Data visualisation using R, for researchers who don't use R

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Abstract

In addition to benefiting reproducibility and transparency, one of the advantages of using R is that researchers have a much larger range of fully customisable data visualisations options than are typically available in point-and-click software, due to the open-source nature of R. These visualisation options not only look attractive, but can increase transparency about the distribution of the underlying data rather than relying on commonly used visualisations of aggregations such as bar charts of means. In this tutorial, we provide a practical introduction to data visualisation using R, specifically aimed at researchers who have little to no prior experience of using R. First we detail the rationale for using R for data visualisation and introduce the "grammar of graphics" that underlies data visualisation using the ggplot package. The tutorial then walks the reader through how to replicate plots that are commonly available in point-and-click software such as histograms and boxplots, as well as showing how the code for these "basic" plots can be easily extended to less commonly available options such as violin-boxplots. The dataset and code used in this tutorial as well as an interactive version with activity solutions, additional resources and advanced plotting options is available at https://osf.io/bj83f/.

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⁹ **Introduction**

¹⁰ Use of the programming language R (R Core Team, 2021) for data processing and
¹¹ statistical analysis by researchers is increasingly common, with an average yearly growth of
¹² 87% in the number of citations of the R Core Team between 2006-2018 (Barrett, 2019). In
¹³ addition to benefiting reproducibility and transparency, one of the advantages of using R is
¹⁴ that researchers have a much larger range of fully customisable data visualisations options
¹⁵ than are typically available in point-and-click software, due to the open-source nature of R.
¹⁶ These visualisation options not only look attractive, but can increase transparency about
¹⁷ the distribution of the underlying data rather than relying on commonly used visualisations
¹⁸ of aggregations such as bar charts of means (Newman & Scholl, 2012).

¹⁹ Yet, the benefits of using R are obscured for many researchers by the perception
²⁰ that coding skills are difficult to learn (Robins, Rountree, & Rountree, 2003). Coupled
²¹ with this, only a minority of psychology programmes currently teach coding skills (Wills,
²² n.d.) with the majority of both undergraduate and postgraduate courses using proprietary
²³ point-and-click software such as SAS, SPSS or Microsoft Excel. While the sophisticated use
²⁴ of proprietary software often necessitates the use of computational thinking skills akin to
²⁵ coding (for instance SPSS scripts or formulas in Excel), we have found that many researchers
²⁶ do not perceive that they already have introductory coding skills. In the following tutorial
²⁷ we intend to change that perception by showing how experienced researchers can redevelop
²⁸ their existing computational skills to utilise the powerful data visualisation tools offered by
²⁹ R.

³⁰ In this tutorial, we aim to provide a practical introduction to data visualisation using
³¹ R, specifically aimed at researchers who have little to no prior experience of using R. First
³² we detail the rationale for using R for data visualisation and introduce the "grammar of
³³ graphics" that underlies data visualisation using the `ggplot2` package. The tutorial then
³⁴ walks the reader through how to replicate plots that are commonly available in point-and-
³⁵ click software such as histograms and boxplots, as well as showing how the code for these
³⁶ "basic" plots can be easily extended to less commonly available options such as violin-
³⁷ boxplots.

³⁸ **Why R for data visualisation?**

³⁹ Data visualisation benefits from the same advantages as statistical analysis when writ-
⁴⁰ ing code rather than using point-and-click software – reproducibility and transparency. The
⁴¹ need for psychological researchers to work in reproducible ways has been well-documented
⁴² and discussed in response to the replication crisis (e.g. Munafò et al., 2017) and we will
⁴³ not repeat those arguments here. However, there is an additional benefit to reproducibility
⁴⁴ that is less frequently acknowledged compared to the loftier goals of improving psychological
⁴⁵ science: if you write code to produce your plots, you can reuse and adapt that code in the
⁴⁶ future rather than starting from scratch each time.

⁴⁷ In addition to the benefits of reproducibility, using R for data visualisation gives the
⁴⁸ researcher almost total control over each element of the plot. Whilst this flexibility can
⁴⁹ seem daunting at first, the ability to write reusable code recipes (and use recipes created

₅₀ by others) is highly advantageous. The level of customisation and the professional outputs
₅₁ available using R has, for instance, lead news outlets such as the BBC (Visual & Journalism,
₅₂ 2019) and the New York Times (Bertini & Stefaner, 2015) to adopt R as their preferred
₅₃ data visualisation tool.

₅₄ **A layered grammar of graphics**

₅₅   There are multiple approaches to data visualisation in R; in this paper we use the
₅₆ popular package[1] `ggplot2` (Wickham, 2016a) which is part of the larger `tidyverse`[2] (Wick-
₅₇ ham, 2017) collection of packages that provide functions for data wrangling, descriptives,
₅₈ and visualisation. A grammar of graphics (Wilkinson, Anand, & Grossman, 2005) is a stan-
₅₉ dardised way to describe the components of a graphic. `ggplot2` uses a layered grammar of
₆₀ graphics (Wickham, 2010), in which plots are built up in a series of layers. It may be helpful
₆₁ to think about any picture as having multiple elements that sit semi-transparently over each
₆₂ other. A good analogy is old Disney movies where artists would create a background and
₆₃ then add moveable elements on top of the background via transparencies.

₆₄   Figure 1 displays the evolution of a simple scatterplot using this layered approach.
₆₅ First, the plot space is built (layer 1); the variables are specified (layer 2); the type of
₆₆ visualisation (known as a `geom`) that is desired for these variables is specified (layer 3) - in
₆₇ this case `geom_point()` is called to visualise individual data points; a second geom is added
₆₈ to include a line of best fit (layer 4), the axis labels are edited for readability (layer 5), and
₆₉ finally, a theme is applied to change the overall appearance of the plot (layer 6).

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[1]The power of R is that it is extendable and open source - put simply, if a function doesn't exist or is
difficult to use, anyone can create a new **package** that contains data and code to allow you to perform new
tasks. You may find it helpful to think of packages as additional apps that you need to download separately
to extend the functionality beyond what comes with "Base R."

[2]Because there are so many different ways to achieve the same thing in R, when Googling for help with
R, it is useful to append the name of the package or approach you are using, e.g., "how to make a histogram
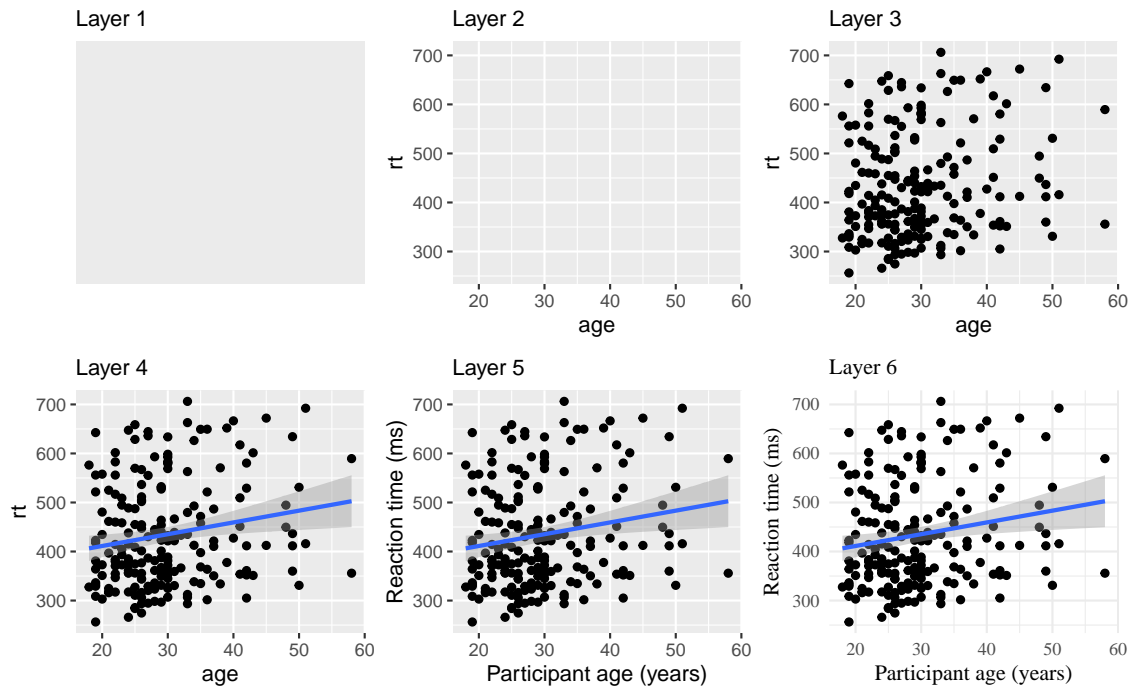ggplot2."

Figure 1. Evolution of a layered plot

70   Importantly, each layer is independent and independently customisable. For example,
71 the size, colour and position of each component can be adjusted, or one could, for example,
72 remove the first geom (the data points) to only visualise the line of best fit, simply by
73 removing the layer that draws the data points (Figure 2). The use of layers makes it easy
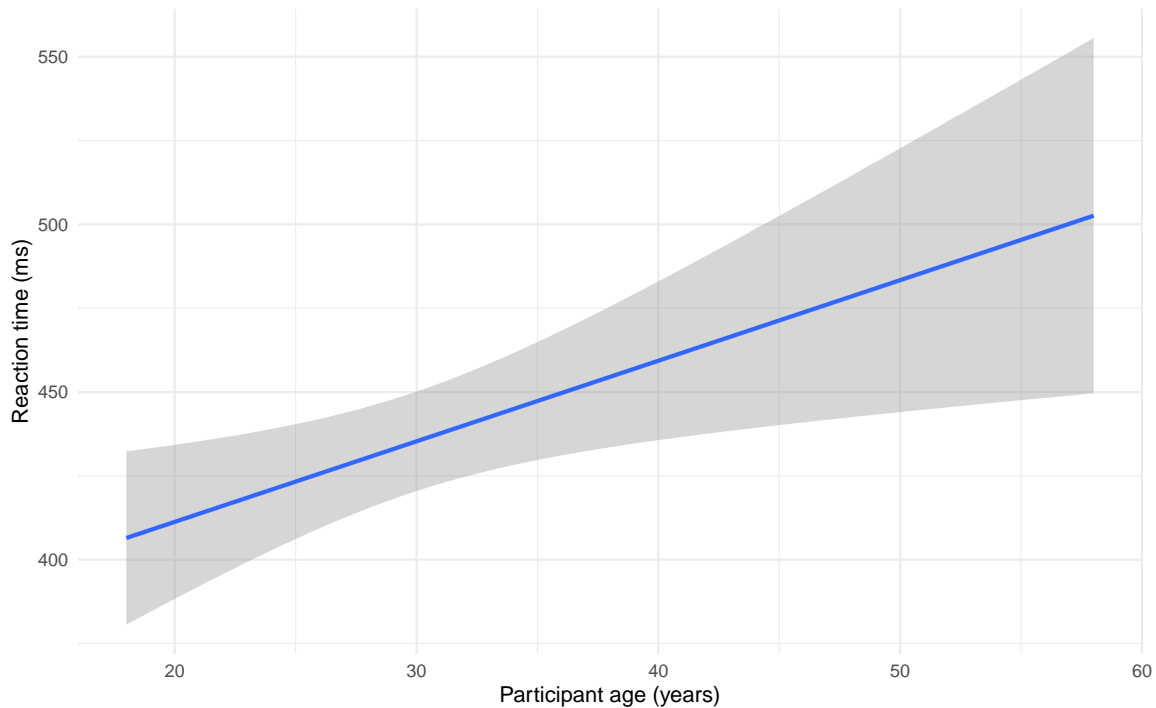74 to build up complex plots step-by-step, and to adapt or extend plots from existing code.

Figure 2. Plot with scatterplot layer removed.

Tutorial components

This tutorial contains three components.

1. A traditional PDF manuscript that can easily be saved, printed, and cited.
2. An online version of the tutorial published at https://psyteachr.github.io/ introdataviz/ that may be easier to copy and paste code from and that also provides the optional activity solutions as well as additional appendices, including code tutorials for advanced plots beyond the scope of this paper and links to additional resources.
3. An Open Science Framework repository published at https://osf.io/bj83f/ that contains the simulated dataset (see below), preprint, and R Markdown workbook.

Simulated dataset

For the purpose of this tutorial, we will use simulated data for a 2 x 2 mixed-design lexical decision task in which participants have to decide whether a presented word is a real word, or a non-word, with 100 participants. There are 100 rows (1 for each participant) and 7 variables:

- Participant information:
  - `id`: Participant ID

92   – `age`: Age

93   • 1 between-subject independent variable (VI):

94   – `language`: Language group (1 = monolingual, 2 = bilingual)

95   • 4 columns for the 2 dependent variables (DVs) for RT and accuracy, crossed by the
96   within-subject IV of condition:

97   – `rt_word`: Reaction time (ms) for word trials
98   – `rt_nonword`: Reaction time (ms) for non-word trials
99   – `acc_word`: Accuracy for word trials
100   – `acc_nonword`: Accuracy for non-word trials

101   For newcomers to R, we would suggest working through this tutorial with the simu-
102   lated dataset, then extending the code to your own datasets with a similar structure, and
103   finally generalising the code to new structures and problems.

Setting up R and RStudio

105   We strongly encourage the use of RStudio (RStudio Team, 2021) to write code in R.
106   R is the programming language whilst RStudio is an *integrated development environment*
107   that makes working with R easier. More information on installing both R and RStudio can
108   be found in the additional resources.

109   Projects are a useful way of keeping all your code, data, and output in one place.
110   To create a new project, open RStudio and click `File - New Project - New Directory`
111   `- New Project`. You will be prompted to give the project a name, and select a location
112   for where to store the project on your computer. Once you have done this, click `Create`
113   `Project`. Download the simulated dataset and code tutorial Rmd file from the online
114   materials and then (`ldt_data.csv`, `workbook.Rmd`) to this folder. The files pane on the
115   bottom right of RStudio should now display this folder and the files it contains - this is
116   known as your *working directory* and it is where R will look for any data you wish to import
117   and where it will save any output you create.

118   This tutorial will require you to use the packages contained with the `tidyverse`
119   collection. Additionally, we will also require use of `patchwork`. To install these packages,
120   copy and paste the below code into the console (the left hand pane) and press enter to
121   execute the code.

```
# only run in the console, never put this in a script
package_list <- c("tidyverse", "patchwork")
install.packages(package_list)
```

122   The R Markdown workbook available in the online materials contains all the code in
123   this tutorial and there is more information and links to additional resources for how to use
124   R Markdown for reproducible reports in the additional resources.

125 The reason that the above install packages code is not included in the workbook
126 is that every time you run the install command code it will install the latest version of
127 the package. Leaving this code in your script can lead you to unintentionally install a
128 package update you didn't want. For this reason, avoid including install code in any script
129 or Markdown document.

Preparing your data

131 Before you start visualising your data, you need to get it into an appropriate format.
132 These preparatory steps can all be dealt with reproducibly using R and the additional re-
133 sources section points to extra tutorials for doing so. However, performing these types of
134 tasks in R can require more sophisticated coding skills and the solutions and tools are de-
135 pendent on the idiosyncrasies of each dataset. For this reason, in this tutorial we encourage
136 the reader to complete data preparation steps using the method they are most comfortable
137 with and to focus on the aim of data visualisation.

138 **Data format.** The simulated lexical decision data is provided in a `csv` (comma-
139 separated variable) file. Functions exist in R to read many other types of data files; the
140 `rio` package's `import()` function can read most types of files. However, `csv` files avoids
141 problems like Excel's insistence on mangling anything that even vaguely resembles a date.
142 You may wish to export your data as a `csv` file that contains only the data you want to
143 visualise, rather than a full, larger workbook. When working with your own data, remove
144 summary rows or additional notes from any files you import. The files you import from
145 should only contain the rows and columns of data you want to plot. You should always
146 check after importing data that the resulting table looks like you expect.

147 **Variable names.** Ensuring that your variable names are consistent can make it
148 much easier to work in R. We recommend using short but informative variable names, for
149 example `rt_word` is preferred over `dv1_iv1` or `reaction_time_word_condition` because
150 these are either hard to read or hard to type.

151 It is also helpful to have a consistent naming scheme, particularly for variable names
152 that require more than one word. Two popular options are `CamelCase` where each new word
153 begins with a capital letter, or `snake_case` where all letters are lower case and words are
154 separated by an underscore. For the purposes of naming variables, avoid using any spaces in
155 variable names (e.g., `rt word`) and consider the additional meaning of a separator beyond
156 making the variable names easier to read. For example, `rt_word`, `rt_nonword`, `acc_word`,
157 and `acc_nonword` all have the DV to the left of the separator and the level of the IV to the
158 right. `rt_word_condition` on the other hand has two separators but only one of them is
159 meaningful and it is useful to be able to split variable names consistently. In this paper, we
160 will use `snake_case` and lower case letters for all variable names so that we don't have to
161 remember where to put the capital letters.

162 When working with your own data, you can rename columns in Excel, but the re-
163 sources listed in the online appendices point to how to rename columns reproducibly with
164 code.

165   **Data values.**   A great benefit to using R is that categorical data can be entered
166 as text.   In the tutorial dataset, language group is entered as 1 or 2, so that we can
167 show you how to recode numeric values into factors with labels. However, we recommend
168 recording meaningful labels rather than numbers from the beginning of data collection to
169 avoid misinterpreting data due to coding errors. Note that values must match *exactly* in
170 order to be considered in the same category and R is case sensitive, so "mono," "Mono,"
171 and "monolingual" would be classified as members of three separate categories.

172   Finally, cells that represent missing data should be left empty rather than containing
173 values like `NA`, `missing` or `999`[3]. A complementary rule of thumb is that each column should
174 only contain one type of data, such as words or numbers, not both.

Getting Started

Loading packages

177   To load the packages that have the functions we need, use the `library()` function.
178 Whilst you only need to install packages once, you need to load any packages you want
179 to use with `library()` every time you start R or start a new session. When you load
180 the `tidyverse`, you actually load several separate packages that are all part of the same
181 collection and have been designed to work well together. R will produce a message that
182 tells you the names of all the packages that have been loaded.

```
library(tidyverse)
library(patchwork)
```

Loading data

184   To load the simulated data we use the function `read_csv()` from the `readr` tidyverse
185 package. Note that there are many other ways of reading data into R, but the benefit of
186 this function is that it enters the data into the R environment in such a way that it makes
187 most sense for other tidyverse packages.

```
dat <- read_csv(file = "ldt_data.csv")
```

188   This code has created an object `dat` into which you have read the data from the file
189 `ldt_data.csv`. This object will appear in the environment pane in the top right. Note
190 that the name of the data file must be in quotation marks and the file extension (`.csv`)
191 must also be included. If you receive the error `...does not exist in current working`
192 `directory` it is highly likely that you have made a typo in the file name (remember R is case
193 sensitive), have forgotten to include the file extension `.csv`, or that the data file you want

---

[3]If your data use a missing value like `NA` or `999`, you can indicate this in the `na` argument of `read_csv()` when you read in your data. For example, `read_csv("data.csv", na = c("", "NA", 999))` allows you to use blank cells `""`, the letters `"NA"`, and the number `999` as missing values.

194 to load is not stored in your project folder. If you get the error `could not find function`
195 it means you have either not loaded the correct package (a common beginner error is to
196 write the code, but not run it), or you have made a typo in the function name.

197   To view the dataset, click `dat` in the environment pane or run `View(dat)` in the
198 console. The environment pane also tells us that the object `dat` has 100 observations of 7
199 variables, and this is a useful quick check to ensure one has loaded the right data. Note
200 that the 7 variables have an additional piece of information `chr` and `num`; this specifies the
201 kind of data in the column. Similar to Excel and SPSS, R uses this information (or variable
202 type) to specify allowable manipulations of data. For instance character data such as the
203 `id` cannot be averaged, while it is possible to do this with numerical data such as the `age`.

Handling numeric factors

205   Another useful check is to use the functions `summary()` and `str()` (structure) to check
206 what kind of data R thinks is in each column. Run the below code and look at the output
207 of each, comparing it with what you know about the simulated dataset:

```
summary(dat)
str(dat)
```

208   Because the factor `language` is coded as 1 and 2, R has categorised this column
209 as containing numeric information and unless we correct it, this will cause problems for
210 visualisation and analysis. The code below shows how to recode numeric codes into labels.

211 • `mutate()` makes new columns in a data table, or overwrites a column;
212 • `factor()` translates the language column into a factor with the labels "monolingual"
213   and "bilingual." You can also use `factor()` to set the display order of a column that
214   contains words. Otherwise, they will display in alphabetical order. In this case we
215   are replacing the numeric data (1 and 2) in the `language` column with the equivalent
216   English labels `monolingual` for 1 and `bilingual` for 2. At the same time we will
217   change the column type to be a factor, which is how R defines categorical data.

```
dat <- dat %>%
  mutate(language = factor(
    x = language, # column to translate
    levels = c(1, 2), # values of the original data in preferred order
    labels = c("monolingual", "bilingual") # labels for display
  ))
```

218   Make sure that you always check the output of any code that you run. If after running
219 this code `language` is full of `NA` values, it means that you have run the code twice. The
220 first time would have worked and transformed the values from 1 to `monolingual` and 2 to
221 `bilingual`. If you run the code again on the same dataset, it will look for the values 1 and

222 2, and because there are no longer any that match, it will return NA. If this happens, you
223 will need to reload the dataset from the csv file.

224   A good way to avoid this is never to overwrite data, but to always store the output
225 of code in new objects (e.g., `dat_recoded`) or new variables (`language_recoded`). For the
226 purposes of this tutorial, overwriting provides a useful teachable moment so we'll leave it
227 as it is.

