return to task on P22

Solution 8

```
ggplot(gapminder[gapminder$year == 1952, ],
       aes(x = log10(gdpPercap), y = lifeExp, size = pop, colour = continent)) +
    geom_point()
```




```
ggplot(gapminder[gapminder$year == 1952, ],
       aes(x = gdpPercap, y = lifeExp, size = pop, colour = continent)) +
    geom_point() + scale_x_log10()
```

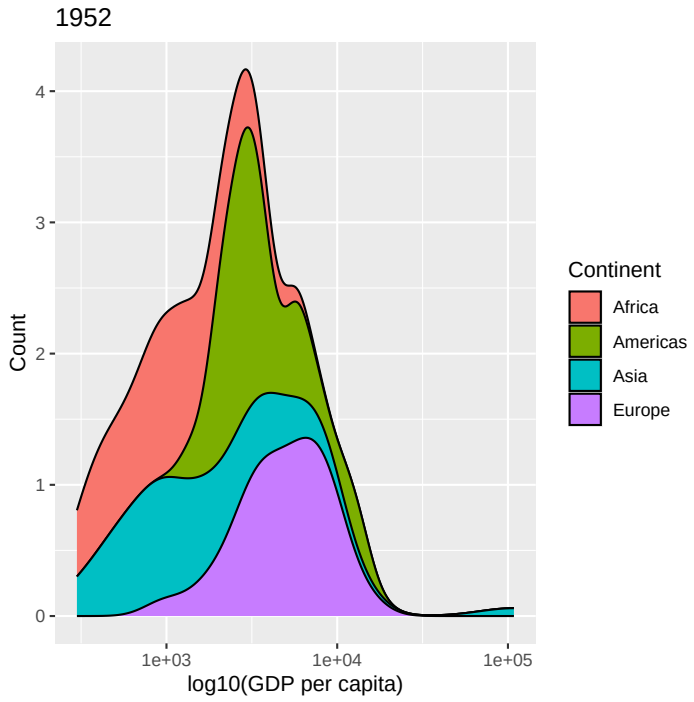


The plots differ purely in the labels for the x-axis.

Return to task on P22

Solution 10

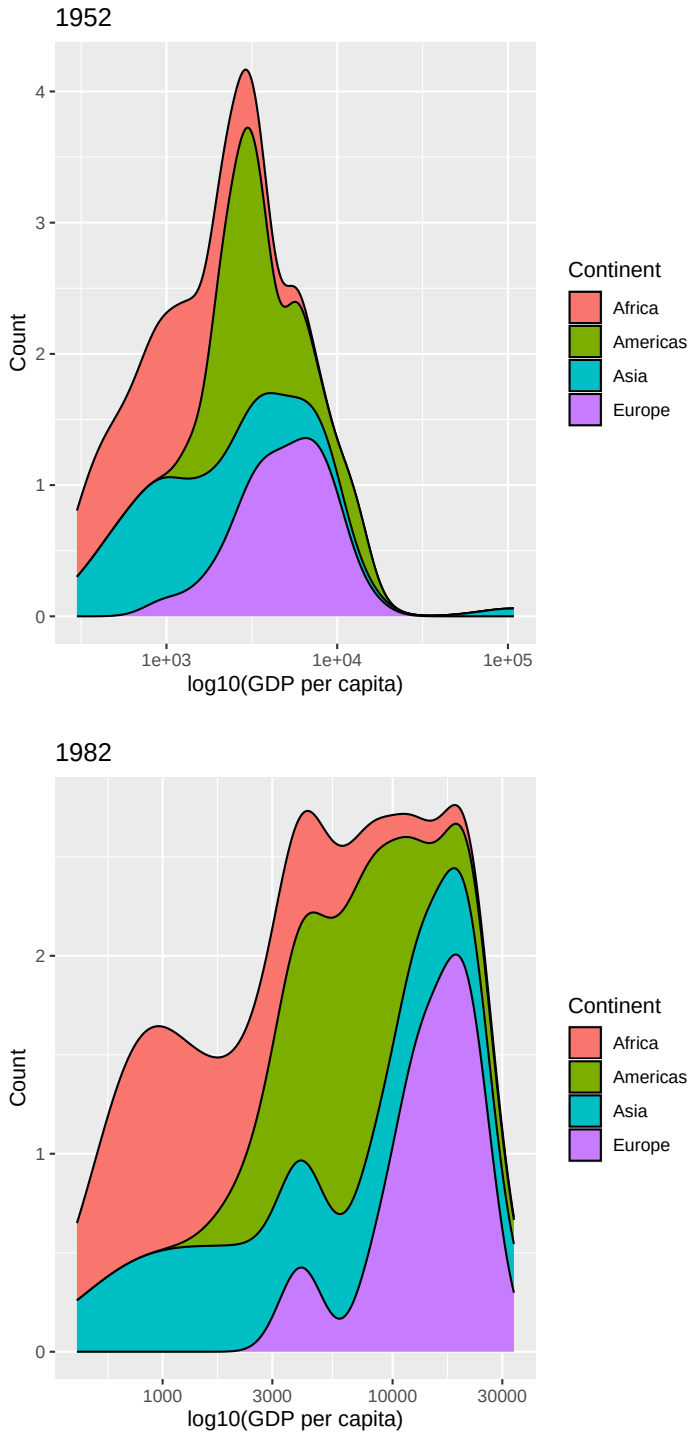
```
ggplot(gapminderNoOc[gapminderNoOc$year == 1952, ],
       aes(x = gdpPercap, fill = continent)) +
    geom_density(position = "stack") +
    scale_x_log10() +
    xlab("log10(GDP per capita)") +
    ylab("Count") +
    ggtitle("1952") +
    labs(fill = "Continent")
```