228 **Argument names**

229   Each function has a list of arguments it can take, and a default order for those
230 arguments. You can get more information on each function by entering `?function_name`
231 into the console, although be aware that learning to read the help documentation in R is a
232 skill in itself. When you are writing R code, as long as you stick to the default order, you
233 do not have to explicitly call the argument names, for example, the above code could also
234 be written as:

```r
dat <- dat %>%
  mutate(language = factor(language,
                           c(1, 2),
                           c("monolingual", "bilingual")))
```

235   One of the challenges in learning R is that many of the "helpful" examples and
236 solutions you will find online do not include argument names and so for novice learners are
237 completely opaque. In this tutorial, we will include the argument names the first time a
238 function is used, however, we will remove some argument names from subsequent examples
239 to facilitate knowledge transfer to the help available online.

240 **Demographic information**

241   You can calculate and plot some basic descriptive information about the demographics
242 of our sample using the imported dataset without any additional wrangling (i.e., data
243 processing). The code below uses the `%>%` operator, otherwise known as the *pipe,* and can
244 be translated as "*and then*". For example, the below code can be read as:

245 • Start with the dataset `dat` *and then;*

246 • Group it by the variable `language` *and then;*

247 • Count the number of observations in each group *and then;*

248 • Remove the grouping

```r
dat %>%
  group_by(language) %>%
  count() %>%
  ungroup()
```

language	n
monolingual	55
bilingual	45

²⁴⁹

250 `group_by()` does not result in surface level changes to the dataset, rather, it changes
251 the underlying structure so that if groups are specified, whatever functions called next are
252 performed separately on each level of the grouping variable, until the grouping is removed
253 with `ungroup()`. The above code therefore counts the number of observations in each
254 group of the variable `language`. If you just need the total number of observations, you
255 could remove the `group_by()` and `ungroup()` lines, which would perform the operation on
256 the whole dataset, rather than by groups:

```
dat %>%
  count()
```

n
100

²⁵⁷

258 Similarly, we may wish to calculate the mean age (and SD) of the sample and we can
259 do so using the function `summarise()` from the `dplyr` tidyverse package.

```
dat %>%
  summarise(mean_age = mean(age),
            sd_age = sd(age),
            n_values = n())
```

mean_age	sd_age	n_values
29.75	8.28	100

²⁶⁰

261 This code produces summary data in the form of a column named `mean_age` that
262 contains the result of calculating the mean of the variable `age`. It then creates `sd_age`
263 which does the same but for standard deviation. Finally, it uses the function `n()` to add
264 the number of values used to calculate the statistic in a column named `n_values` - this is
265 a useful sanity check whenever you make summary statistics.

266 Note that the above code will not save the result of this operation, it will simply
267 output the result in the console. If you wish to save it for future use, you can store it in an
268 object by using the `<-` notation and print it later by typing the object name.

```
age_stats <- dat %>%
  summarise(mean_age = mean(age),
            sd_age = sd(age),
            n_values = n())
```

269 Finally, the `group_by()` function will work in the same way when calculating sum-
270 mary statistics – the output of the function that is called after `group_by()` will be produced
271 for each level of the grouping variable.

```
dat %>%
  group_by(language) %>%
  summarise(mean_age = mean(age),
            sd_age = sd(age),
            n_values = n()) %>%
  ungroup()
```

language	mean_age	sd_age	n_values
monolingual	27.96	6.78	55
bilingual	31.93	9.44	45

Bar chart of counts

For our first plot, we will make a simple bar chart of counts that shows the number of participants in each `language` group.

```
ggplot(data = dat, mapping = aes(x = language)) +
  geom_bar()
```
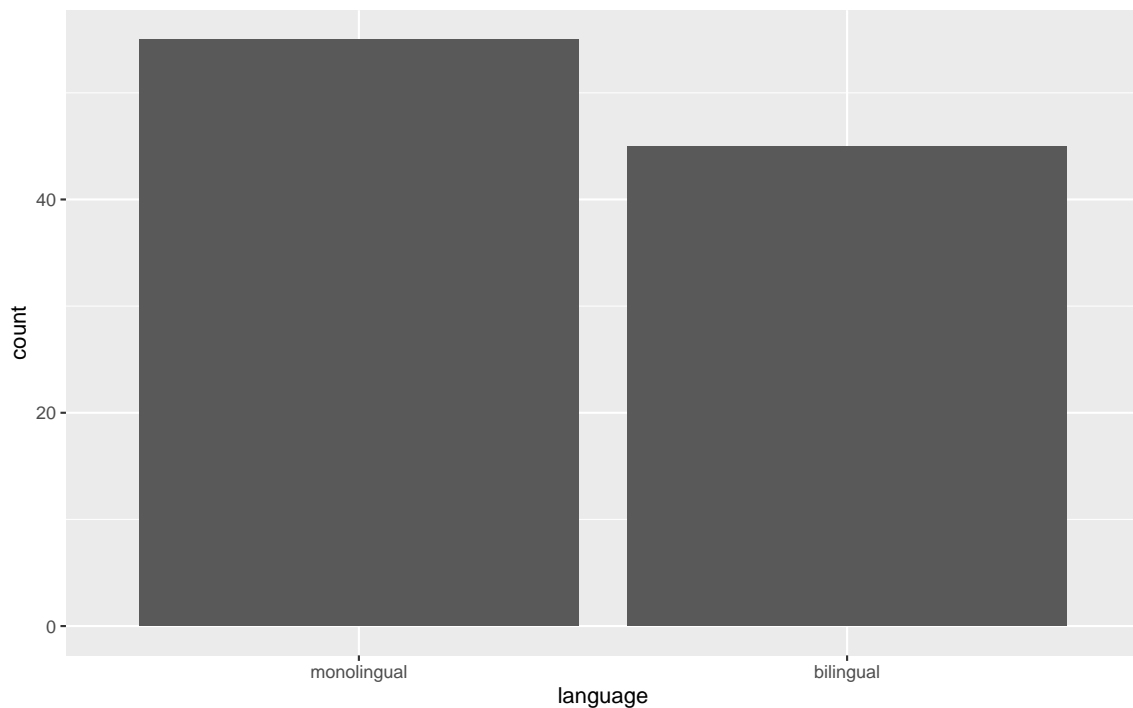

Figure 3. Bar chart of counts.

The first line of code sets up the base of the plot.

- `data` specifies which data source to use for the plot

²⁷⁸   • `mapping` specifies which variables to map to which aesthetics (`aes`) of the plot. Aes-
²⁷⁹   thetic mappings describe how variables in the data are mapped to visual properties
²⁸⁰   (aesthetics) of geoms.

²⁸¹   • `x` specifies which variable to put on the x-axis

²⁸²   The second line of code adds a `geom`, and is connected to the base code with `+`.
²⁸³ In this case, we ask for `geom_bar()`. Each `geom` has an associated default statistic. For
²⁸⁴ `geom_bar()`, the default statistic is to count the data passed to it. This means that you
²⁸⁵ do not have to specify a `y` variable when making a bar plot of counts; when given an `x`
²⁸⁶ variable `geom_bar()` will automatically calculate counts of the groups in that variable. In
²⁸⁷ this example, it counts the number of data points that are in each category of the `language`
²⁸⁸ variable.

²⁸⁹   The base layer and the geoms you add as layers work in symbiosis so it is worthwhile
²⁹⁰ checking the mapping rules as these are related to the default statistic for the plot's geom.

Plotting existing aggregates and percent

²⁹²   If your dataset already has the counts that you want to plot, you can set
²⁹³ `stat="identity"` inside of `geom_bar()` to use that number instead of counting rows.
²⁹⁴ For example, there is currently no function to plot percentages rather than counts within
²⁹⁵ `ggplot2`, you need to calculate these and store them in a new object that is then used as
²⁹⁶ the dataset.

²⁹⁷   Notice that we are now omitting the names of the arguments `data` and `mapping` in
²⁹⁸ the `ggplot()` function.

```r
dat_percent <- dat %>%      # start with the data in dat
  count(language) %>%       # count rows per language (makes a new column called n)
  mutate(percent = (n/sum(n)*100)) # make a new column 'percent' equal to
                                   # n divided by the sum of n times 100

ggplot(dat_percent, aes(x = language, y = percent)) +
  geom_bar(stat="identity")
```
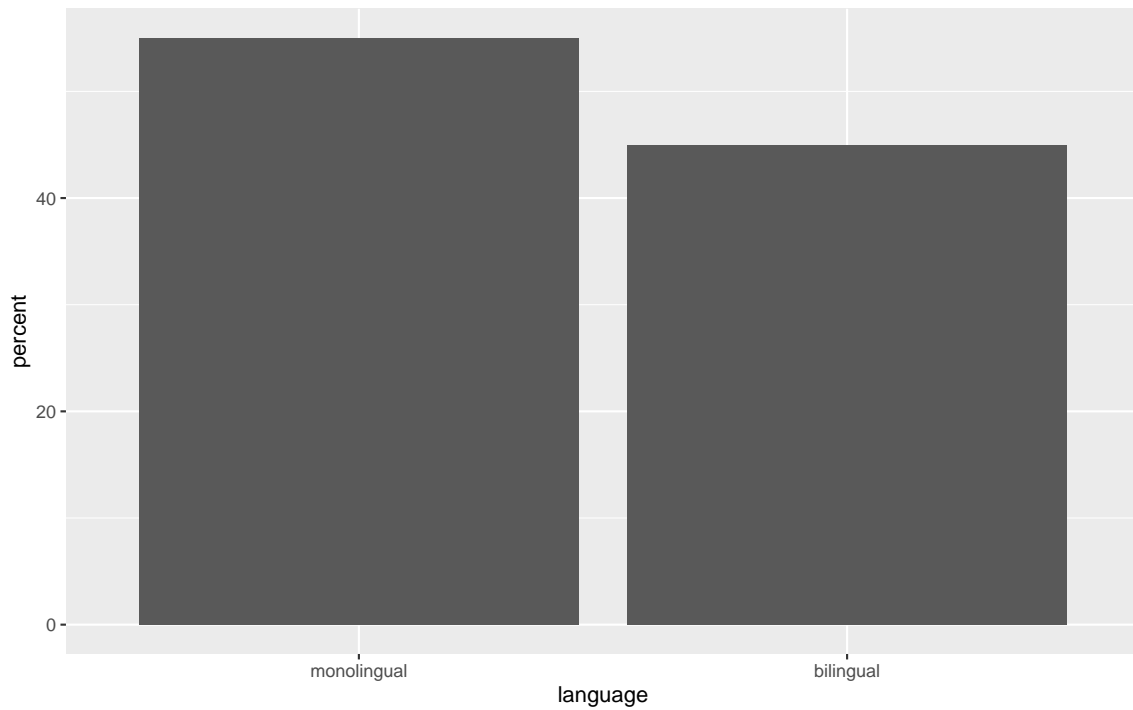
Figure 4. Bar chart of pre-calculated counts.

Histogram

The code to plot a histogram of `age` is very similar to the code used for the bar chart. We start by setting up the plot space, the dataset we want to use, and mapping the variables to the relevant axis. In this case, we want to plot a histogram with `age` on the x-axis:
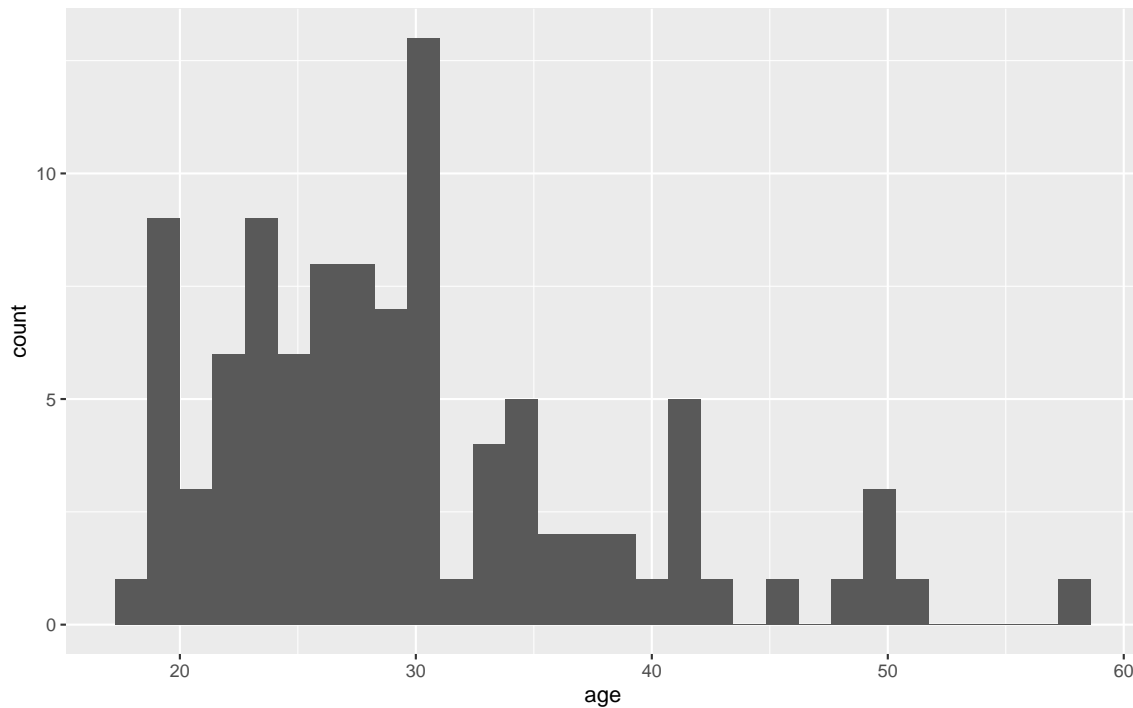
```
ggplot(dat, aes(x = age)) +
  geom_histogram()
```

Figure 5. Histogram of ages.

304   The base statistic for `geom_histogram()` is also count, and by default
305 `geom_histogram()` divides the x-axis into "bins" and counts how many observations are
306 in each bin and so the y-axis does not need to be specified. When you run the code
307 to produce the histogram, you will get the message `stat_bin() using bins = 30. Pick`
308 `better value with binwidth`. This means that, by default, `geom_histogram()` divides
309 the x-axis into 30 bins. You can change this by either setting the number of bins (e.g., `bins`
310 `= 20`) or the width of each bin (e.g., `binwidth = 5`) as an argument.

```
ggplot(dat, aes(x = age)) +
  geom_histogram(binwidth = 5)
```
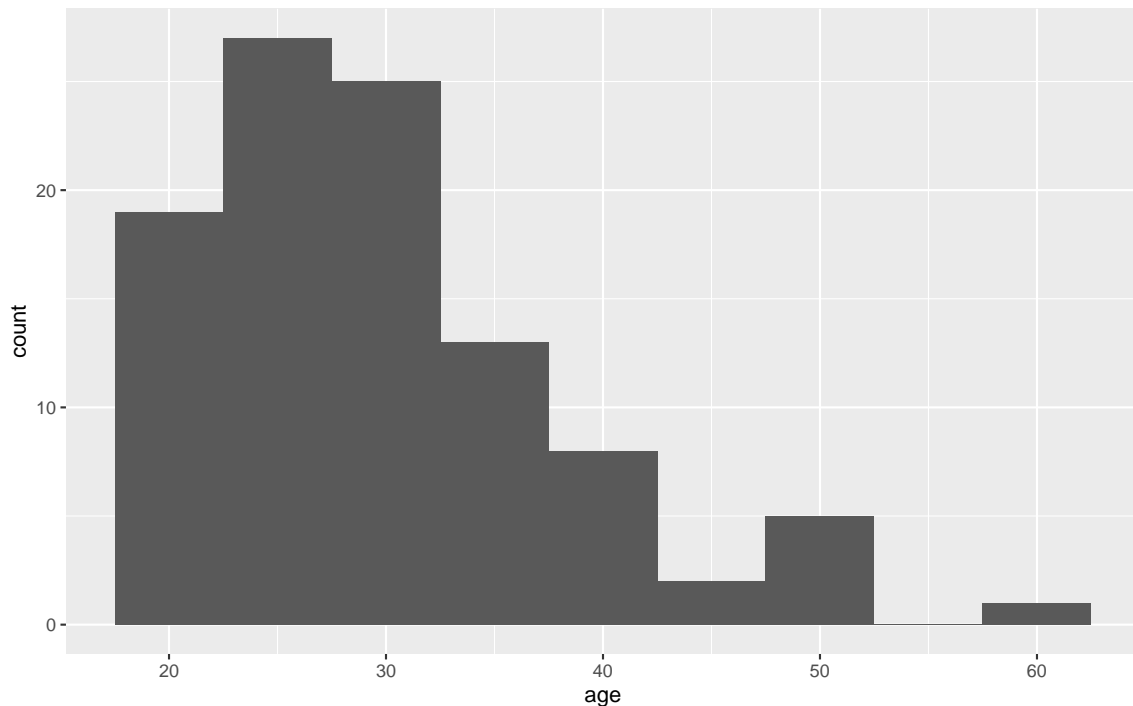
Figure 6. Histogram of ages where each bin covers five years.

Customisation 1

So far we have made basic plots with the default visual appearance. Before we move on to the experimental data we will introduce some simple visual customisation options. There are many ways in which you can control or customise the visual appearance of figures in R. However, once you understand the logic of one, it becomes easier to understand others that you may see in other examples. Visual appearance of elements can be customised within a geom itself, within the aesthetic mapping, or by connecting additional layers with `+`. In this section we look at the simplest and most commonly-used customisations: changing colours, adding axis labels, and adding themes.

Changing colours. For our basic bar chart, you can control colours used to display the bars by setting `fill` (internal colour) and `colour` (outline colour) inside the geom function. This methods changes **all** the bars; we will show you later how to set fill or colour separately for different groups.

```
ggplot(dat, aes(age)) +
  geom_histogram(binwidth = 1,
                 fill = "white",
                 colour = "black")
```
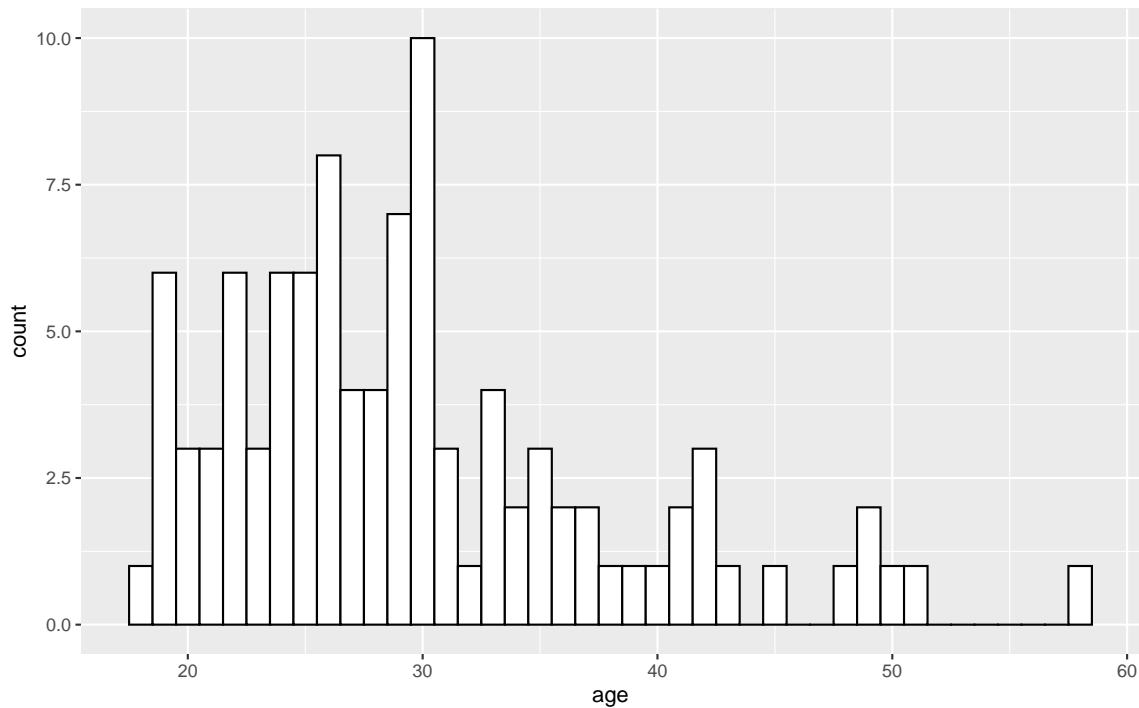
Figure 7. Histogram with custom colors for bar fill and line colors.

Editing axis names and labels.   To edit axis names and labels you can connect
`scale_*` functions to your plot with `+` to add layers. These functions are part of `ggplot2`
and the one you use depends on which aesthetic you wish to edit (e.g., x-axis, y-axis, fill,
colour) as well as the type of data it represents (discrete, continuous).

For the bar chart of counts, the x-axis is mapped to a discrete (categorical) variable
whilst the y-axis is continuous. For each of these there is a relevant scale function with
various elements that can be customised. Each axis then has its own function added as a
layer to the basic plot.

```
ggplot(dat, aes(language)) +
  geom_bar() +
  scale_x_discrete(name = "Language group",
                   labels = c("Monolingual", "Bilingual")) +
  scale_y_continuous(name = "Number of participants",
                     breaks = c(0,10,20,30,40,50))
```
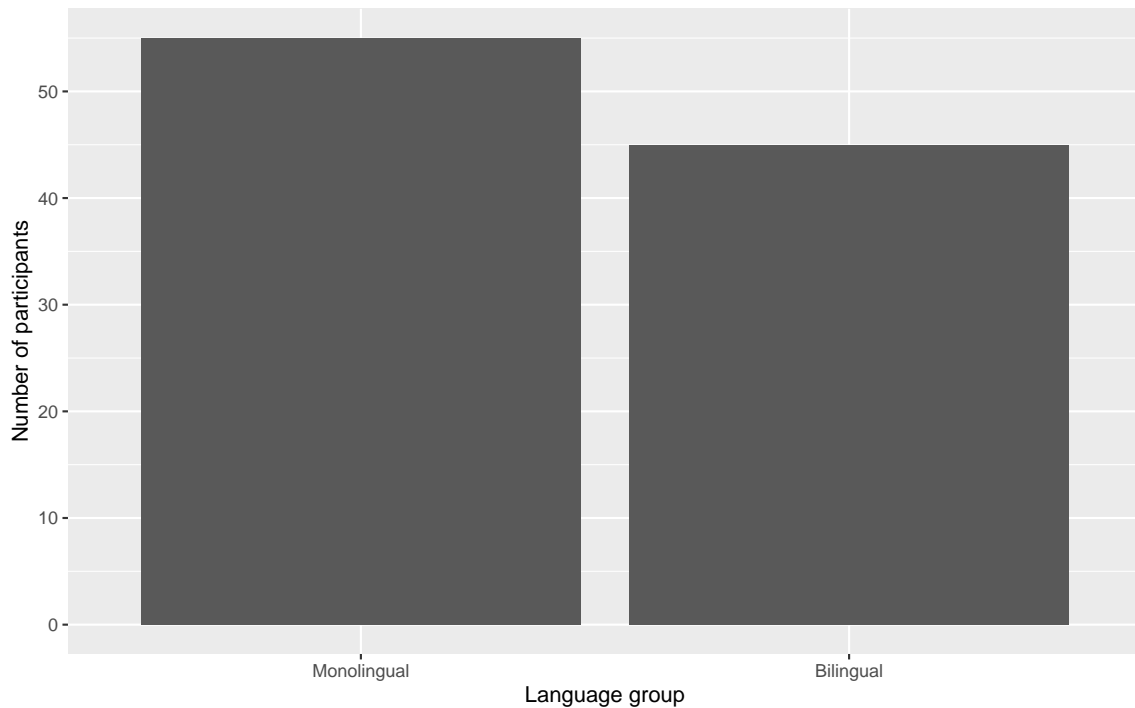
Figure 8. Bar chart with custom axis labels.

- **name** controls the overall name of the axis (note the use of quotation marks)

- **labels** controls the names of the conditions with a discrete variable.

- **c()** is a function that you will see in many different contexts and is used to combine multiple values. In this case, the labels we want to apply are combined within **c()** by enclosing each word within their own parenthesis, and are in the order displayed on the plot. A very common error is to forget to enclose multiple values in **c()**.

- **breaks** controls the tick marks on the axis. Again because there are multiple values, they are enclosed within **c()** although because they are numeric and not text, they do not need quotation marks.

Discrete vs. continuous errors. Another very common error is to map the wrong type of **scale_** function to a variable. Try running the below code:

```
# produces an error
ggplot(dat, aes(language)) +
  geom_bar() +
  scale_x_continuous(name = "Language group",
                     labels = c("Monolingual", "Bilingual"))
```

This will produce the error **Discrete value supplied to continuous scale** because we have used a **continuous** scale function, despite the fact that x-axis variable is

345 discrete. If you get this error (or the reverse), check the type of data on each axis and the
346 function you have used.

347   **Adding a theme.** ggplot2 has a number of built-in visual themes that you can
348 apply as an extra layer. The below code updates the x-axis and y-axis labels to the his-
349 togram, but also applies `theme_minimal()`. Each part of a theme can be independently
350 customised, which may be necessary, for example, if you have journal guidelines on fonts
351 for publication. There are further instructions for how to do this in the online appendices.

```r
ggplot(dat, aes(age)) +
  geom_histogram(binwidth = 1, fill = "wheat", color = "black") +
  scale_x_continuous(name = "Participant age (years)") +
  theme_minimal()
```
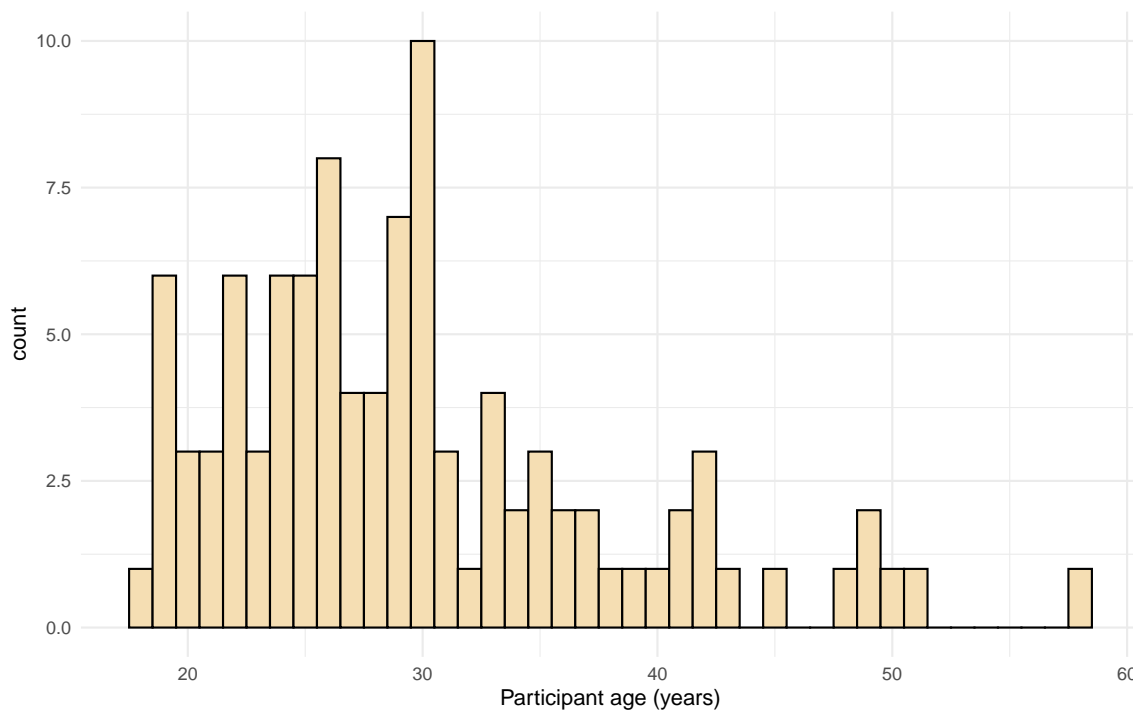

Figure 9. Histogram with a custom theme.

352   You can set the theme globally so that all subsequent plots use a theme.

```r
theme_set(theme_minimal())
```

353   If you wished to return to the default theme, change the above to specify
354 `theme_grey()`.

Activities 1

Before you move on try the following:

1. Add a layer that edits the **name** of the y-axis histogram label to `Number of participants`.

2. Change the colour of the bars in the bar chart to red.

3. Remove `theme_minimal()` from the histogram and instead apply one of the other available themes. To find out about other available themes, start typing `theme_` and the auto-complete will show you the available options - this will only work if you have loaded the `tidyverse` library with `library(tidyverse)`.

Transforming Data

Data formats

To visualise the experimental reaction time and accuracy data using `ggplot2`, we first need to reshape the data from wide-format to long-format and it is this step that can cause friction with novice users of R. Traditionally, psychologists have been taught data skills using wide-format data. Wide-format data typically has one row of data for each participant with separate columns for each score or variable. Where there are repeated-measures variables, the dependent variable is split across different columns with one measurement for each condition and where there is a between groups variable, a separate column is added to encode the group to which a participant or observation belongs.

The simulated lexical decision data is currently in wide-format (see Table 1) where each participant's aggregated[4] reaction time and accuracy for each level of the within-subject variable is split across multiple columns.

Wide-format is popular because it is intuitive to read and easy to enter data into as all the data for one participant is contained within a single row. However, for the purposes of analysis, and particularly for analysis using R, this format is unsuitable. Whilst it is intuitive to read by a human, the same is not true for a computer. Wide-format data concatenates multiple pieces of information in a single column, for example in Table 1, `rt_word` contains information related to both a DV and one level of an IV. In comparison, long-format data separates the DV from the IV's so that each column represents only one variable. The less intuitive part is that long data has multiple rows for each participant and a column that encodes the level of the IV (`word` or `nonword`). In essence, the long-format encodes repeated-measures variable in the same way as a between-group variable

---

[4]In this tutorial we have chosen to gloss over the data processing steps that must occur to get from the raw data to aggregated values. This type of processing requires a more extensive tutorial than we can provide in the current paper. More importantly, it is still possible to use R for data visualisation having done the preparatory steps using existing workflows in Excel and SPSS, so long as the file is saved/exported as a `.csv` file. We bypass these initial steps and focus on tangible outputs that may then encourage further mastery of reproducible methods. Collectively we tend to call the steps for reshaping data and for processing raw data or for getting data ready to use statistical functions "wrangling."

Table 1
Data in wide format.

id	age	language	rt_word	rt_nonword	acc_word	acc_nonword
S001	22	monolingual	379.46	516.82	99	90
S002	33	monolingual	312.45	435.04	94	82
S003	23	monolingual	404.94	458.50	96	87
S004	28	monolingual	298.37	335.89	92	76
S005	26	monolingual	316.42	401.32	91	83
S006	29	monolingual	357.17	367.34	96	78

Table 2
Data in the correct format for visualization.

id	age	language	condition	rt	acc
S001	22	monolingual	word	379.46	99
S001	22	monolingual	nonword	516.82	90
S002	33	monolingual	word	312.45	94
S002	33	monolingual	nonword	435.04	82
S003	23	monolingual	word	404.94	96
S003	23	monolingual	nonword	458.50	87

in SPSS. Wickham (2014) provides a comprehensive overview of the benefits of a similar format known as tidy data, which is a standard way of mapping a dataset to its structure, but for the purposes of this tutorial there are two important rules: each column should be a *variable* and each row should be an *observation.*

Moving from using wide-form to long-form datasets can require a conceptual shift on the part of the researcher and one that usually only comes with practice and repeated exposure[5]. For our example dataset, adhering to these rules for reshaping the data would produce Table 2. Rather than different observations of the same dependent variable being split across columns, there is now a single column for the DV reaction time, and a single column for the DV accuracy. Each participant now has multiple rows of data, one for each observation (i.e., for each participant there will be as many rows as there are levels of the within-subject IV). Although there is some repetition of age and language group, each row is unique when looking at the combination of measures.

The benefits and flexibility of this format will hopefully become apparent as we progress through the tutorial, however, a useful rule of thumb when working with data in R for visualisation is that *anything that shares an axis should probably be in the same column.* For example, a simple boxplot showing reaction time by condition would display the variable `condition` on the x-axis with bars representing both the `word` and `nonword` data, and `rt` on the y-axis. Therefore, all the data relating to `condition` should be in one column, and all the data relating to `rt` should be in a separate single column, rather than being split like in wide-format data.

---

[5]That is to say, if you are new to R, know that many before you have struggled with this conceptual shift - it does get better, it just takes time and your preferred choice of cursing.

Transforming data

⁴⁰⁹   We have chosen a 2 x 2 design with two DVs as we anticipate that this is a design
⁴¹⁰ many researchers will be familiar with and may also have existing datasets with a similar
⁴¹¹ structure. However, it is worth normalising that trial-and-error is part of the process of
⁴¹² learning how to apply these functions to new datasets and structures. Data visualisation
⁴¹³ can be a useful way to scaffold learning these data transformations because they can provide
⁴¹⁴ a concrete visual check as to whether you have done what you intended to do with your
⁴¹⁵ data.

⁴¹⁶   **Step 1: `pivot_longer()`.** The first step is to use the function `pivot_longer()`
⁴¹⁷ to transform the data to long-form. We have purposefully used a more complex dataset
⁴¹⁸ with two DVs for this tutorial to aid researchers applying our code to their own datasets.
⁴¹⁹ Because of this, we will break down the steps involved to help show how the code works.

⁴²⁰   This first code ignores that the dataset has two DVs, a problem we will fix in step 2.
⁴²¹ The pivot functions can be easier to show than tell - you may find it a useful exercise to
⁴²² run the below code and compare the newly created object `long` (Table 3) with the original
⁴²³ `dat` Table 1 before reading on.

```
long <- pivot_longer(data = dat,
                     cols = rt_word:acc_nonword,
                     names_to = "dv_condition",
                     values_to = "dv")
```

⁴²⁴ • As with the other tidyverse functions, the first argument specifies the dataset to use
⁴²⁵   as the base, in this case `dat`. This argument name is often dropped in examples.

⁴²⁶ • `cols` specifies all the columns you want to transform. The easiest way to visualise this
⁴²⁷   is to think about which columns would be the same in the new long-form dataset and
⁴²⁸   which will change. If you refer back to Table 1, you can see that `id`, `age`, and `language`
⁴²⁹   all remain, while the columns that contain the measurements of the DVs change. The
⁴³⁰   colon notation `first_column:last_column` is used to select all variables from the
⁴³¹   first column specified to the second. In our code, `cols` specifies that the columns we
⁴³²   want to transform are `rt_word` to `acc_nonword`.

⁴³³ • `names_to` specifies the name of the new column that will be created.

⁴³⁴ • Finally, `values_to` names the new column that will contain the measurements, in this
⁴³⁵   case we'll call it `dv`. At this point you may find it helpful to go back and compare `dat`
⁴³⁶   and `long` again to see how each argument matches up with the output of the table.

⁴³⁷   **Step 2: `pivot_longer()` adjusted.** The problem with the above long-form data-
⁴³⁸ set is that because we have ignored that there are two DVs, `dv_condition` still continues
⁴³⁹ to conflate two variables - it has information about the type of DV and the condition of
⁴⁴⁰ the IV. To account for this, we include a new argument `names_sep` and adjust `name_to` to
⁴⁴¹ specify the creation of two new columns. Note that we are pivoting the same wide-format
⁴⁴² dataset `dat` as we did in step 1.

Table 3
Data in long format with mixed DVs.

id	age	language	dv_condition	dv
S001	22	monolingual	rt_word	379.46
S001	22	monolingual	rt_nonword	516.82
S001	22	monolingual	acc_word	99.00
S001	22	monolingual	acc_nonword	90.00
S002	33	monolingual	rt_word	312.45
S002	33	monolingual	rt_nonword	435.04

Table 4
Data in long format with dv type and condition in separate columns.

id	age	language	dv_type	condition	dv
S001	22	monolingual	rt	word	379.46
S001	22	monolingual	rt	nonword	516.82
S001	22	monolingual	acc	word	99.00
S001	22	monolingual	acc	nonword	90.00
S002	33	monolingual	rt	word	312.45
S002	33	monolingual	rt	nonword	435.04

- `names_sep` specifies how to split up the variable name in cases where it has multiple components. This is when taking care to name your variables consistently and meaningfully pays off. Because the word to the left of the separator (`_`) is always the DV type and the word to the right is always the condition of the within-subject IV, it is easy to automatically split the columns.

- Note that when specifying more than one column name, they must be combined using `c()` and be enclosed in their own quotation marks.

```
long2 <- pivot_longer(data = dat,
                      cols = rt_word:acc_nonword,
                      names_sep = "_",
                      names_to = c("dv_type", "condition"),
                      values_to = "dv")
```

Step 3: `pivot_wider()`. Although we have now split the columns so that there are separate variables for the DV type and level of condition, because we have two DVs, there is an additional bit of wrangling required to get the data in the right format for plotting.

In the current long-form dataset, the column `dv` contains both reaction time and accuracy measures and keeping in mind the rule of thumb that *anything that shares an axis should probably be in the same column,* this creates a problem because we cannot plot two different units of measurement on the same axis. To fix this we need to use the function `pivot_wider()`. Again, we would encourage you at this point to compare `long2` and `dat_long` with the below code to try and map the connections before reading on.

```
dat_long <- pivot_wider(long2,
                        names_from = "dv_type",
                        values_from = "dv")
```

- The first argument is again the dataset you wish to work from, in this case `long2`. We have removed the argument name `data` in this example.

- `names_from` acts somewhat like the reverse of `names_to` from `pivot_longer()`. It will take the values from the variable specified and use these as variable names, i.e., in this case, the values of `rt` and `acc` that are currently in the `dv_type` column, and turn these into the column names.

- Finally, `values_from` specifies the values to fill the new columns with. In this case, the new columns `rt` and `acc` will be filled with the values that were in `dv`. Again, it can be helpful to compare each dataset with the code to see how it aligns.

This final long-form data should look like Table 2.

If you are working with a dataset with only one DV, note that only step 1 of this process would be necessary. Also, be careful not to calculate demographic descriptive statistics from this long-form dataset. Because the process of transformation has introduced some repetition for these variables, the wide-form dataset where 1 row = 1 participant should be used for demographic information. Finally, the three step process noted above is broken down for teaching purposes, in reality, one would likely do this in a single pipeline of code, for example:

```
dat_long <- pivot_longer(data = dat,
                         cols = rt_word:acc_nonword,
                         names_sep = "_",
                         names_to = c("dv_type", "condition"),
                         values_to = "dv") %>%
  pivot_wider(names_from = "dv_type",
              values_from = "dv")
```

Histogram 2

Now that we have the experimental data in the right form, we can begin to create some useful visualizations. First, to demonstrate how code recipes can be reused and adapted, we will create histograms of reaction time and accuracy. The below code uses the same template as before but changes the dataset (`dat_long`), the bin-widths of the histograms, the x variable to display (`rt/acc`), and the name of the x-axis.

```
ggplot(dat_long, aes(x = rt)) +
  geom_histogram(binwidth = 10, fill = "white", colour = "black") +
```

```
    scale_x_continuous(name = "Reaction time (ms)")

ggplot(dat_long, aes(x = acc)) +
  geom_histogram(binwidth = 1, fill = "white", colour = "black") +
  scale_x_continuous(name = "Accuracy (0-100)")
```
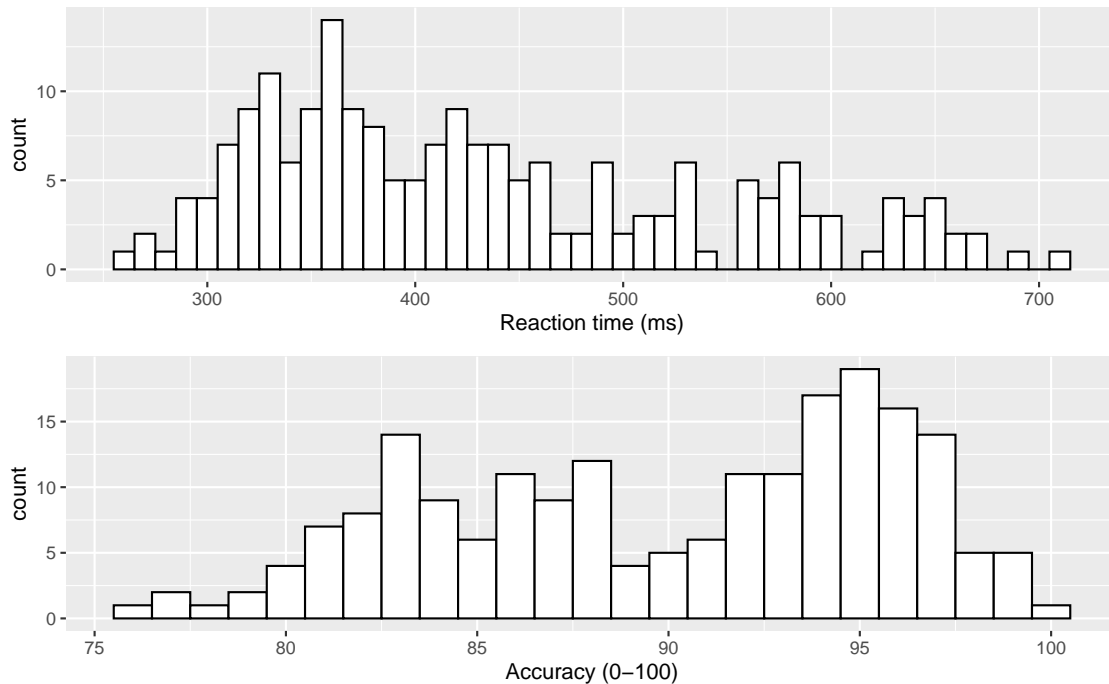

Figure 10. Histograms showing the distribution of reaction time (top) and accuracy (bottom)

Density plots

The layer system makes it easy to create new types of plots by adapting existing recipes. For example, rather than creating a histogram, we can create a smoothed density plot by calling `geom_density()` rather than `geom_histogram()`. The rest of the code remains identical.

```
ggplot(dat_long, aes(x = rt)) +
  geom_density()+
  scale_x_continuous(name = "Reaction time (ms)")
```
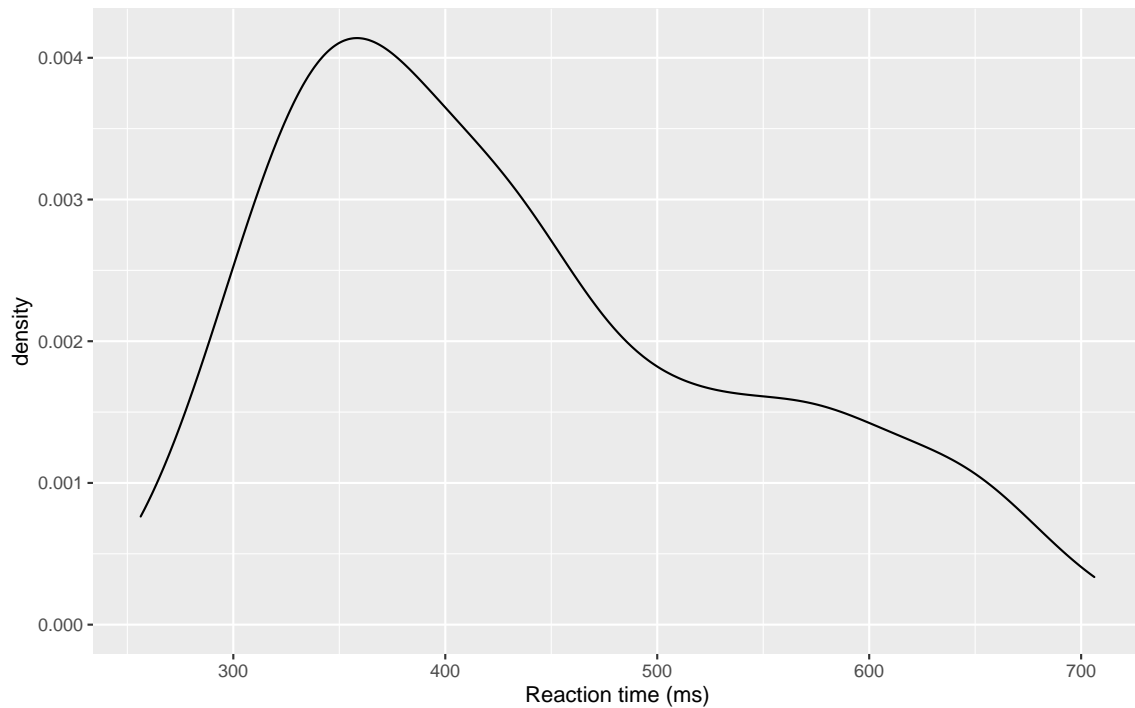
Figure 11. Density plot of reaction time.