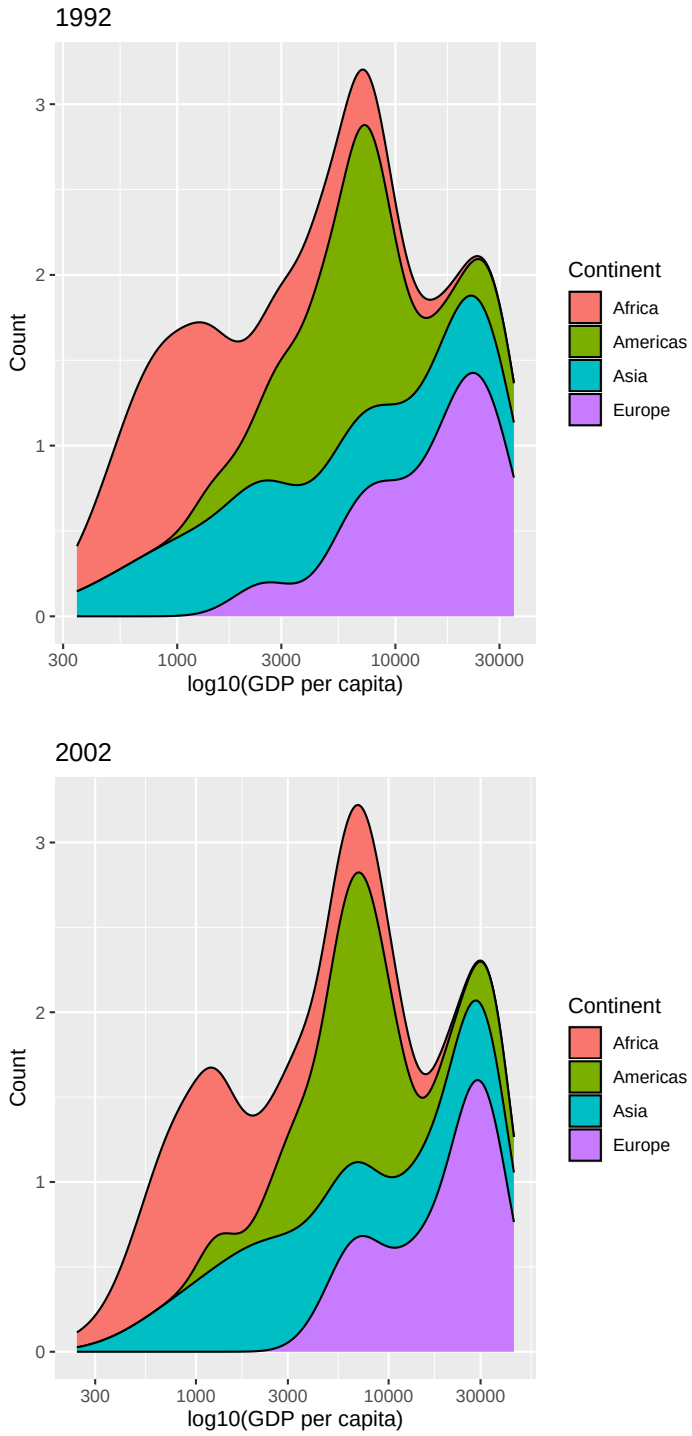


Return to task on P29

Solution 11

```
plotGapminder_gg <- function(data, year) {
    p <- ggplot(data[data$year == year, ],
       aes(x = gdpPercap, fill = continent)) +
    geom_density(position = "stack") +
    scale_x_log10() +
    xlab("log10(GDP per capita)") +
    ylab("Count") +
    ggtitle(year) +
    labs(fill = "Continent")
    print(p)
}
for(i in c(1952, 1982, 1992, 2002)) {
    plotGapminder_gg(gapminderNoOc, i)
}
```


1952
Count
log10(GDP per capita)
1e+03
1e+04
1e+05
0
1
2
3
4
Continent
Africa
Americas
Asia
Europe
1982
Count
log10(GDP per capita)