487   **Grouped density plots.**   Density plots are most useful for comparing the distri-
488 butions of different groups of data. Because the dataset is now in long format, it makes it
489 easier to map another variable to the plot because each variable is contained within a single
490 column.

491 • In addition to mapping `rt` to the x-axis, we specify the `fill` aesthetic to fill the
492   visualisation of each level of the `condition` variable with different colours.
493 • Because the density plots are overlapping, we set `alpha = 0.75` to make the geoms
494   75% transparent.
495 • As with the x and y-axis scale functions, we can edit the names and labels of our fill
496   aesthetic by adding on another `scale_*` layer.
497 • Note that the `fill` here is set inside the `aes()` function, which tells ggplot to set
498   the fill differently for each value in the `condition` column. You cannot specify which
499   colour here (e.g., `fill="red"`), like you could when you set `fill` inside the `geom_*()`
500   function before.

```
ggplot(dat_long, aes(x = rt, fill = condition)) +
  geom_density(alpha = 0.75)+
  scale_x_continuous(name = "Reaction time (ms)") +
  scale_fill_discrete(name = "Condition",
                      labels = c("Word", "Non-word"))
```
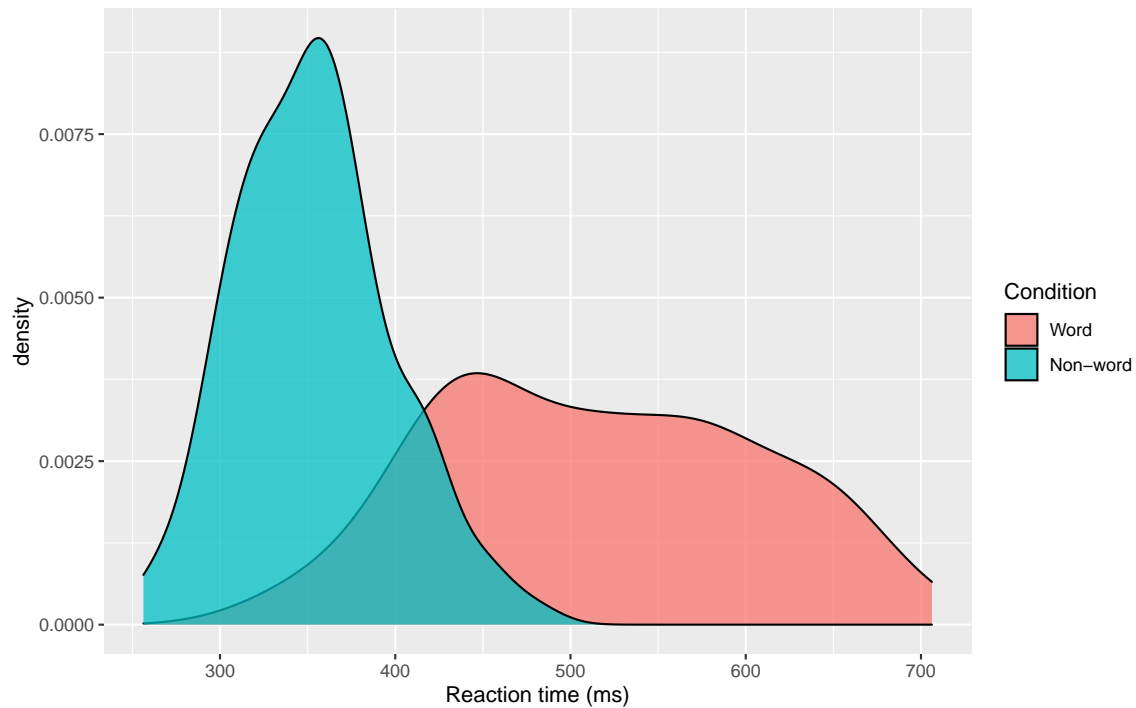
Figure 12. Density plot of reaction times grouped by condition.

Scatterplots

Scatterplots are created by calling `geom_point()` and require both an x and y variable to be specified in the mapping.

```
ggplot(dat_long, aes(x = rt, y = age)) +
  geom_point()
```
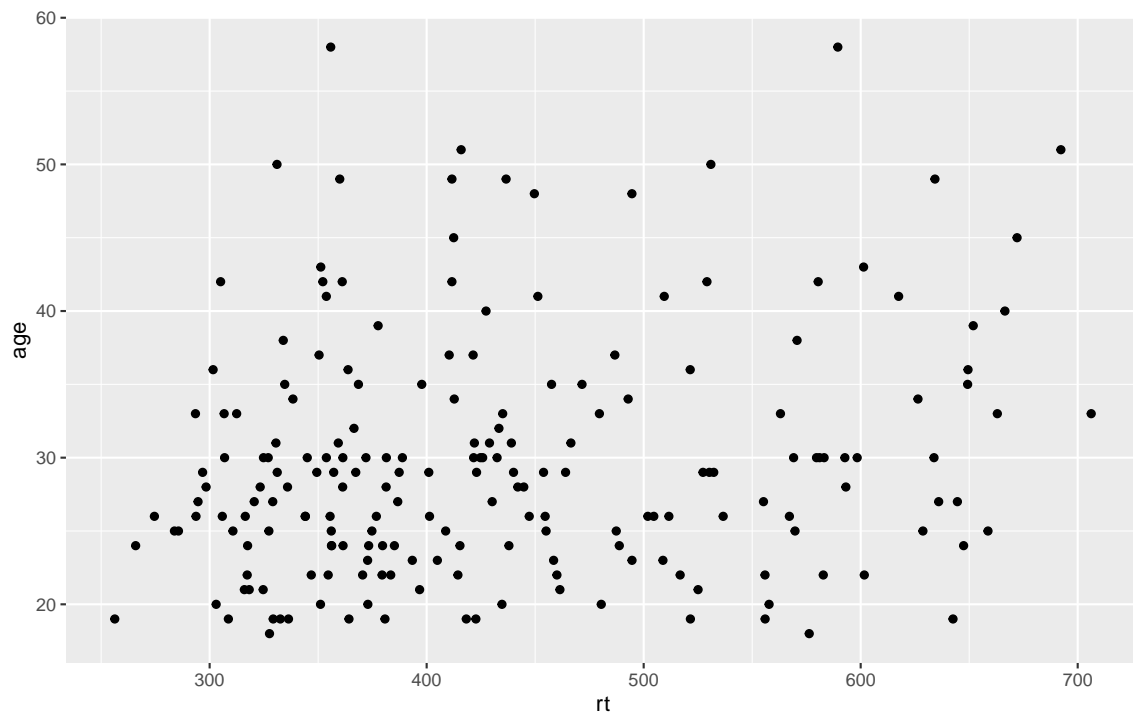
Figure 13. Point plot of reaction time versus age.

⁵⁰⁴ A line of best fit can be added with an additional layer that calls the function
⁵⁰⁵ geom_smooth(). The default is to draw a LOESS or curved regression line, however, a
⁵⁰⁶ linear line of best fit can be specified using method = "lm". By default, geom_smooth()
⁵⁰⁷ will also draw a confidence envelope around the regression line, this can be removed by
⁵⁰⁸ adding se = FALSE to geom_smooth(). A common error is to try and use geom_line() to
⁵⁰⁹ draw the line of best fit, which whilst a sensible guess, will not work (try it).

```
ggplot(dat_long, aes(x = rt, y = age)) +
  geom_point() +
  geom_smooth(method = "lm")
```

Figure 14. Line of best fit for reaction time versus age.

₅₁₀   **Grouped scatterplots.** Similar to the density plot, the scatterplot can also be
₅₁₁ easily adjusted to display grouped data. For `geom_point()`, the grouping variable is mapped
₅₁₂ to `colour` rather than `fill` and the relevant `scale_` function is added.

```r
ggplot(dat_long, aes(x = rt, y = age, colour = condition)) +
  geom_point() +
  geom_smooth(method = "lm") +
  scale_colour_discrete(name = "Condition",
                        labels = c("Word", "Non-word"))
```

Figure 15. Grouped scatter plot of reaction time versus age by condition.

513 **Transforming data 2**

514   Following the rule that *anything that shares an axis should probably be in the same*
515 *column* means that we will frequently need our data in long-form when using `ggplot2`,
516 however, there are some cases when wide-form is necessary. For example, we may wish to
517 visualise the relationship between reaction time in the word and non-word conditions. The
518 easiest way to achieve this in our case would simply be to use the original wide-form data
519 as the input:

```
ggplot(dat, aes(x = rt_word, y = rt_nonword, colour = language)) +
  geom_point() +
  geom_smooth(method = "lm")
```
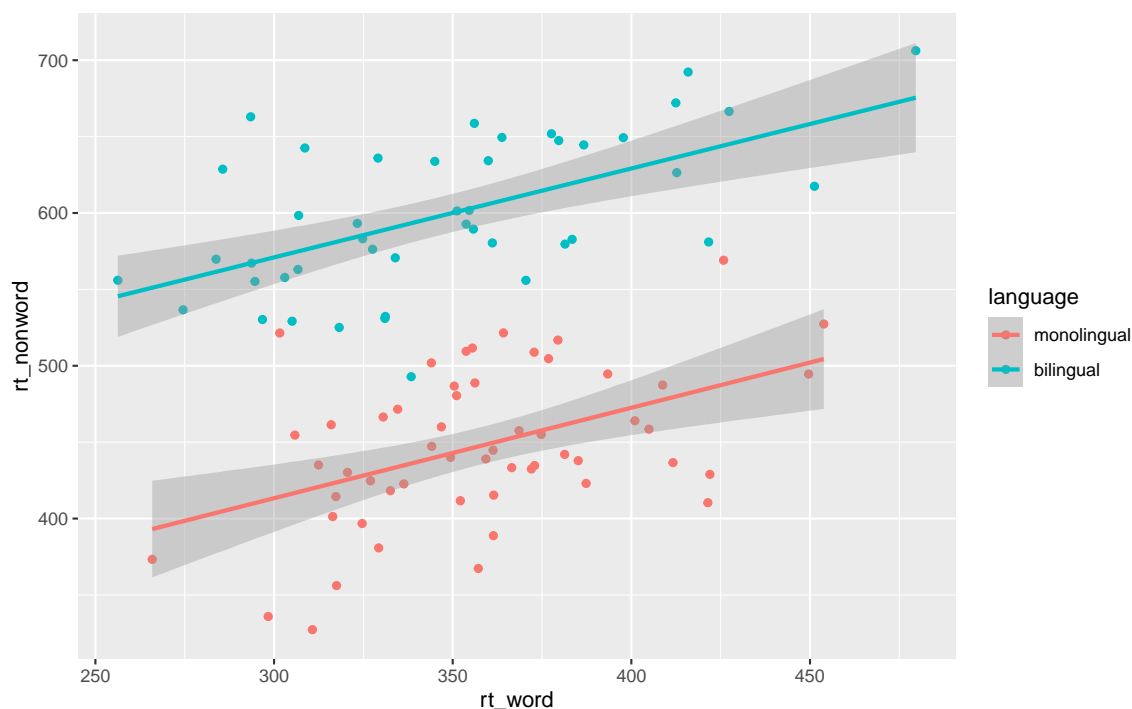
Figure 16. Scatterplot with data grouped by langauge group

520   However, there may also be cases when you do not have an original wide-form version
521 and you can use the `pivot_wider()` function to transform from long to wide.

```
dat_wide <- dat_long %>%
  pivot_wider(id_cols = "id",
              names_from = "condition",
              values_from = c(rt,acc))
```

id	rt_word	rt_nonword	acc_word	acc_nonword
S001	379.4585	516.8176	99	90
S002	312.4513	435.0404	94	82
S003	404.9407	458.5022	96	87
S004	298.3734	335.8933	92	76
S005	316.4250	401.3214	91	83
S006	357.1710	367.3355	96	78

Customisation 2

524   **Accessible colour schemes.**   One of the drawbacks of using `ggplot2` for visualisa-
525 tion is that the default colour scheme is not accessible (or visually appealing). The red and
526 green default palette is difficult for colour-blind people to differentiate, and also does not
527 display well in grey scale. You can specify exact custom colours for your plots, but one easy

528 option is to use a custom colour palette. These take the same arguments as their default
529 `scale` sister functions for updating axis names and labels, but display plots in contrasting
530 colours that can be read by colour-blind people and that also print well in grey scale. For
531 categorical colours, the "Set2," "Dark2" and "Paired" palettes from the `brewer` scale func-
532 tions are colourblind-safe. For continuous colours, such as when colour is representing the
533 magnitude of a correlation in a tile plot, the `viridis` scale functions provide a number of
534 different colourblind and greyscale-safe options.

```
ggplot(dat_long, aes(x = rt, y = age, colour = condition)) +
  geom_point() +
  geom_smooth(method = "lm") +
  scale_color_brewer(palette = "Dark2",
                     name = "Condition",
                     labels = c("Word", "Non-word"))
```
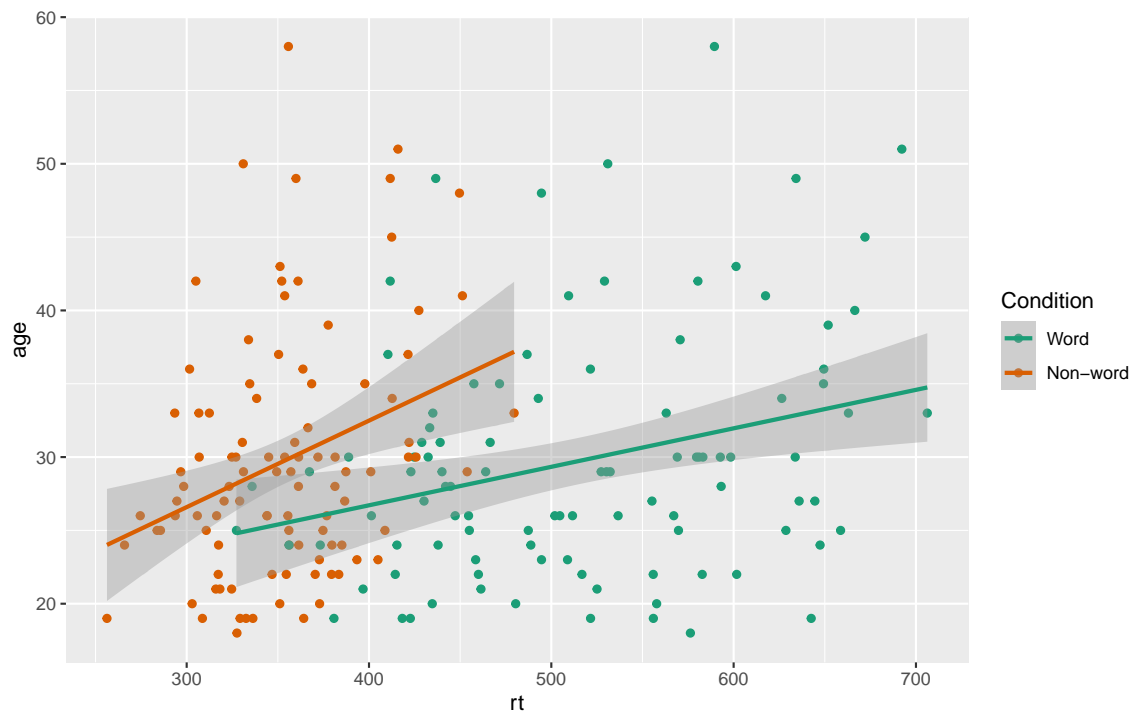

Figure 17. Use the Dark2 brewer colour scheme for accessibility.

535 **Specifying axis `breaks` with `seq()`**

536   Previously, when we have edited the `breaks` on the axis labels, we have done so
537 manually, typing out all the values we want to display on the axis. For example, the below
538 code edits the y-axis so that `age` is displayed in increments of 5.

```
ggplot(dat_long, aes(x = rt, y = age)) +
  geom_point() +
  scale_y_continuous(breaks = c(20,25,30,35,40,45,50,55,60))
```
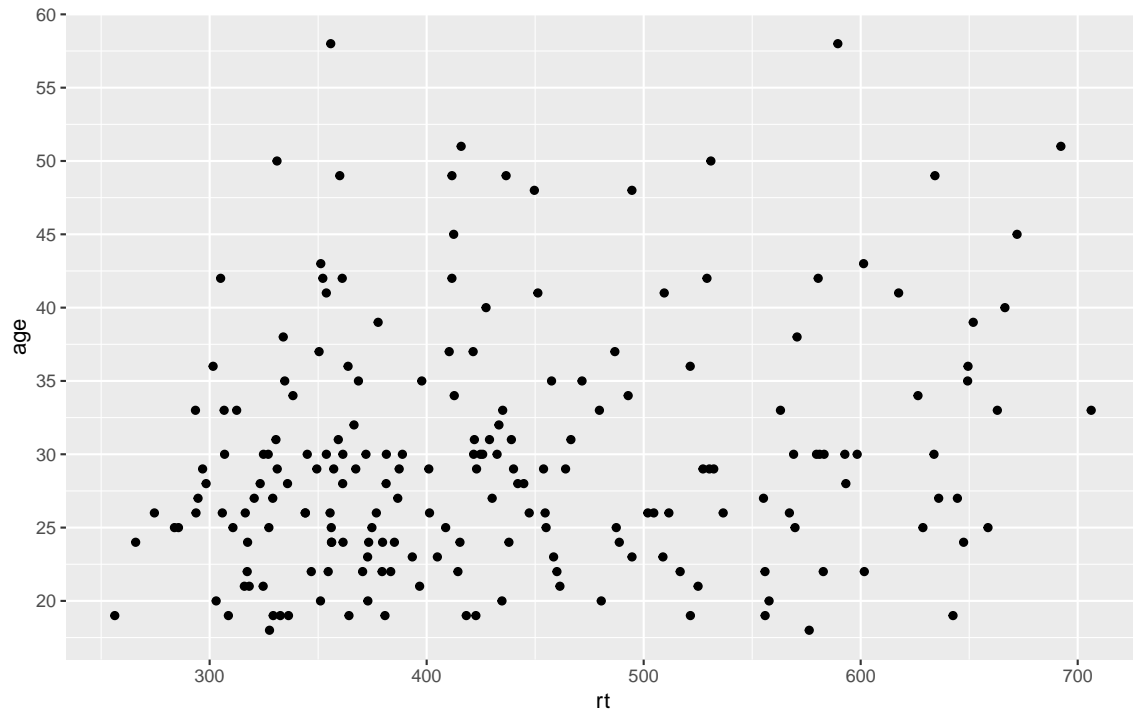

Figure 18

539   However, this is somewhat inefficient. Instead, we can use the function `seq()` to
540 specify the first and last value and the increments `by` which the breaks should display
541 between these two values.

```
ggplot(dat_long, aes(x = rt, y = age)) +
  geom_point() +
  scale_y_continuous(breaks = seq(20,60, by = 5))
```
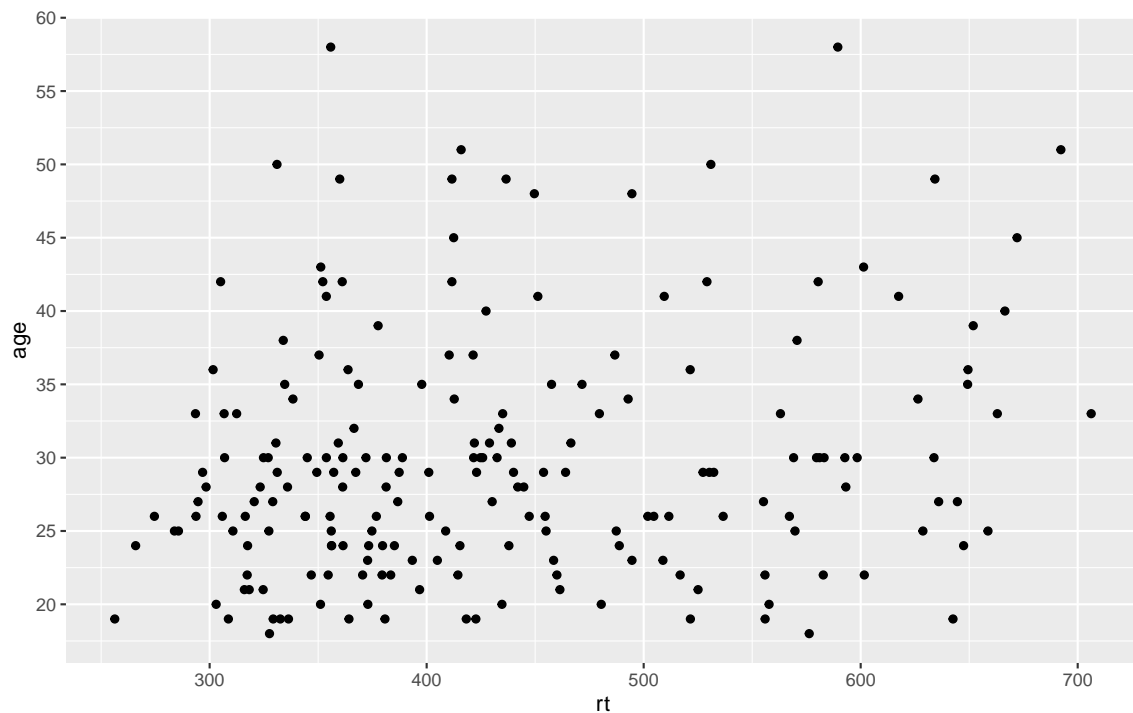
Figure 19

542 **Activities 2**

543   Before you move on try the following:

544   1. Use `fill` to created grouped histograms that display the distributions for `rt` for each
545   `language` group separately and also edit the fill axis labels. Try adding `position =`
546   `"dodge"` to `geom_histogram()` to see what happens.

547   2. Use `scale_*_*()` functions to edit the name of the x and y-axis on the scatterplot

548   3. Use `se = FALSE` to remove the confidence envelope from the scatterplots

549   4. Remove `method = "lm"` from `geom_smooth()` to produce a curved regression line.

550   5. Replace the default `scale_fill_*()` on the grouped density plot with a colour-blind
551   friendly version.

552   **Representing Summary Statistics**

553   The layering approach that is used in `ggplot2` to make figures comes into its own
554 when you want to include information about the distribution and spread of scores. In this
555 section we introduce different ways of including summary statistics on your figures.

⁵⁵⁶ **Boxplots**

⁵⁵⁷   As with `geom_point()`, the boxplot geom also require an x and y-variable to be
⁵⁵⁸ specified. In this case, x must be a discrete, or categorical variable, whilst y must be
⁵⁵⁹ continuous.

```
ggplot(dat_long, aes(x = condition, y = acc)) +
  geom_boxplot()
```
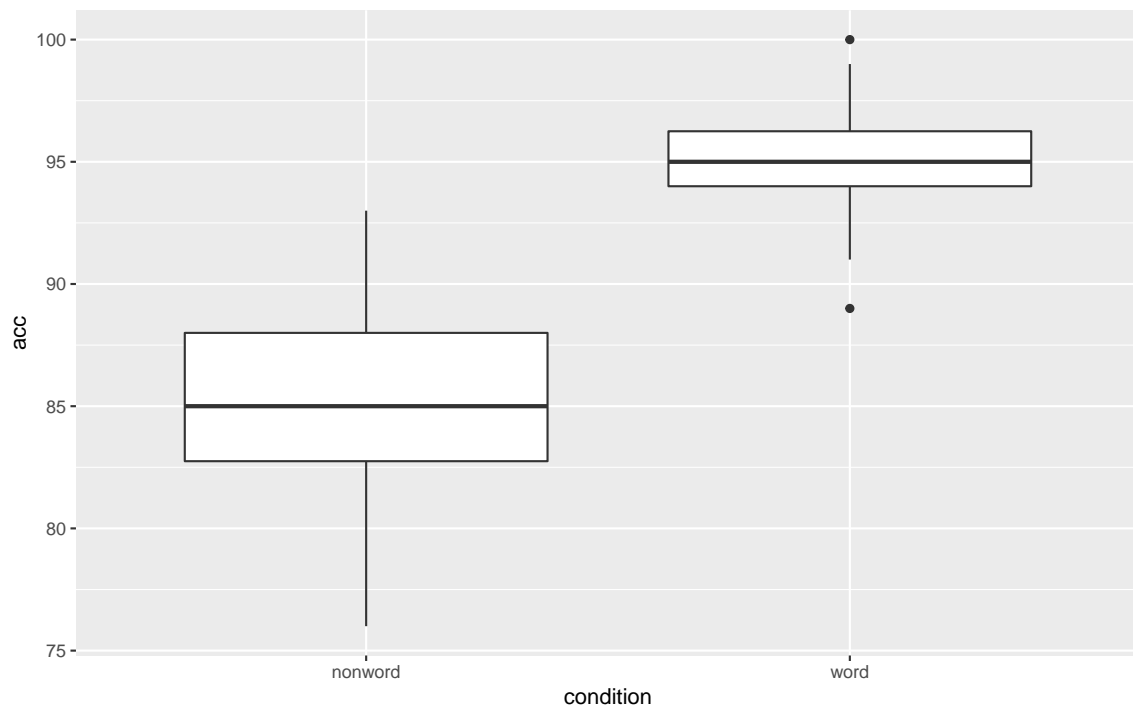

Figure 20. Basic boxplot.

⁵⁶⁰   **Grouped boxplots.** As with histograms and density plots, `fill` can be used to
⁵⁶¹ create grouped boxplots. This looks like a lot of complicated code at first glance, but most
⁵⁶² of it is just editing the axis labels.

```
ggplot(dat_long, aes(x = condition, y = acc, fill = language)) +
  geom_boxplot() +
  scale_fill_brewer(palette = "Dark2",
                    name = "Group",
                    labels = c("Bilingual", "Monolingual")) +
  theme_classic() +
  scale_x_discrete(name = "Condition",
                   labels = c("Word", "Non-word")) +
  scale_y_continuous(name = "Accuracy")
```
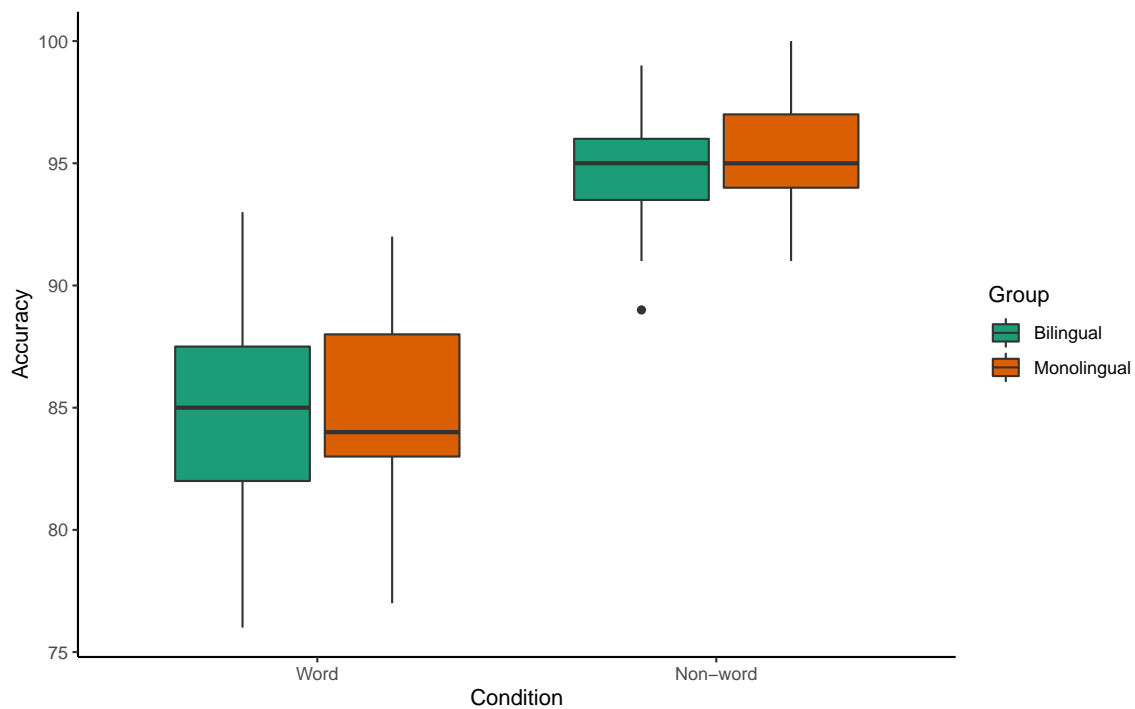
Figure 21. Grouped boxplots

Violin plots

Violin plots display the distribution of a dataset and can be created by calling `geom_violin()`. They are so-called because the shape they make sometimes looks something like a violin. They are essentially a mirrored density plot on its side. Note that the below code is identical to the code used to draw the boxplots above, except for the call to `geom_violin()` rather than `geom_boxplot()`.

```
ggplot(dat_long, aes(x = condition, y = acc, fill = language)) +
  geom_violin() +
  scale_fill_brewer(palette = "Dark2",
                    name = "Group",
                    labels = c("Bilingual", "Monolingual")) +
  theme_classic() +
  scale_x_discrete(name = "Condition",
                   labels = c("Word", "Non-word")) +
  scale_y_continuous(name = "Accuracy")
```
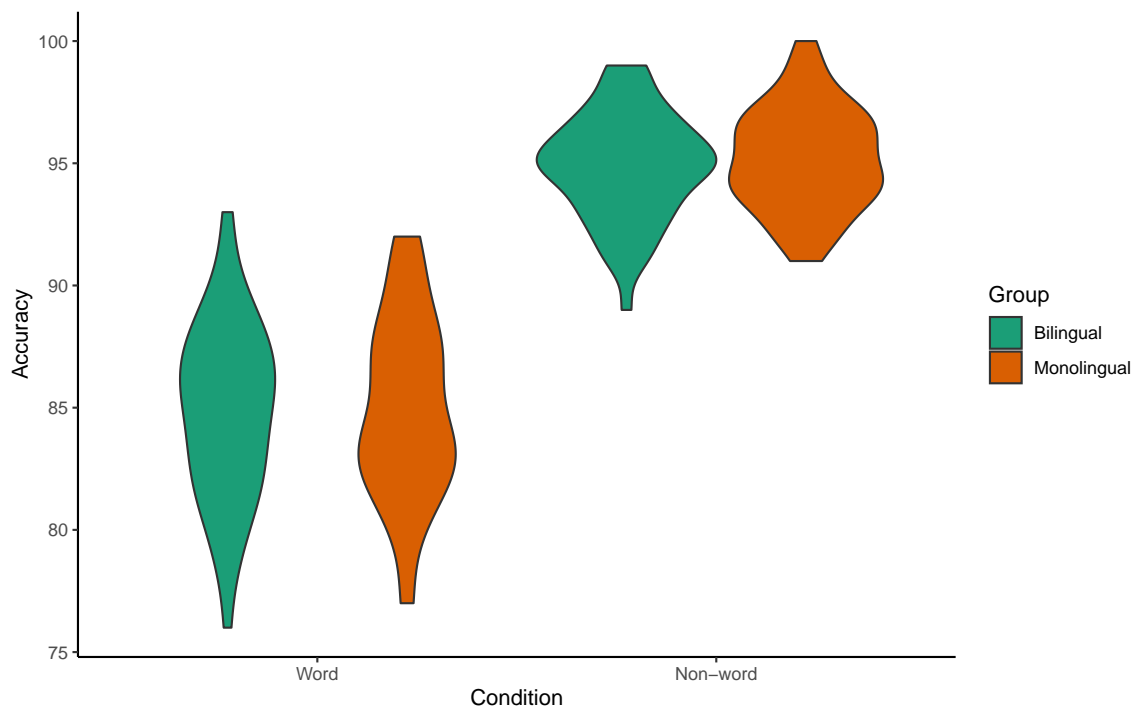
Figure 22. Violin plot.

Bar chart of means

⁵⁷⁰ Commonly, rather than visualising distributions of raw data researchers will wish
⁵⁷¹ to visualise means using a bar chart with error bars. As with SPSS and Excel, `ggplot2`
⁵⁷² requires you to calculate the summary statistics and then plot the summary. There are at
⁵⁷³ least two ways to do this, in the first you make a table of summary statistics as we did
⁵⁷⁴ earlier when calculating the participant demographics and then plot that table. The second
⁵⁷⁵ approach is to calculate the statistics within a layer of the plot. That is the approach we
⁵⁷⁶ will use below.

⁵⁷⁷ First we present code for making a bar chart. The code for bar charts is here because
⁵⁷⁸ it is a common visualisation that is familiar to most researchers, however, we would urge
⁵⁷⁹ you to use a visualisation that provides more transparency about the distribution of the
⁵⁸⁰ raw data, such as the violin-boxplots we will present in the next section.

⁵⁸¹ To summarise the data into means we use a new function `stat_summary`. Rather than
⁵⁸² calling a `geom_*` function, we call `stat_summary()` and specify how we want to summarise
⁵⁸³ the data and how we want to present that summary in our figure.

⁵⁸⁴ • `fun` specifies the summary function that gives us the y-value we want to plot, in this
⁵⁸⁵   case, `mean`.

⁵⁸⁶ • `geom` specifies what shape or plot we want to use to display the summary. For the
⁵⁸⁷   first layer we will specify `bar`. As with the other geom-type functions we have shown

588 you, this part of the `stat_summary()` function is tied to the aesthetic mapping in the
589 first line of code. The underlying statistics for a bar chart means that we must specify
590 and IV (x-axis) as well as the DV (y-axis).

```
ggplot(dat_long, aes(x = condition, y = rt)) +
  stat_summary(fun = "mean", geom = "bar")
```
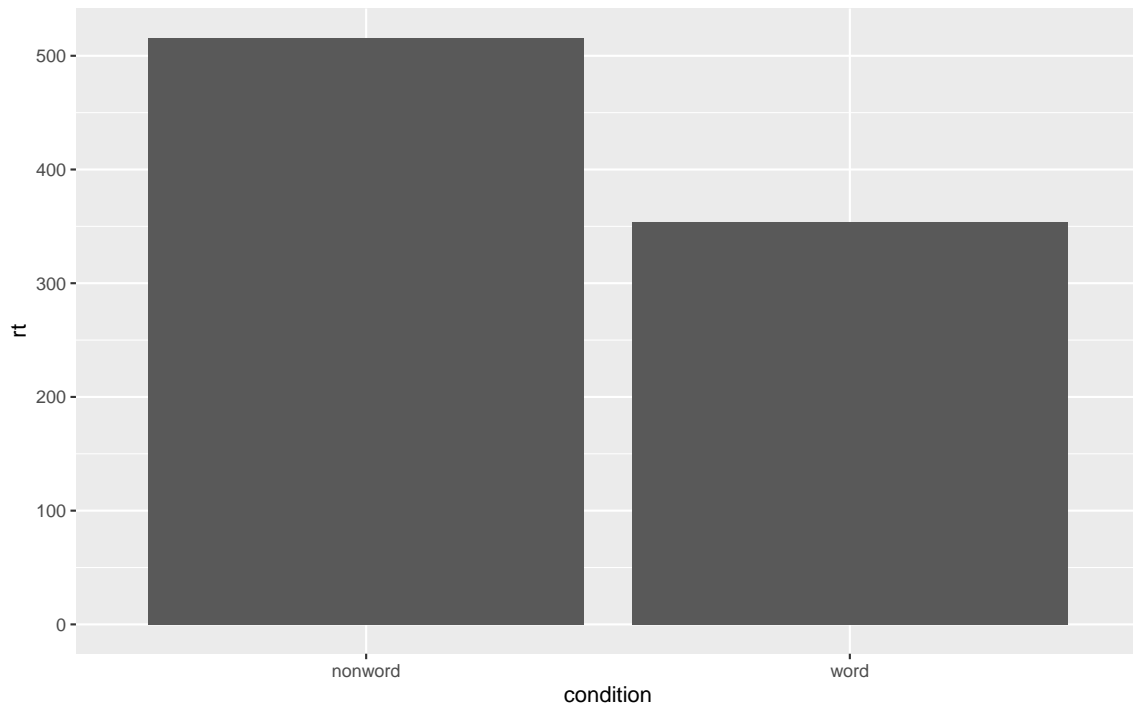

Figure 23. Bar plot of means.

591 To add the error bars, another layer is added with a second call to `stat_summary`.
592 This time, the function represents the type of error bars we wish to draw, you can choose
593 from `mean_se` for standard error, `mean_cl_normal` for confidence intervals, or `mean_sdl` for
594 standard deviation. `width` controls the width of the error bars - try changing the value to
595 see what happens.

596 • Whilst `fun` returns a single value (y) per condition, `fun.data` returns the y-values we
597   want to plot plus their minimum and maximum values, in this case, `mean_se`

```
ggplot(dat_long, aes(x = condition, y = rt)) +
  stat_summary(fun = "mean", geom = "bar") +
  stat_summary(fun.data = "mean_se",
               geom = "errorbar",
               width = .2)
```
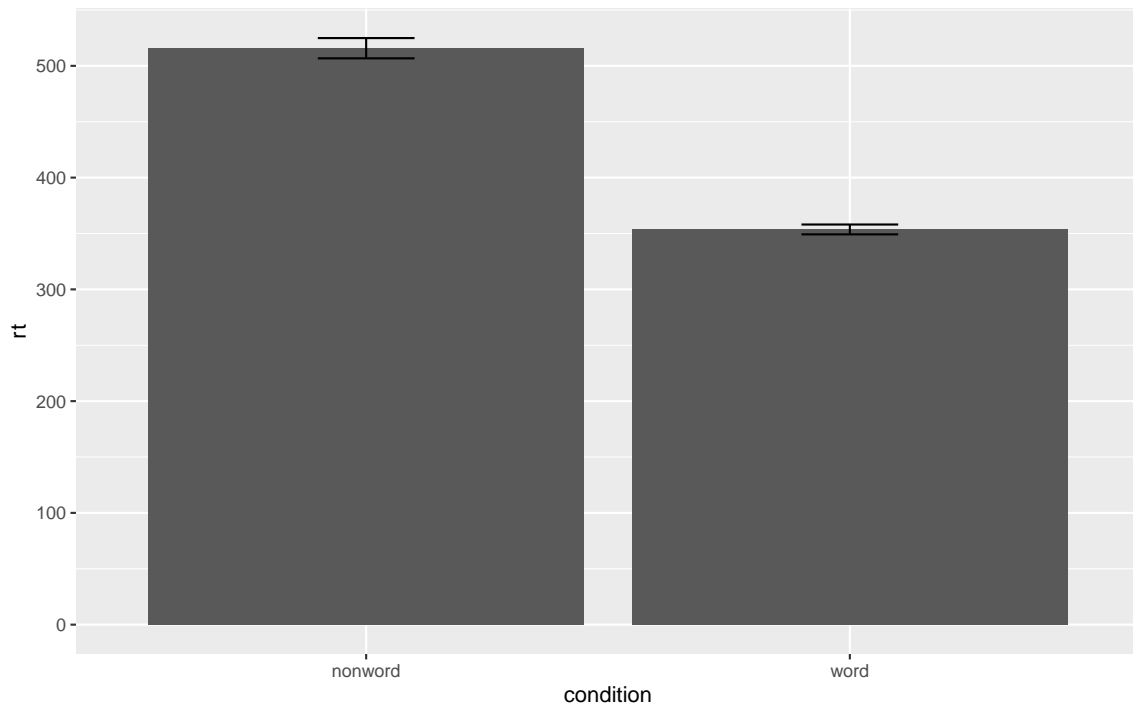
Figure 24. Bar plot of means with error bars representing SE.

Violin-boxplot

The power of the layered system for making figures is further highlighted by the ability to combine different types of plots. For example, rather than using a bar chart with error bars, one can easily create a single plot that includes density of the distribution, confidence intervals, means and standard errors. In the below code we first draw a violin plot, then layer on a boxplot, a point for the mean (note `geom = "point"` instead of `"bar"`) and standard error bars (`geom = "errorbar"`). This plot does not require much additional code to produce than the bar plot with error bars, yet the amount of information displayed is vastly superior.

- `fatten = NULL` in the boxplot geom removes the median line, which can make it easier to see the mean and error bars. Including this argument will result in the warning message `Removed 1 rows containing missing values (geom_segment)` and is not a cause for concern. Removing this argument will reinstate the median line.

```
ggplot(dat_long, aes(x = condition, y= rt)) +
  geom_violin() +
  # remove the median line with fatten = NULL
  geom_boxplot(width = .2,
               fatten = NULL) +
  stat_summary(fun = "mean", geom = "point") +
```

```
stat_summary(fun.data = "mean_se",
             geom = "errorbar",
             width = .1)
```
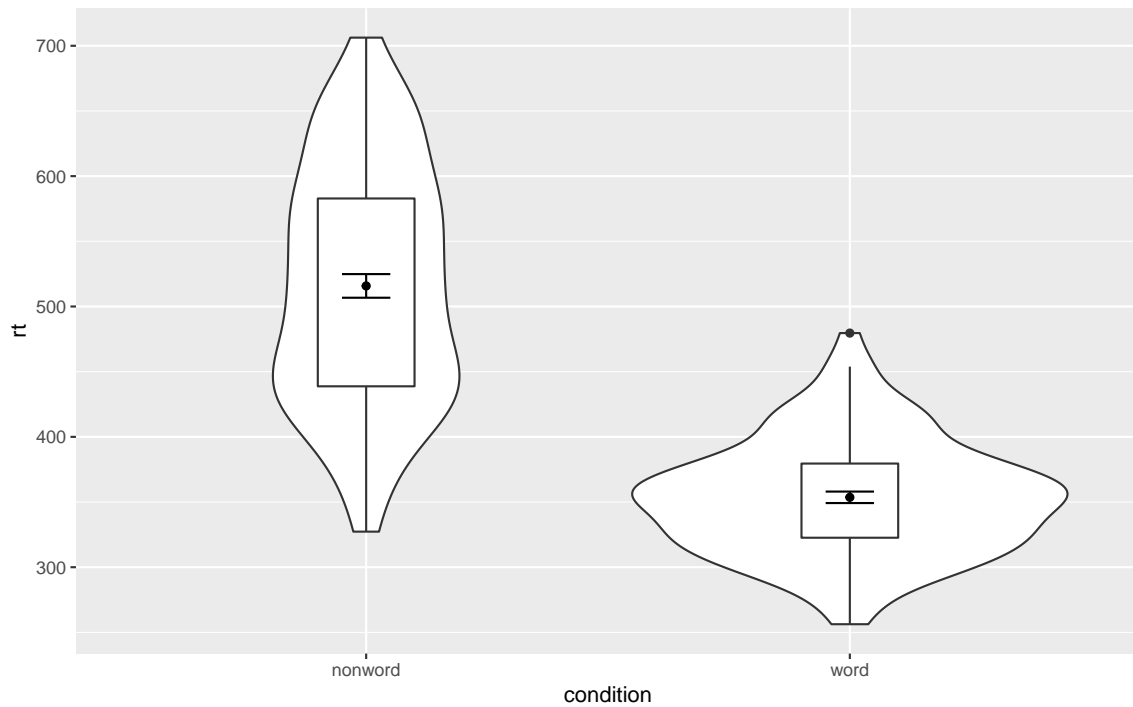

Figure 25. Violin-boxplot with mean dot and standard error bars.