1000
3000
10000
30000
0
1
2
Continent
Africa
Americas
Asia
Europe



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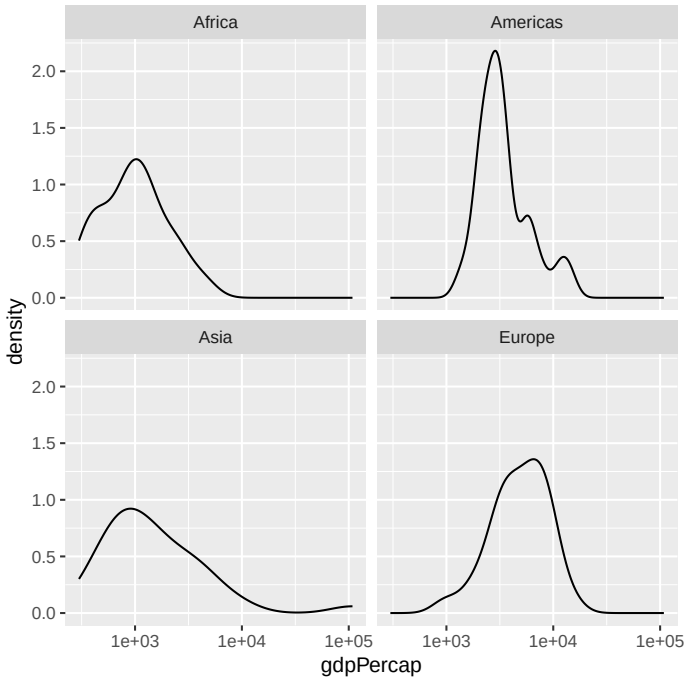
Solution 12

```
ggplot(gapminderNoOc[gapminderNoOc$year == 1952, ],
       aes(x = gdpPercap)) +
    geom_density()  +
    scale_x_log10()  +
    facet_wrap(~ continent)
```



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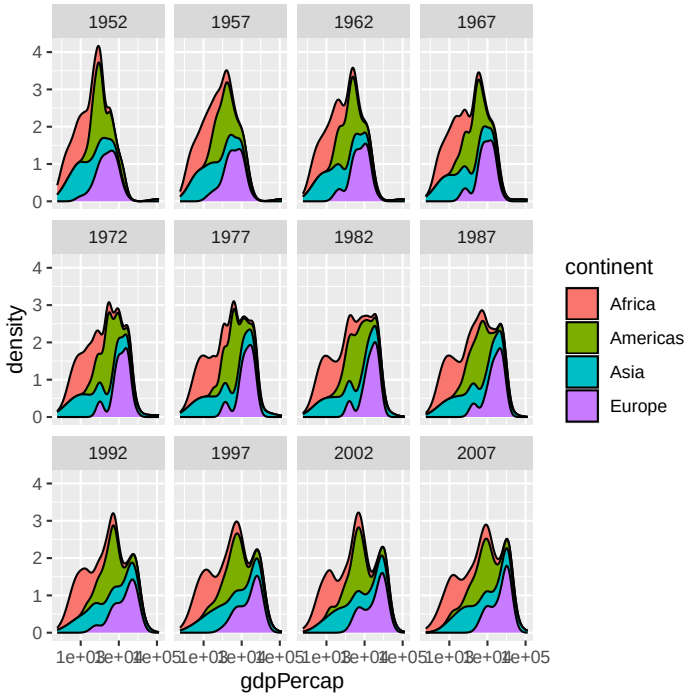
Solution 13

```
ggplot(gapminderNoOc,
       aes(x = gdpPercap, fill = continent)) +
    geom_density(position = "stack") +
    scale_x_log10() +
    facet_wrap(~ year)
```