⁶¹¹   It is important to note that the order of the layers matters and it is worth experiment-
⁶¹²   ing with the order to see where the order matters. For example, if we call `geom_boxplot()`
⁶¹³   followed by `geom_violin()`, we get the following mess:

```
ggplot(dat_long, aes(x = condition, y= rt)) +
  geom_boxplot() +
  geom_violin() +
  stat_summary(fun = "mean",  geom = "point") +
  stat_summary(fun.data = "mean_se",
               geom = "errorbar",
               width = .1)
```
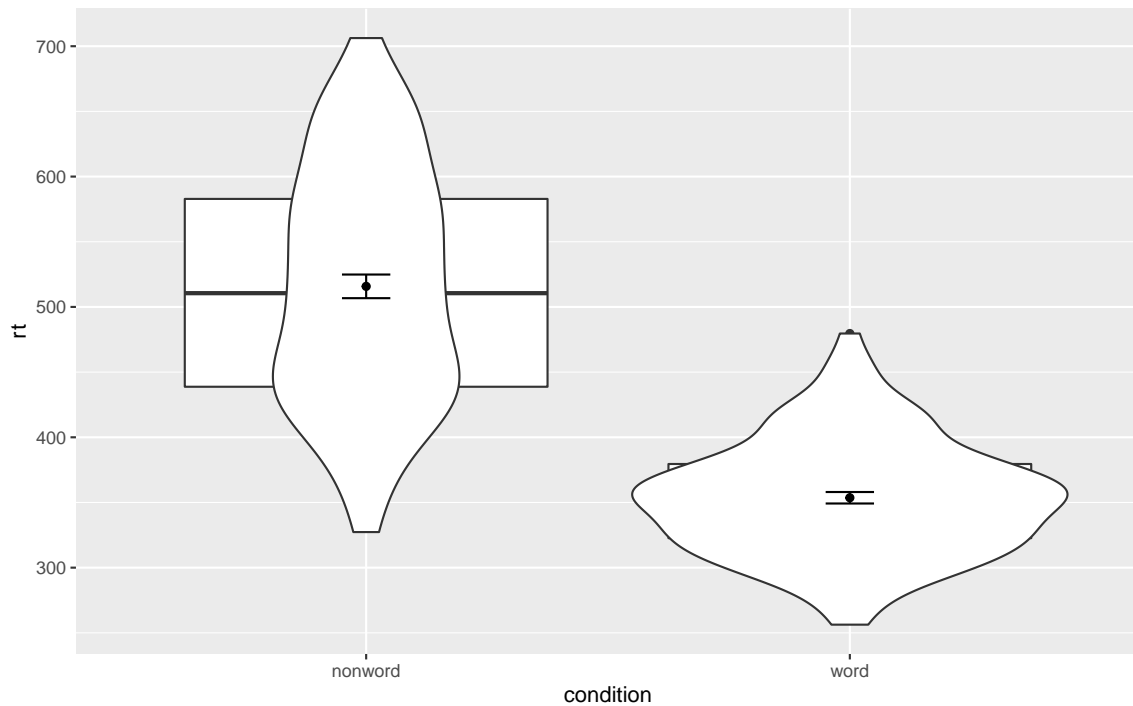
Figure 26. Plot with the geoms in the wrong order.

⁶¹⁴   **Grouped violin-boxplots.** As with previous plots, another variable can be
⁶¹⁵ mapped to `fill` for the violin-boxplot. (Remember to add a colourblind-safe palette.)
⁶¹⁶ However, simply adding `fill` to the mapping causes the different components of the plot
⁶¹⁷ to become misaligned because they have different default positions:

```
ggplot(dat_long, aes(x = condition, y= rt, fill = language)) +
  geom_violin() +
  geom_boxplot(width = .2,
               fatten = NULL) +
  stat_summary(fun = "mean",  geom = "point") +
  stat_summary(fun.data = "mean_se",
               geom = "errorbar",
               width = .1) +
  scale_fill_brewer(palette = "Dark2")
```
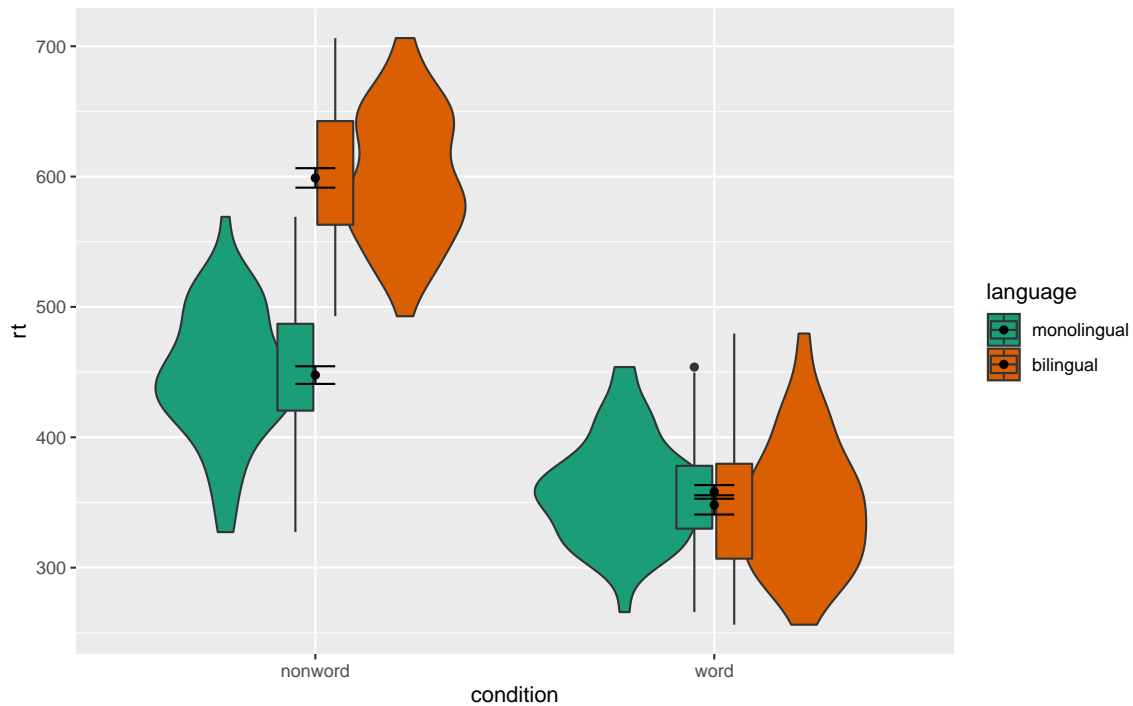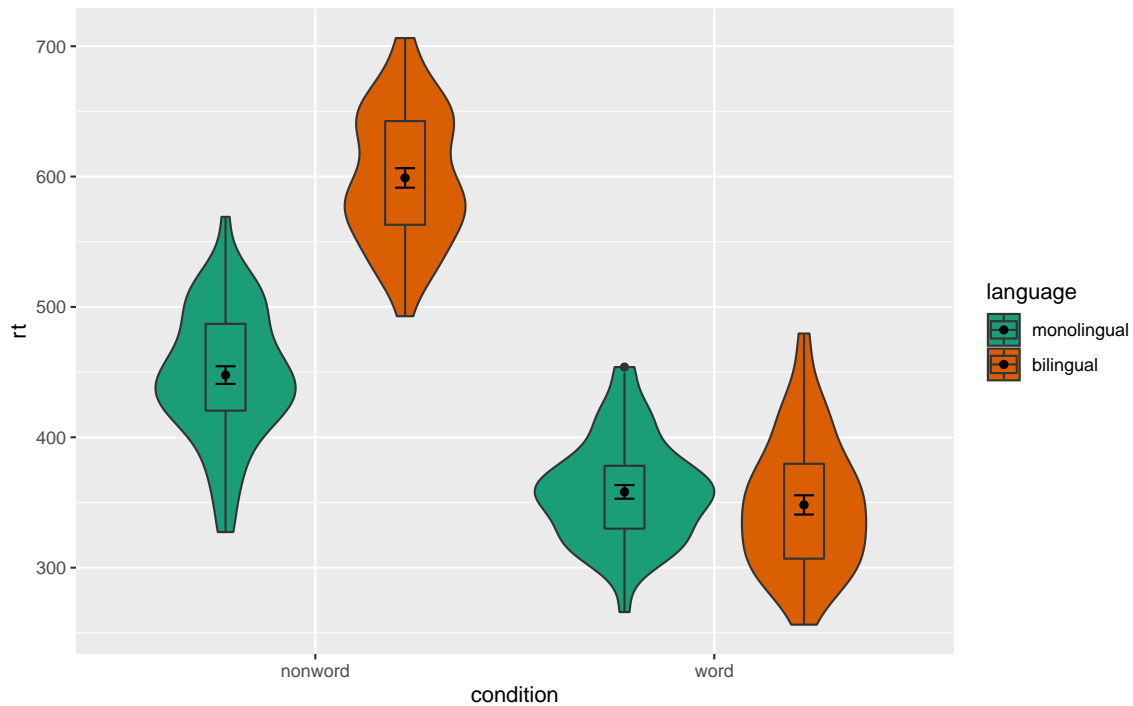
Figure 27. Grouped violin-boxplots without repositioning.

618   To rectify this we need to adjust the argument `position` for each of the misaligned
619 layers. `position_dodge()` instructs R to move (dodge) the position of the plot component
620 by the specified value; finding what value looks best can sometimes take trial and error.

```r
# set the offset position of the geoms
pos <- position_dodge(0.9)

ggplot(dat_long, aes(x = condition, y= rt, fill = language)) +
  geom_violin(position = pos) +
  geom_boxplot(width = .2,
               fatten = NULL,
               position = pos) +
  stat_summary(fun = "mean",
               geom = "point",
               position = pos) +
  stat_summary(fun.data = "mean_se",
               geom = "errorbar",
               width = .1,
               position = pos) +
  scale_fill_brewer(palette = "Dark2")
```

Figure 28. Grouped violin-boxplots with repositioning.

Customisation part 3

Combining multiple type of plots can present an issue with the colours, particularly when the fill and line colours are similar. For example, it is hard to make out the boxplot against the violin plot above.

There are a number of solutions to this problem. One solution is to adjust the transparency of each layer using `alpha`. The exact values needed can take trial and error:

```r
ggplot(dat_long, aes(x = condition, y= rt, fill = language,
                     group = paste(condition, language))) +
  geom_violin(alpha = 0.25, position = pos) +
  geom_boxplot(width = .2,
               fatten = NULL,
               alpha = 0.75,
               position = pos) +
  stat_summary(fun = "mean",
               geom = "point",
               position = pos) +
  stat_summary(fun.data = "mean_se",
               geom = "errorbar",
               width = .1,
               position = pos) +
```

```
scale_fill_brewer(palette = "Dark2")
```
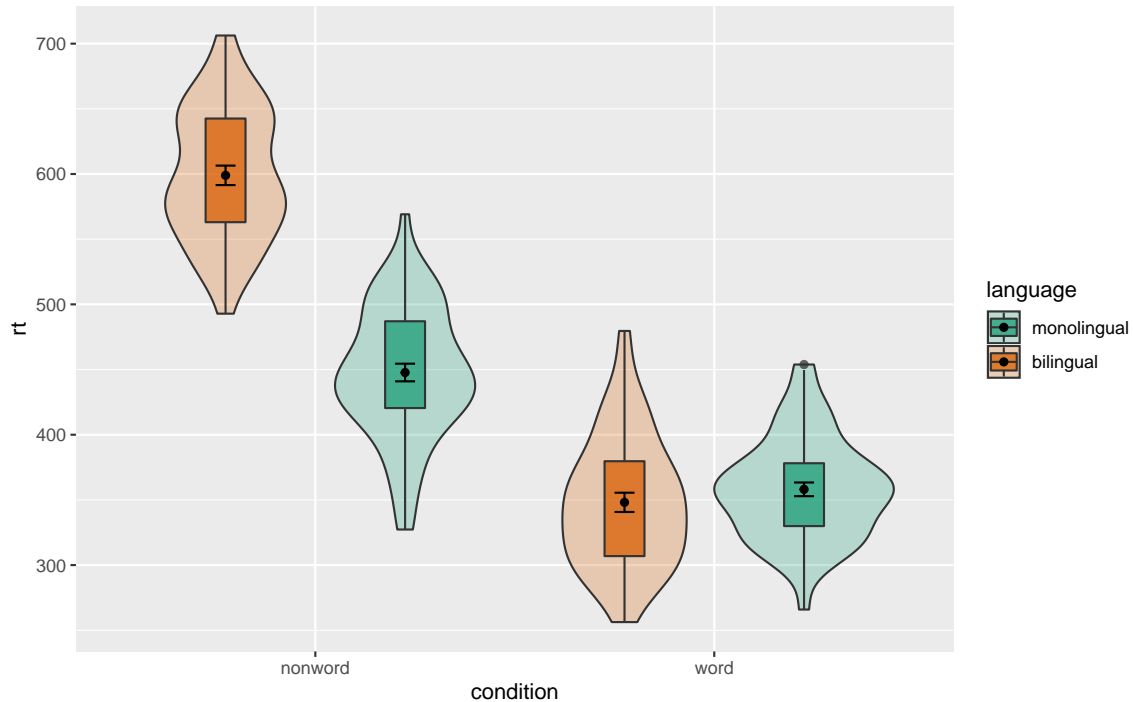

Figure 29. Using transparency on the fill color.

627   Alternatively, we can change the fill of individual geoms by adding `fill = "colour"`
628 to each relevant geom. In the example below, we fill the boxplots with white. Since all
629 of the boxplots are no longer being filled according to language, but you still want a four
630 separate boxplots, you have to add an extra mapping to `geom_boxplot()` to specify that
631 you want the output grouped by the interaction of condition and language.

```
ggplot(dat_long, aes(x = condition, y= rt, fill = language)) +
  geom_violin(position = pos) +
  geom_boxplot(width = .2, fatten = NULL,
               mapping = aes(group = interaction(condition, language)),
               fill = "white",
               position = pos) +
  stat_summary(fun = "mean",
               geom = "point",
               position = pos) +
  stat_summary(fun.data = "mean_se",
               geom = "errorbar",
               width = .1,
               position = pos) +
  scale_fill_brewer(palette = "Dark2")
```
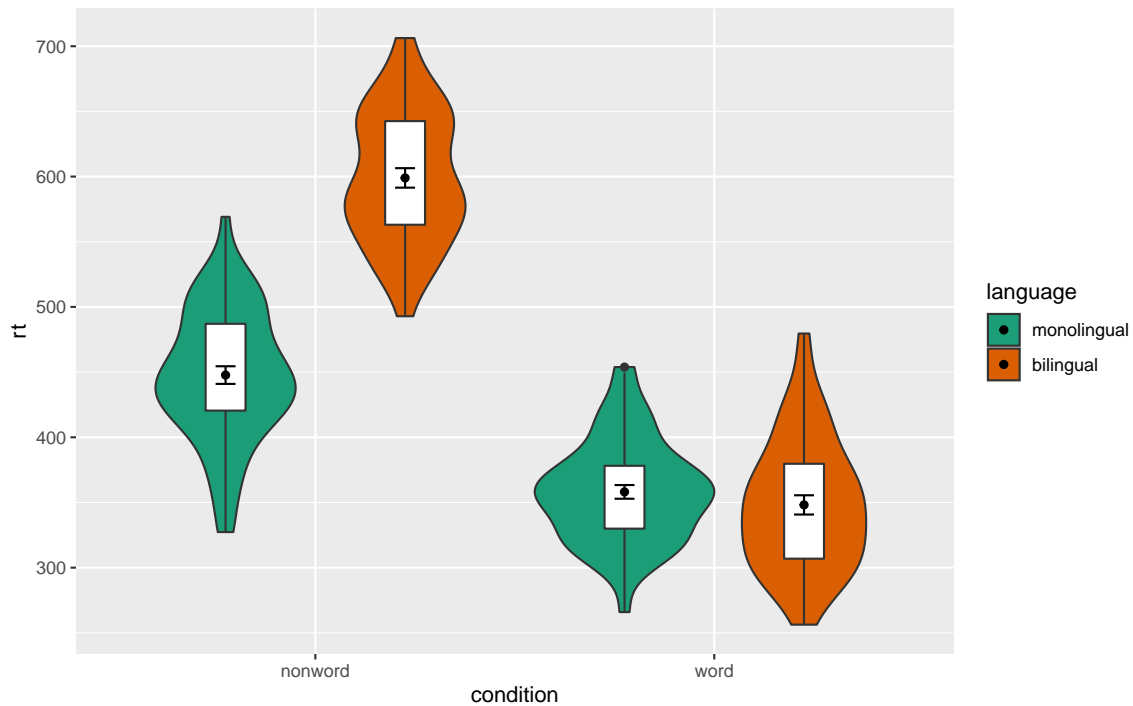
Figure 30. Manually changing the fill color.

Activities 3

Before you go on, do the following:

1. Review all the code you have run so far. Try to identify the commonalities between each plot's code and the bits of the code you might change if you were using a different dataset.

2. Take a moment to recognise the complexity of the code you are now able to read.

3. For the violin-boxplot, for `geom = "point"`, try changing `fun` to `median`

4. For the violin-boxplot, for `geom = "errorbar"`, try changing `fun.data` to `mean_cl_normal` (for 95% CI)

5. Go back to the grouped density plots and try changing the transparency with `alpha`.

Multi-part Plots

Interaction plots

Interaction plots are commonly used to help display or interpret a factorial design. Just as with the bar chart of means, interaction plots represent data summaries and so they are built up with a series of calls to `stat_summary()`.

647   • **shape** acts much like `fill` in previous plots, except that rather than producing dif-
648   ferent colour fills for each level of the IV, the data points are given different shapes.

649   • **size** lets you change the size of lines and points. You usually don't want different
650   groups to be different sizes, so this option is set inside the relevant `geom_*()` function,
651   not inside the `aes()` function.

652   • **scale_color_manual()** works much like `scale_color_discrete()` except that it
653   lets you specify the colour values manually, instead of then being automatically ap-
654   plied based on the palette you choose/default to. You can specify RGB colour values
655   or a list of predefined colour names - all available options can be found by run-
656   ning `colours()` in the console. Other manual scales are also available, for example,
657   `scale_fill_manual`.

```r
ggplot(dat_long, aes(x = condition, y = rt,
                     shape = language,
                     group = language,
                     color = language)) +
  stat_summary(fun = "mean", geom = "point", size = 3) +
  stat_summary(fun = "mean", geom = "line") +
  stat_summary(fun.data = "mean_se", geom = "errorbar", width = .2) +
  scale_color_manual(values = c("blue", "darkorange")) +
  theme_classic()
```
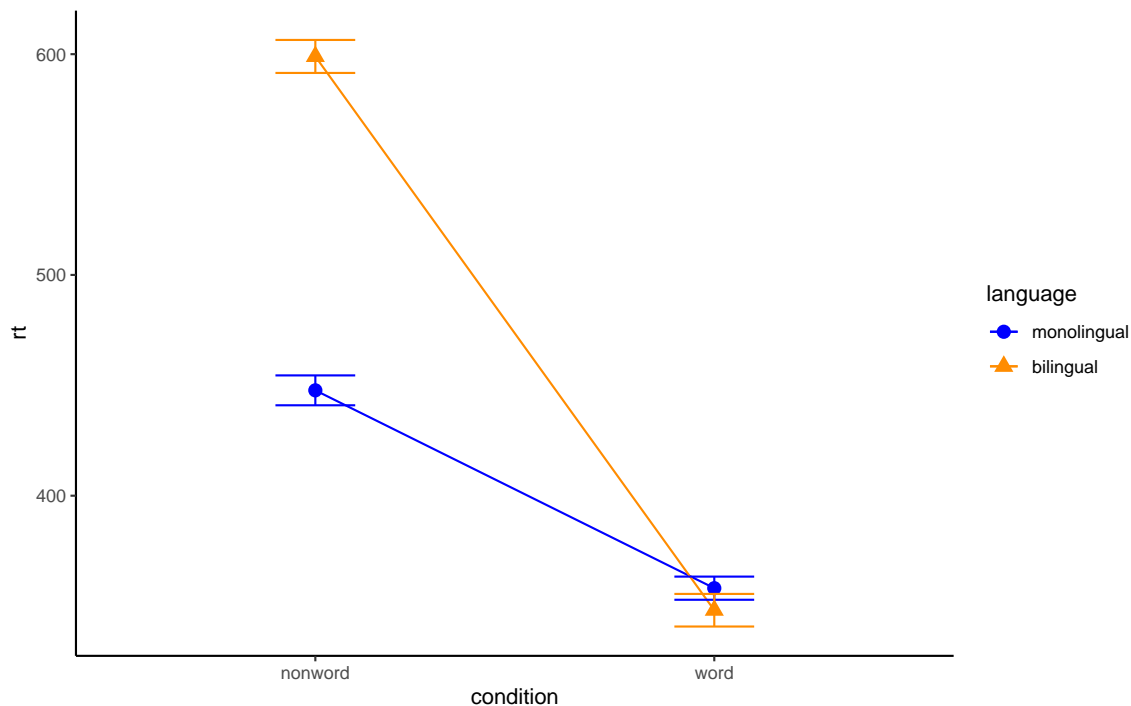

Figure 31. Interaction plot.