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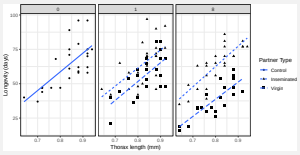
Solution 14

ggplot2

For comparison `ggplot2` and base R versions of the code are provided. You can see how much easier it is to produce a plot like this using `ggplot2`! Note that in the base R code we have used the `lm()` function to fit a **linear regression model** to each subset of data in order to produce the fitted lines. We do not cover **statistical modelling in R** in this workshop, but if you are interested, there is a workshop here where you can learn more.

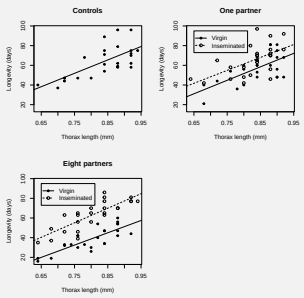
```
## produce summary plot
ggplot(ff, aes(y = longevity, x = thorax,
        linetype = partner.type,
        shape = partner.type)) +
    geom_point() +
    stat_smooth(method = "lm", se = FALSE) +
    facet_wrap(~partners) +
    labs(linetype = "Partner Type",
         shape = "Partner Type") +
    ylab("Longevity (days)") +
    xlab("Thorax length (mm)") +
    theme_bw()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Base R

```
## set up 2 x 2 grid of plots
par(mfrow = c(2, 2))

## plot controls (set range to be the range of the data
## so that it's the same on all plots)
plot(ff$thorax[ff$partner.type == "Control"],
    ff$longevity[ff$partner.type == "Control"],
    pch = 20, xlab = "Thorax length (mm)",
    ylab = "Longevity (days)", main = "Controls",
    xlim = range(ff$thorax), ylim = range(ff$longevity))

## fit linear model and add fitted line using abline()
temp_lm <- lm(longevity ~ thorax,
    data = ff[ff$partner.type == "Control", ])
abline(coef(temp_lm)[1], coef(temp_lm)[2])

titles <- c("One partner", "Eight partners")
partners <- c("1", "8")
for(i in 1:length(titles)) {
    ## extract subset of data for brevity of code
    temp <- ff[ff$partners == partners[i], ]

    ## set point characters
    temp_pch <- rep(20, nrow(temp))
    temp_pch[temp$partner.type != "Virgin"] <- 1

    ## produce plot
    plot(temp$thorax, temp$longevity,
        xlab = "Thorax length (mm)", ylab = "Longevity (days)",
        xlim = range(ff$thorax), ylim = range(ff$longevity),
        main = titles[i], pch = temp_pch)

    ## fit linear models and add fitted lines using abline()
    temp_lm <- lm(longevity ~ thorax,
        data = temp[temp$partner.type == "Virgin", ])
    abline(coef(temp_lm)[1], coef(temp_lm)[2])
    temp_lm <- lm(longevity ~ thorax,
        data = temp[temp$partner.type == "Inseminated", ])
    abline(coef(temp_lm)[1], coef(temp_lm)[2], lty = 2)

    ## add legend
    legend(0.65, 95, pch = c(20, 1), lty = 1:2,
        legend = c("Virgin", "Inseminated"))
}
## reset par
par(mfrow = c(1, 1))
```



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Additional information

Analogous base R code

Here is a version of the same plot using base R graphics functions, with some explanation of the different steps.

Firstly, plot the `iris$Sepal.Width` vector against the `iris$Sepal.Length` vector, adding some informative axis labels.