Combined interaction plots

A more complex interaction plot can be produced that takes advantage of the layers to visualise not only the overall interaction, but the change across conditions for each participant.

This code is more complex than all prior code because it does not use a universal mapping of the plot aesthetics. In our code so far, the aesthetic mapping (`aes`) of the plot has been specified in the first line of code as all layers have used the same mapping, however, is is also possible for each layer to use a different mapping.

- The first call to `ggplot()` sets up the default mappings of the plot that will be used unless otherwise specified - the `x`, `y` and `group` variable. Note two additions are `shape` and `linetype` that will vary those elements according to the language variable.
- `geom_point()` overrides the default mapping by setting its own `colour` to draw the data points from each language group in a different colour. `alpha` is set to a low value to aid readability. Note that because the aesthetic override was defined within the geom function, the colours are not represented in the legend.
- Similarly, `geom_line()` overrides the default grouping variable so that a line is drawn to connect the individual data points for each *participant* (`group = id`) rather than each language group, and also sets the colours. The default line type is also overridden and set for all lines to be solid.
- Finally, the calls to `stat_summary()` remain largely as they were, with the exception of setting `colour = "black"` and `size = 2` so that the overall means and error bars can be more easily distinguished from the individual data points. Because they do not specify an individual mapping, they use the defaults (e.g., the lines are connected by language group). For the error bars the lines are again made solid.

```
ggplot(dat_long, aes(x = condition, y = rt,
                     group = language, shape = language)) +
  geom_point(aes(colour = language),alpha = .2) +
  geom_line(aes(group = id, colour = language), alpha = .2) +
   stat_summary(fun = "mean", geom = "point", size = 2, colour = "black") +
  stat_summary(fun = "mean", geom = "line", colour = "black") +
  stat_summary(fun.data = "mean_se", geom = "errorbar",
               width = .2, colour = "black") +
  scale_color_brewer(palette = "Dark2") +
  theme_minimal()
```
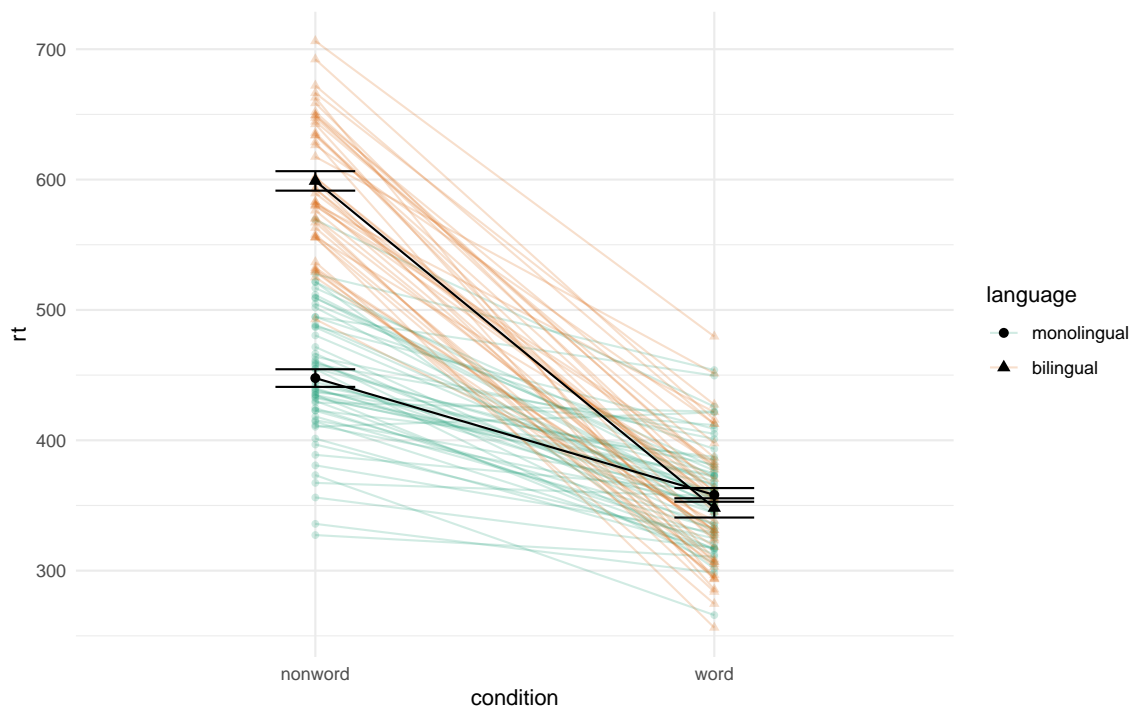
Figure 32. Interaction plot with by-participant data

682 **Facets**

683   So far we have produced single plots that display all the desired variables in one,
684 however, there are situations in which it may be useful to create separate plots for each
685 level of a variable. The below code is an adaptation of the code used to produce the grouped
686 scatterplot (see Figure 27) in which it may be easier to see how the relationship changes
687 when the data are not overlaid.

688   • Rather than using `colour = condition` to produce different colours for each level of
689   condition, this variable is instead passed to `facet_wrap()`.
690   •

```
ggplot(dat_long, aes(x = rt, y = age)) +
  geom_point() +
  geom_smooth(method = "lm") +
  facet_wrap(facets = vars(condition))
```
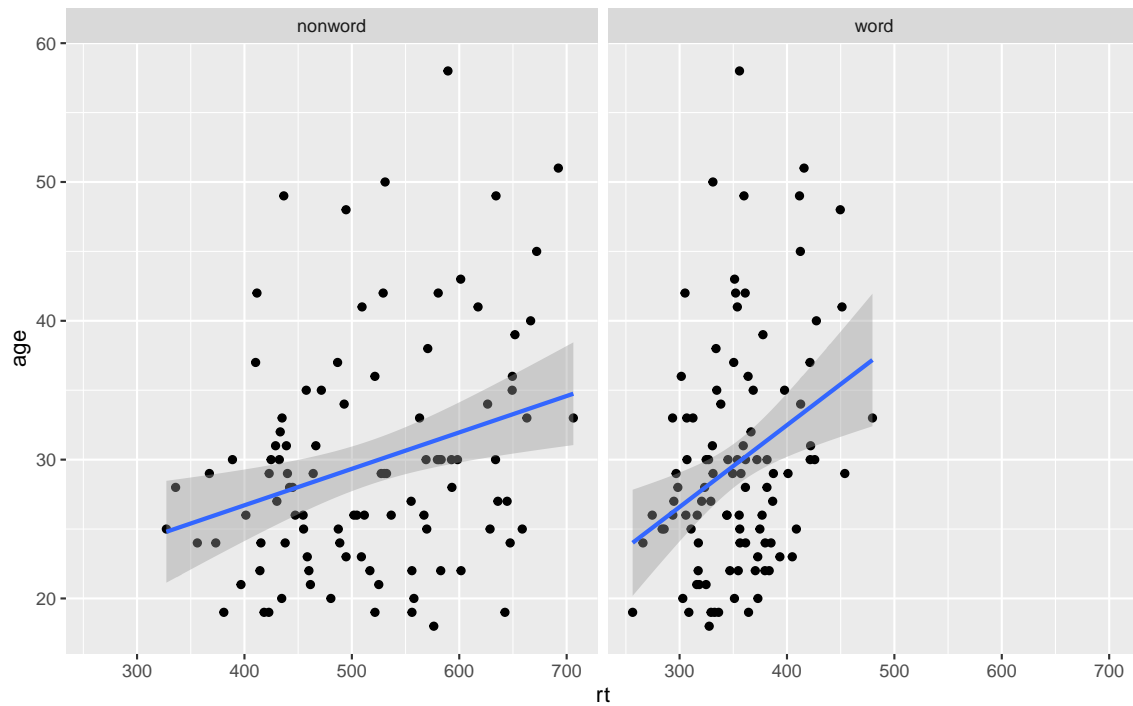
Figure 33. Faceted scatterplot

691   As another example, we can use `facet_wrap()` as an alternative to the grouped
692 violin-boxplot (see Figure 28) in which the variable `language` is passed to `facet_wrap()`
693 rather than `fill`. Using the tilde (`~`) to specify which factor is faceted is an alternative to
694 using `facets = vars(factor)` like above.

```
ggplot(dat_long, aes(x = condition, y= rt)) +
  geom_violin() +
  geom_boxplot(width = .2, fatten = NULL) +
  stat_summary(fun = "mean", geom = "point") +
  stat_summary(fun.data = "mean_se", geom = "errorbar", width = .1) +
  facet_wrap(~language) +
  theme_minimal()
```
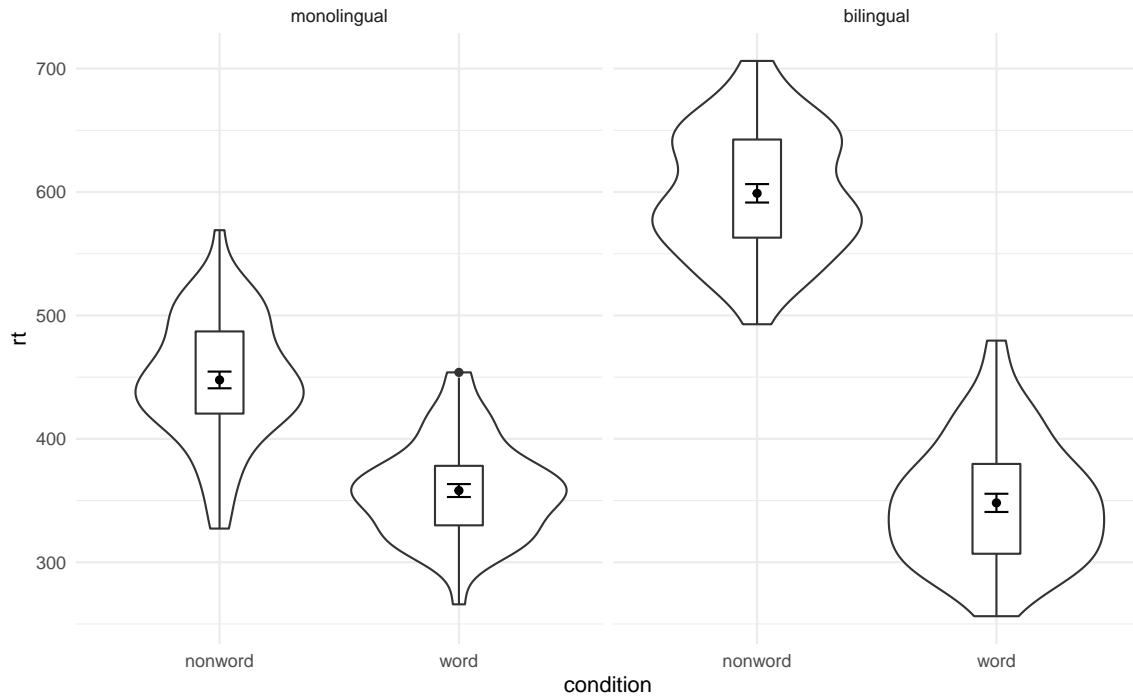
Figure 34. Facted violin-boxplot

Finally, note that editing the labels for faceted variables involves converting the
`language` column into a factor. This allows you to set the order of the `levels` and the
`labels` to display.

```
ggplot(dat_long, aes(x = condition, y= rt)) +
  geom_violin() +
  geom_boxplot(width = .2, fatten = NULL) +
  stat_summary(fun = "mean", geom = "point") +
  stat_summary(fun.data = "mean_se", geom = "errorbar", width = .1) +
  facet_wrap(~factor(language,
                     levels = c("monolingual", "bilingual"),
                     labels = c("Monolingual participants",
                                "Bilingual participants"))) +
  theme_minimal()
```
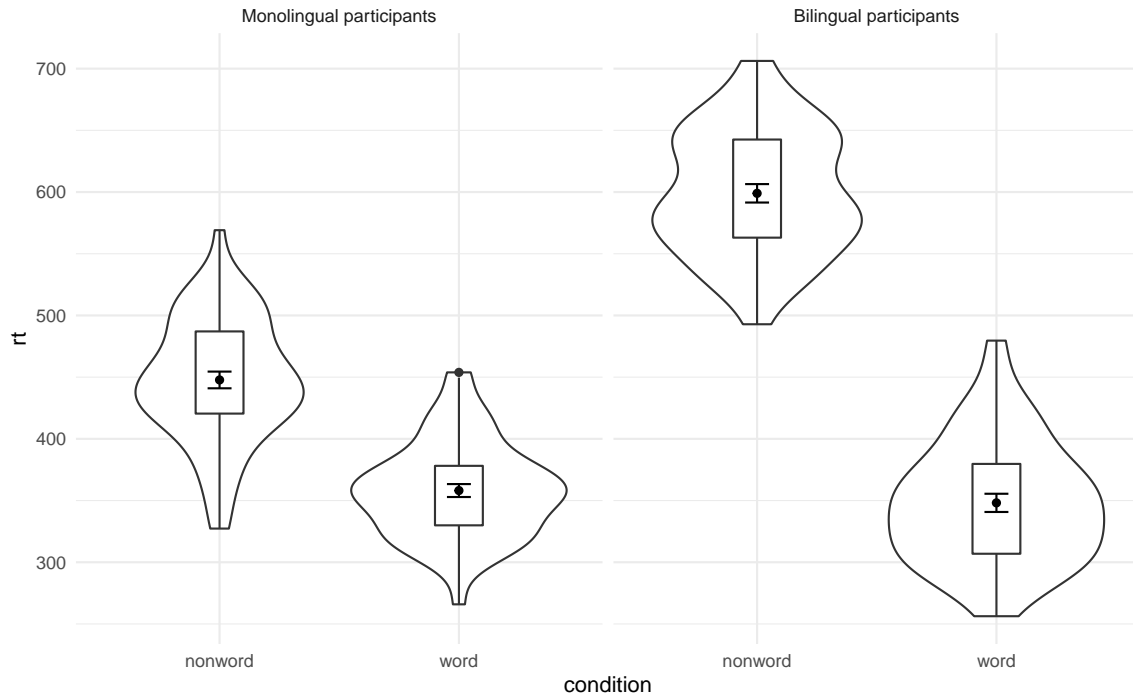
Figure 35. Faceted violin-boxplot with updated labels

698 **Storing plots**

699   Just like with datasets, plots can be saved to objects. The below code saves the
700 histograms we produced for reaction time and accuracy to objects named `p1` and `p2`. These
701 plots can then be viewed by calling the object name in the console.

```
p1 <- ggplot(dat_long, aes(x = rt)) +
  geom_histogram(binwidth = 10, color = "black")

p2 <- ggplot(dat_long, aes(x = acc)) +
  geom_histogram(binwidth = 1, color = "black")
```

702   Importantly, layers can then be added to these saved objects. For example, the below
703 code adds a theme to the plot saved in `p1` and saves it as a new object `p3`. This is important
704 because many of the examples of `ggplot2` code you will find in online help forums use the
705 `p +` format to build up plots but fail to explain what this means, which can be confusing
706 to beginners.

```
p3 <- p1 + theme_minimal()
```

Saving plots as images

In addition to saving plots to objects for further use in R, the function `ggsave()` can be used to save plots as images on your hard drive. The only required argument for `ggsave` is the file name of the image file you will create, complete with file extension (this can be "eps," "ps," "tex," "pdf," "jpeg," "tiff," "png," "bmp," "svg" or "wmf"). By default, `ggsave()` will save the last plot displayed, however, you can also specify a specific plot object if you have one saved.

```r
ggsave(filename = "my_plot.png") # save last displayed plot
ggsave(filename = "my_plot.png", plot = p3) # save plot p3
```

The width, height and resolution of the image can all be manually adjusted and the help documentation for is useful here (type `?ggsave` in the console to access the help).

Multiple plots

As well as creating separate plots for each level of a variable using `facet_wrap()`, you may also wish to display multiple different plots together and the `patchwork` package provides an intuitive way to do this. `patchwork` does not require the use of any functions once it is loaded with `library(patchwork)`, you simply need to save the plots you wish to combine to objects as above and use the operators `+`, `/` `()` and `|` to specify the look of the final figure.

Combining two plots. Two plots can be combined side-by-side or stacked on top of each other. These combined plots could also be saved to an object and then passed to `ggsave`.

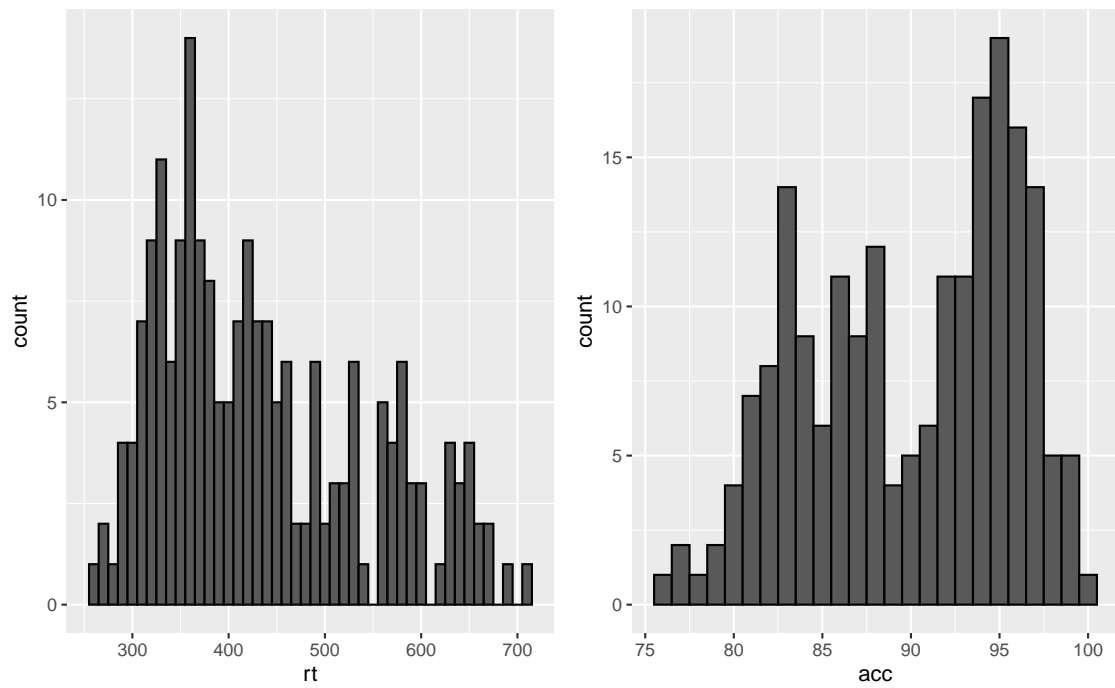```r
p1 + p2 # side-by-side
```

*Figure 36*. Side-by-side plots with patchwork
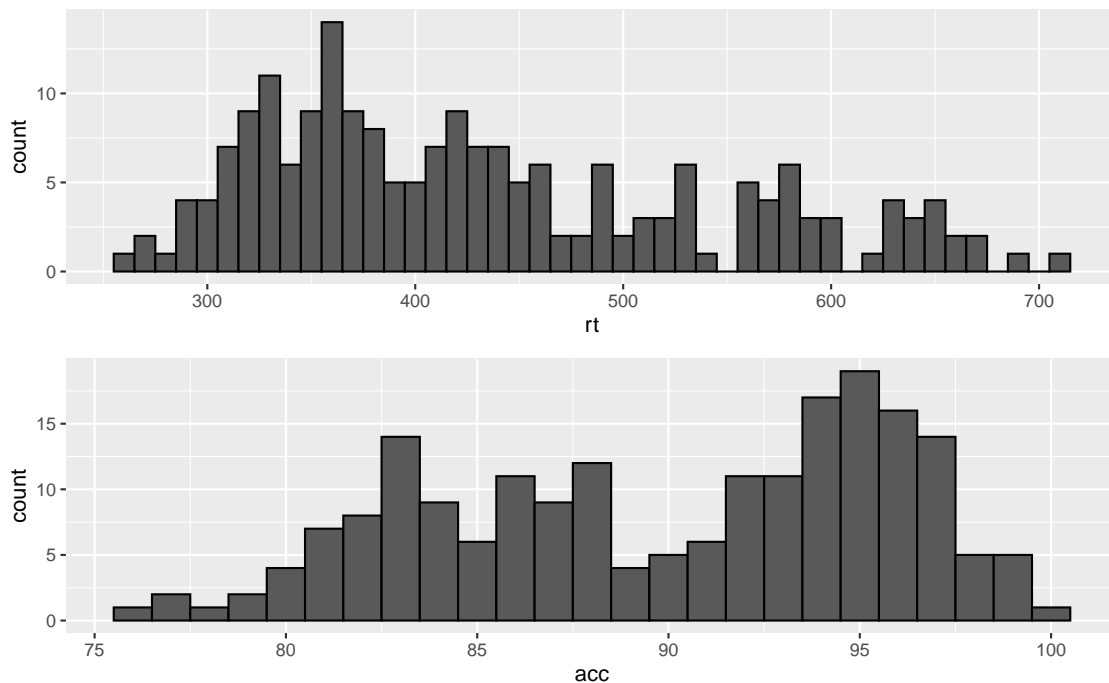
```
p1 / p2 # stacked
```

*Figure 37.* Stacked plots with patchwork

**Combining three or more plots.** Three or more plots can be combined in a number of ways and the `patchwork` syntax is relatively easy to grasp with a few examples and a bit of trial and error. First, we save the complex interaction plot and faceted violin-boxplot to objects named `p5` and `p6`.