```
## produce scatterplot
plot(iris$Sepal.Length, iris$Sepal.Width,
     xlab = "Sepal Length (cm)", ylab = "Sepal Width (cm)")
```

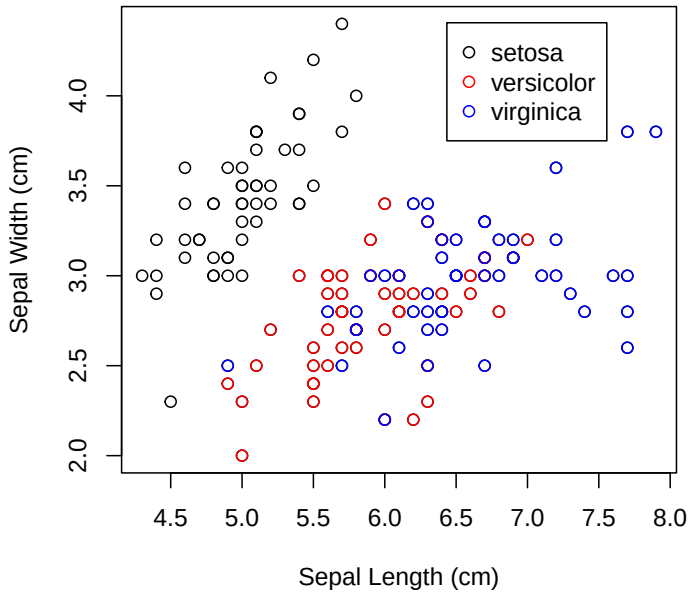
Now we will use the `points()` function to overlay points on an existing plot, manually colouring by the different species.

```
points(iris$Sepal.Length[iris$Species == "versicolor"],
       iris$Sepal.Width[iris$Species == "versicolor"], col = "red")
points(iris$Sepal.Length[iris$Species == "virginica"],
       iris$Sepal.Width[iris$Species == "virginica"], col = "blue")
```

Finally we add a legend. We could set the position of the legend manually, but the objects `par("usr")` provides the coordinates of the plot region in the form `c(x1, x2, y1, y2)`, where `x1` is the lower bound for the x-axis, and `x2` is the upper bound for the x-axis, and similarly for `y1` and `y2`. It is up to us to set the correct mapping of colours and point shapes to the text labels, and to figure out the optimum positioning. See the helps files: `?plot`, `?points` and `?legend` for more details.

```
## add legend
legend(par("usr")[2] * 0.8, par("usr")[4] * 0.98,
       legend = c("setosa", "versicolor", "virginica"),
       pch = c(1, 1, 1),
       col = c("black", "red", "blue"))
```

The final plot looks like:



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Analogous base R code

Let's start by visualising the variable `Sepal.Length` using a kernel density plot:

```
## kernel density of sepal length
plot(density(iris$Sepal.Length))
```

Remember that we can extract a named column from a `data.frame` using the `$` operator. The `density()` function is a simple function in R that takes a `vector` argument and returns a kernel density object, which we can then plot using the generic `plot()` function.

Now let's try to plot different kernel density plots for the three different species. We could do this as separate plots, and use our standard subsetting notation to extract the correct elements of the data frame in each case:

```
## plot Sepal.Length for setosa
plot(density(iris$Sepal.Length[iris$Species == "setosa"]))

## plot Sepal.Length for versicolor
plot(density(iris$Sepal.Length[iris$Species == "versicolor"]))

## plot Sepal.Length for virginica
plot(density(iris$Sepal.Length[iris$Species == "virginica"]))
```

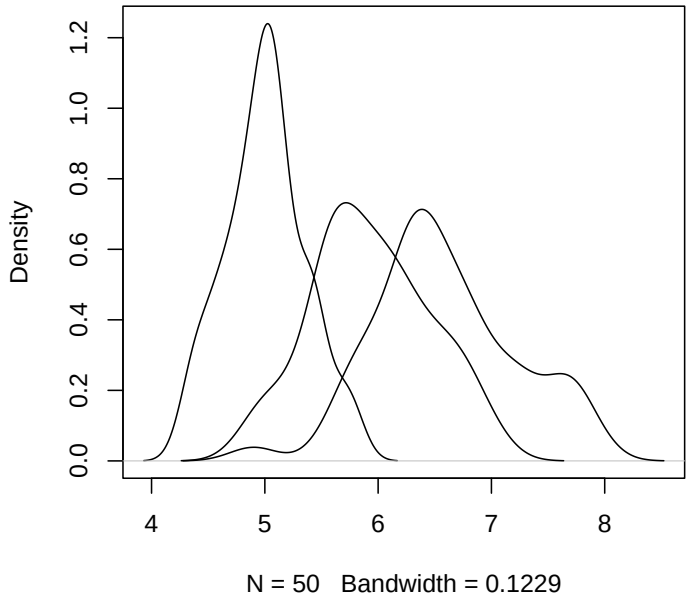
What about if we want to add all three density lines to the same plot?

```
## place kernel density estimates on the same plot
plot(density(iris$Sepal.Length[iris$Species == "setosa"]), main = "")
lines(density(iris$Sepal.Length[iris$Species == "versicolor"]))
lines(density(iris$Sepal.Length[iris$Species == "virginica"]))
```

Notice the use of the `lines()` function to allow a line to be added to an existing plot (in an analogous manner to the `points()` function used in the earlier scatterplot example).

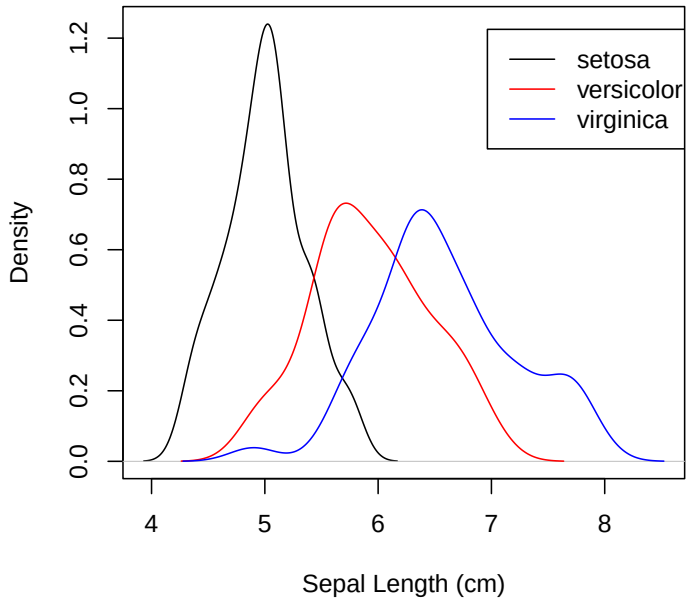
Notice that the limits of the x- and y-axes in this case are set by the range of the initial `setosa` sepal lengths, and hence the density plots for the other two species extend beyond the plot window. Let's try again, but this time setting the bounds for the plots manually. To do this we calculate the x and y ranges for each density plot separately, and then take the maximum values across the different species. We then use the `xlim` and `ylim` arguments to the `plot()` function in order to set the ranges:

```
## produce densities
setosa_dens <- density(iris$Sepal.Length[iris$Species == "setosa"])
versicolor_dens <- density(iris$Sepal.Length[iris$Species == "versicolor"])
virginica_dens <- density(iris$Sepal.Length[iris$Species == "virginica"])

## extract x-ranges and y-ranges
xlims <- range(c(setosa_dens$x, versicolor_dens$x, virginica_dens$x))
ylims <- range(c(setosa_dens$y, versicolor_dens$y, virginica_dens$y))

## produce plot
plot(density(iris$Sepal.Length[iris$Species == "setosa"]),
     xlim = xlims, ylim = ylims, main = "")
lines(density(iris$Sepal.Length[iris$Species == "versicolor"]))
lines(density(iris$Sepal.Length[iris$Species == "virginica"]))
```



This is better, but still not very informative. Let's add some colour and a legend, and tidy up the axis labels.

```
## produce plot
plot(density(iris$Sepal.Length[iris$Species == "setosa"]),
    xlim = xlims, ylim = ylims, main = "", xlab = "Sepal Length (cm)")
lines(density(iris$Sepal.Length[iris$Species == "versicolor"]), col = "red")
lines(density(iris$Sepal.Length[iris$Species == "virginica"]), col = "blue")

## add legend to top-right corner
legend(par("usr")[2] * 0.8, par("usr")[4] * 0.95,
       legend = c("setosa", "versicolor", "virginica"),
       lty = c(1, 1, 1),
       col = c("black", "red", "blue"))
```



Notice that this is quite a simple plot, but required a series of steps to render in base R. We needed to calculate manual limits for the axes, plot the three species separately, and then add a custom legend to the plot, none of which is necessary with `ggplot2`.

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