```
p5 <- ggplot(dat_long, aes(x = condition, y = rt,
                           group = language,
                           shape = language)) +
  geom_point(aes(colour = language),
             alpha = .2) +
  geom_line(aes(group = id, colour = language),
             alpha = .2) +
  stat_summary(fun = "mean",
               geom = "point",
               size = 2,
               colour = "black") +
  stat_summary(fun = "mean",
               geom = "line",
               colour = "black") +
  stat_summary(fun.data = "mean_se",
               geom = "errorbar",
               width = .2,
               colour = "black") +
```

```
  theme_minimal()

p6 <- ggplot(dat_long, aes(x = condition, y= rt)) +
  geom_violin() +
  geom_boxplot(width = .2, fatten = NULL) +
  stat_summary(fun = "mean", geom = "point") +
  stat_summary(fun.data = "mean_se", geom = "errorbar", width = .1) +
  facet_wrap(~factor(language,
                     levels = c("monolingual", "bilingual"),
                     labels = c("Monolingual participants",
                                "Bilingual participants"))) +
  theme_minimal()
```

⁷³⁰   The exact layout of your plots will depend upon a number of factors. Try running
⁷³¹ the below examples and adjust the use of the operators to see how they change the layout.
⁷³² Each line of code will draw a different figure.

```
p1 /p5 / p6
(p1 + p6) / p5
p6 | p1 / p5
```

⁷³³ **Customisation part 4**

⁷³⁴   **Axis labels.**   Previously when we edited the main axis labels we used the `scale_`
⁷³⁵ functions to do so. These functions are useful to know because they allow you to customise
⁷³⁶ each aspect of the scale, for example, the breaks and limits. However, if you only need to
⁷³⁷ change the main axis `name`, there is a quicker way to do so using `labs()`. The below code
⁷³⁸ adds a layer to the plot that changes the axis labels for the histogram saved in `p1` and adds
⁷³⁹ a title and subtitle. The title and subtitle do not conform to APA standards (more on APA
⁷⁴⁰ formatting in the additional resources), however, for presentations and social media they
⁷⁴¹ can be useful.

```
p5 + labs(x = "Type of word",
          y = "Reaction time (ms)",
          title = "Language group by word type interaction plot",
          subtitle = "Reaction time data")
```
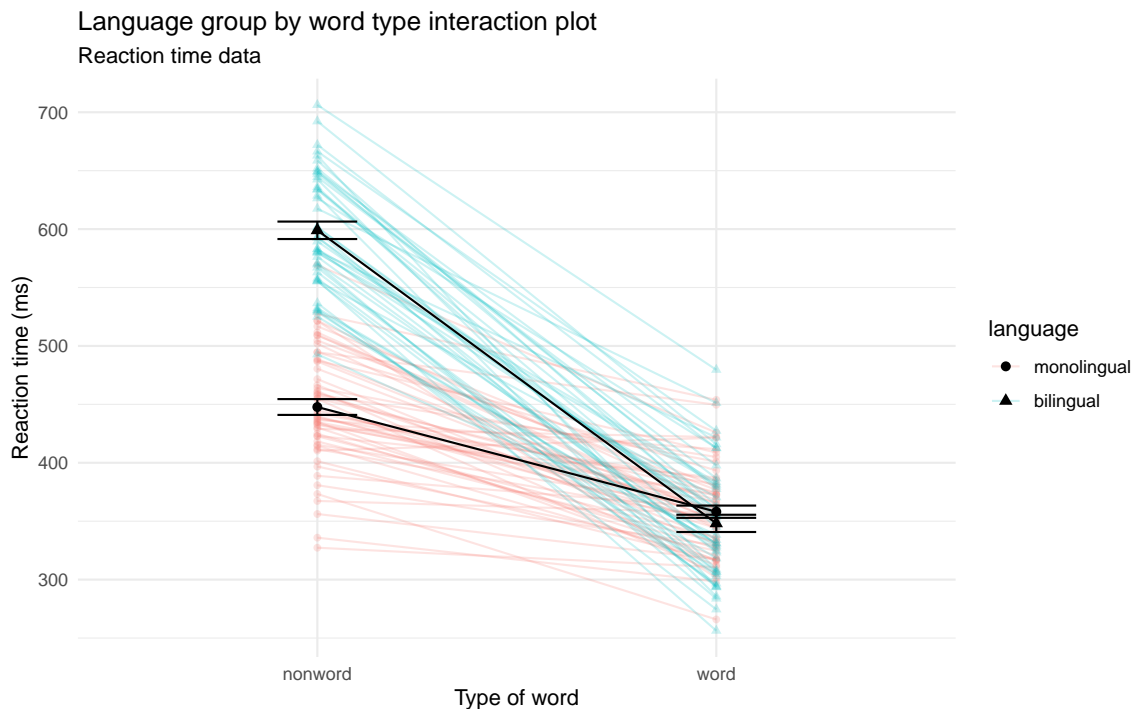
Figure 38. Plot with edited labels and title

742   You can also use `labs()` to remove axis labels, for example, try adjusting the above
743 code to `x = NULL`.

744   **Redundant aesthetics.** So far when we have produced plots with colours, the
745 colours were the only way that different levels of a variable were indicated, but it is some-
746 times preferable to indicate levels with both colour and other means, such as facets or x-axis
747 categories.

748   The code below adds `fill = language` to the violin-boxplots that are also faceted
749 by language. We adjust `alpha` and use the brewer colour palette to customise the colours.

```
ggplot(dat_long, aes(x = condition, y= rt, fill = language)) +
  geom_violin(alpha = .4) +
  geom_boxplot(width = .2, fatten = NULL, alpha = .6) +
  stat_summary(fun = "mean", geom = "point") +
  stat_summary(fun.data = "mean_se", geom = "errorbar", width = .1) +
  facet_wrap(~factor(language,
                     levels = c("monolingual", "bilingual"),
                     labels = c("Monolingual participants",
                                "Bilingual participants"))) +
  theme_minimal() +
  scale_fill_brewer(palette = "Dark2")
```
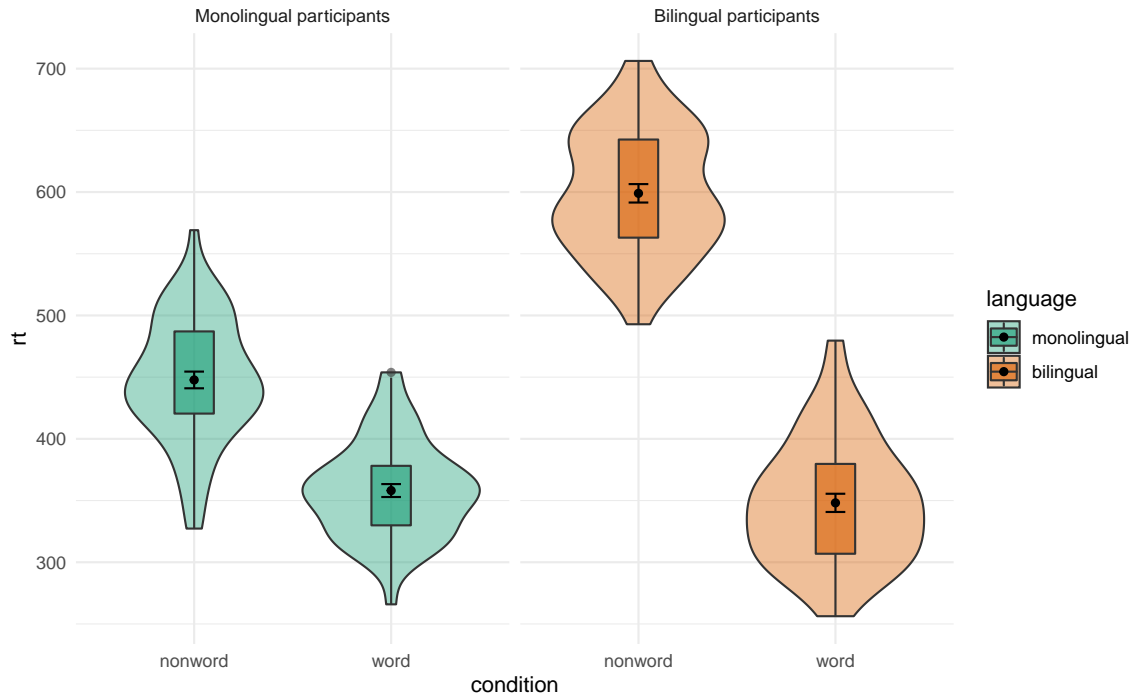
Figure 39. Violin-boxplot with redundant legend

Specifying a `fill` variable means that by default, R produces a legend for that variable. However, the use of colour is redundant with the facet labels, so you can remove this legend with the `guides` function.

```r
ggplot(dat_long, aes(x = condition, y= rt, fill = language)) +
  geom_violin(alpha = .4) +
  geom_boxplot(width = .2, fatten = NULL, alpha = .6) +
  stat_summary(fun = "mean", geom = "point") +
  stat_summary(fun.data = "mean_se", geom = "errorbar", width = .1) +
  facet_wrap(~factor(language,
                     levels = c("monolingual", "bilingual"),
                     labels = c("Monolingual participants",
                                "Bilingual participants"))) +
  theme_minimal() +
  scale_fill_brewer(palette = "Dark2") +
  guides(fill = "none")
```
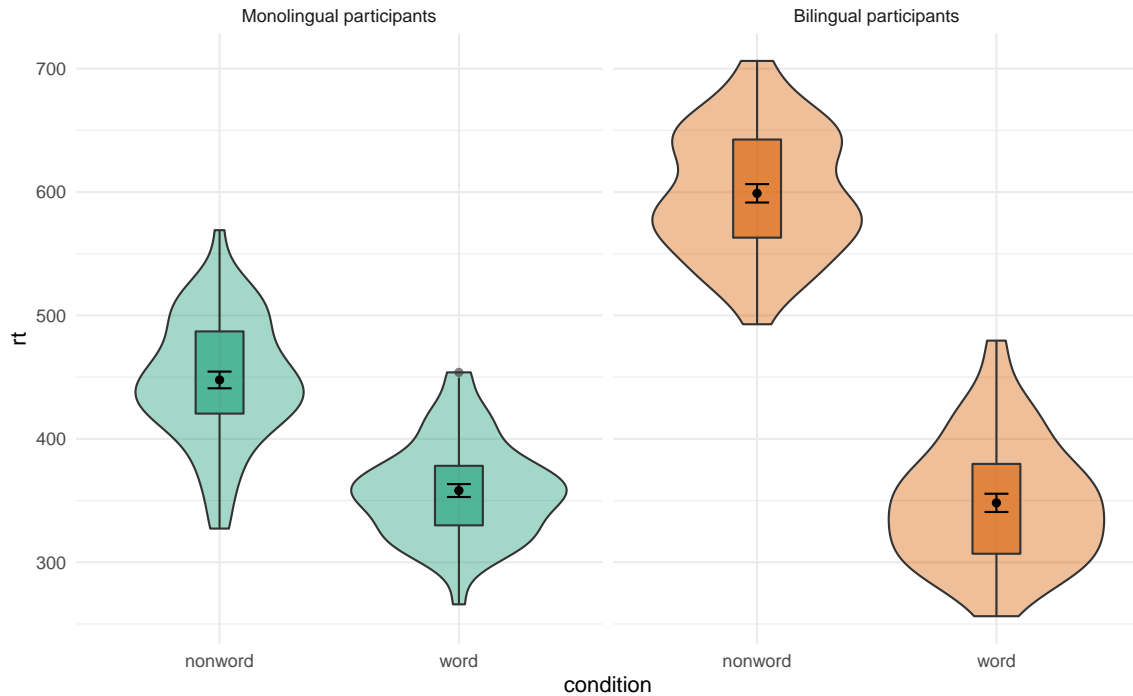
Figure 40. Plot with suppressed redundant legend

Activities 4

⁷⁵⁴   Before you go on, do the following:

⁷⁵⁵   1. Rather than mapping both variables (`condition` and `language`) to a single interaction
⁷⁵⁶   plot with individual participant data, instead produce a faceted plot that separates the
⁷⁵⁷   monolingual and bilingual data. All visual elements should remain the same (colours
⁷⁵⁸   and shapes) and you should also take care not to have any redundant legends.

⁷⁵⁹   2. Choose your favourite three plots you've produced so far in this tutorial, tidy them
⁷⁶⁰   up with axis labels, your preferred colour scheme, and any necessary titles, and then
⁷⁶¹   combine them using `patchwork`. If you're feeling particularly proud of them, post
⁷⁶²   them on Twitter using #PsyTeachR.

Advanced Plots

⁷⁶⁴   This tutorial has but scratched the surface of the visualisation options available using
⁷⁶⁵   R - in the additional online resources we provide some further advanced plots and cus-
⁷⁶⁶   tomisation options for those readers who are feeling confident with the content covered in
⁷⁶⁷   this tutorial, however, the below plots give an idea of what is possible, and represent the
⁷⁶⁸   favourite plots of the authorship team.

⁷⁶⁹   We   will   use   some   custom   functions: `geom_split_violin()`   and
⁷⁷⁰ `geom_flat_violin()`, which you can access through the `introdataviz` package.
⁷⁷¹ These functions are modified from (Allen et al., 2021).

```
# how to install the introdataviz package to get split and half violin plots
devtools::install_github("psyteachr/introdataviz")
```

Split-violin plots

⁷⁷³   Split-violin plots remove the redundancy of mirrored violin plots and make it easier
⁷⁷⁴ to compare the distributions between multiple conditions.
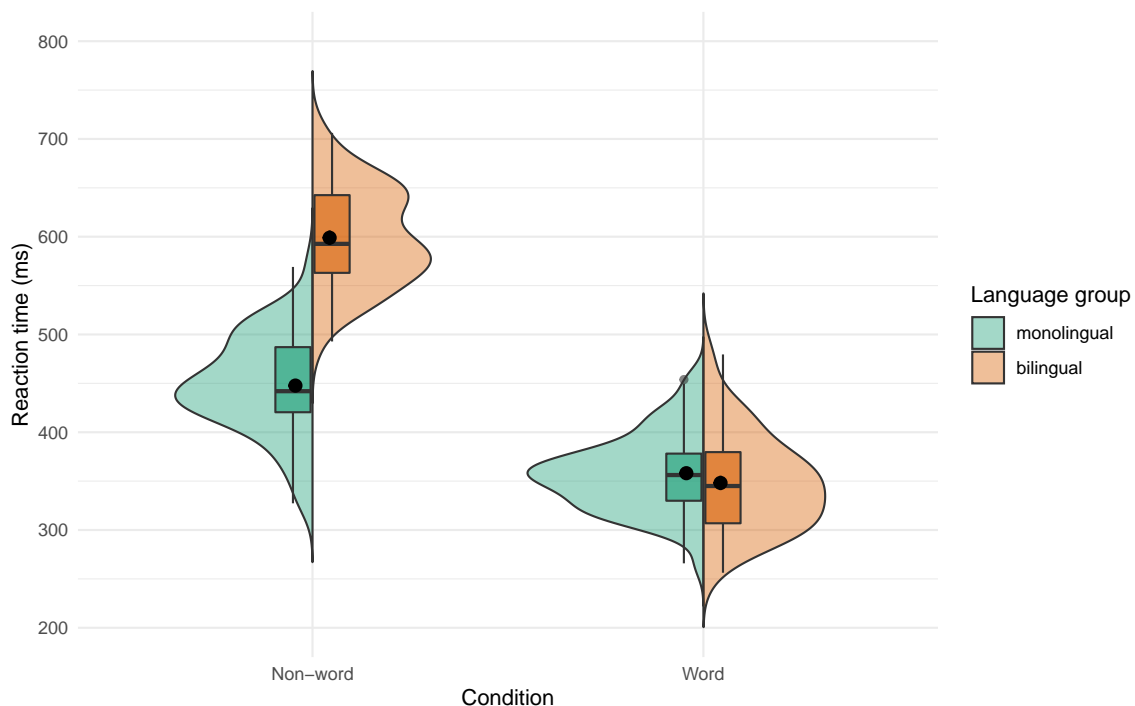
Figure 41. Split-violin plot

Raincloud plots

⁷⁷⁶   Raincloud plots combine a density plot, boxplot, raw data points, and any desired
⁷⁷⁷ summary statistics for a complete visualisation of the data. They are so called because the
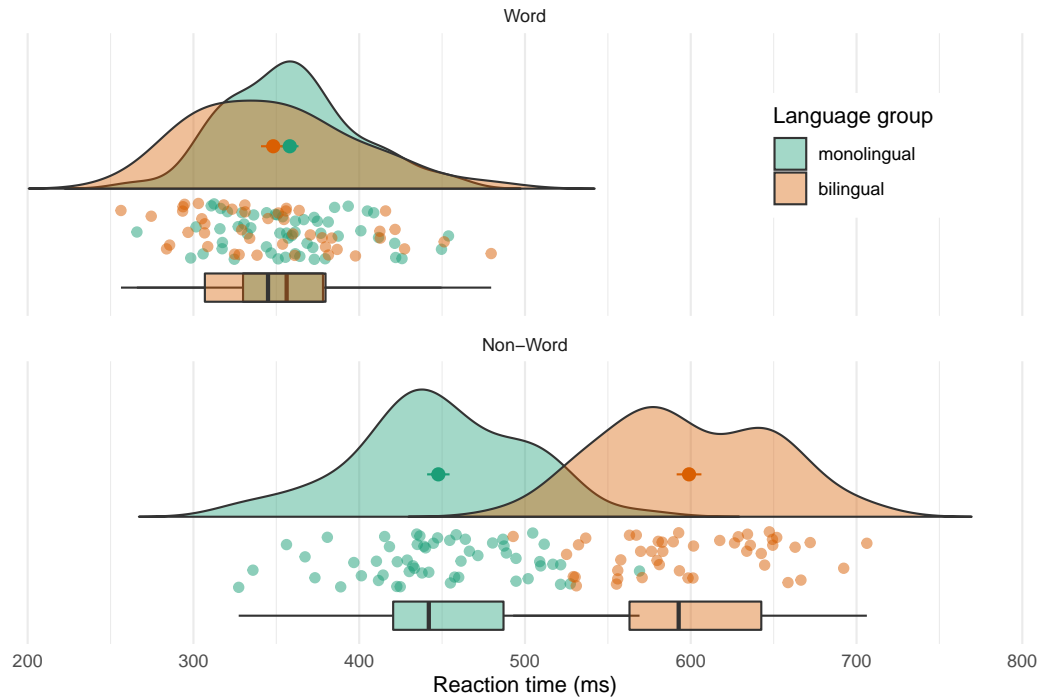⁷⁷⁸ density plot plus raw data is reminiscent of a rain cloud.

Figure 42. Raincloud plot

Ridge plots

Ridge plots are a series of density plots and show the distribution of numeric values for several groups. Figure 43 shows data from (Nation, 2017) and demonstrates how effective this type of visualisation can be to convey a lot of information very intuitively whilst being visually attractive.
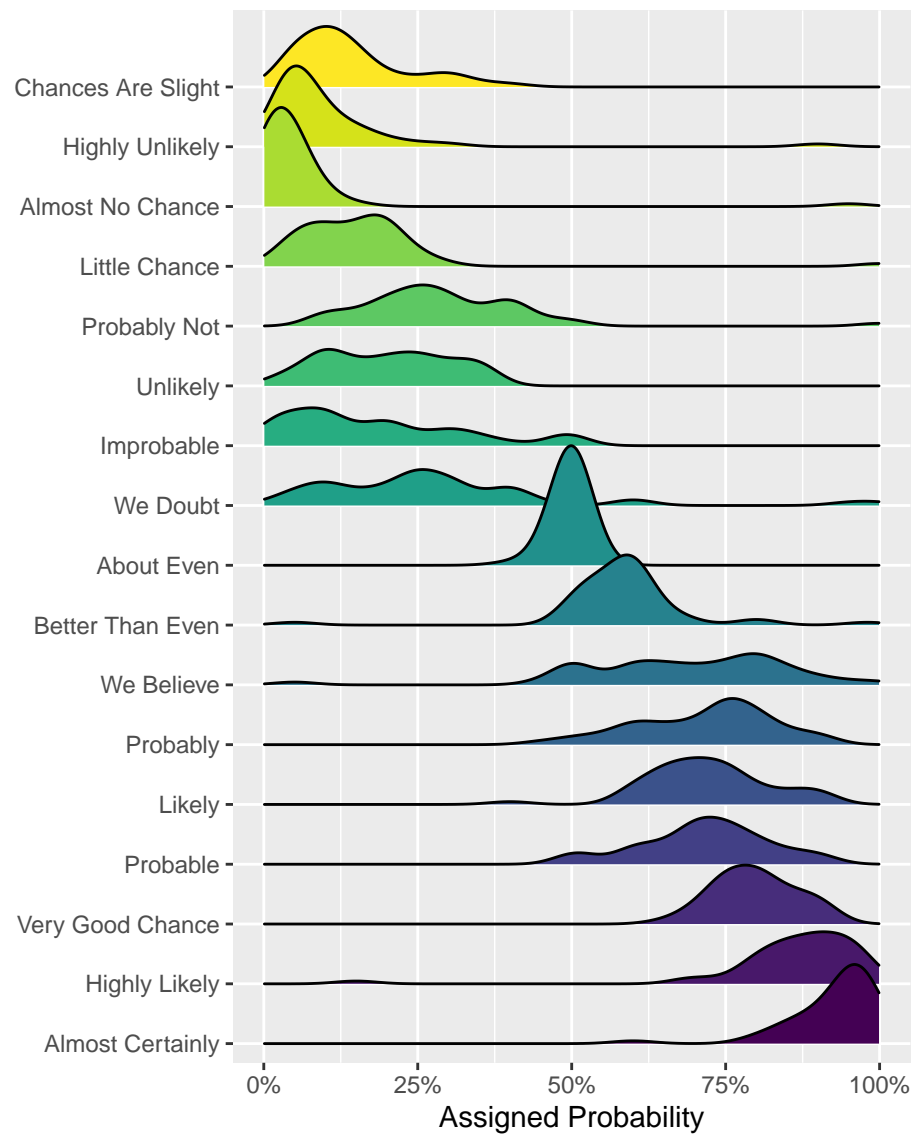
Figure 43. A ridge plot.

Alluvial plots

Alluvial plots visualise multi-level categorical data through flows that can easily be traced in the diagram.
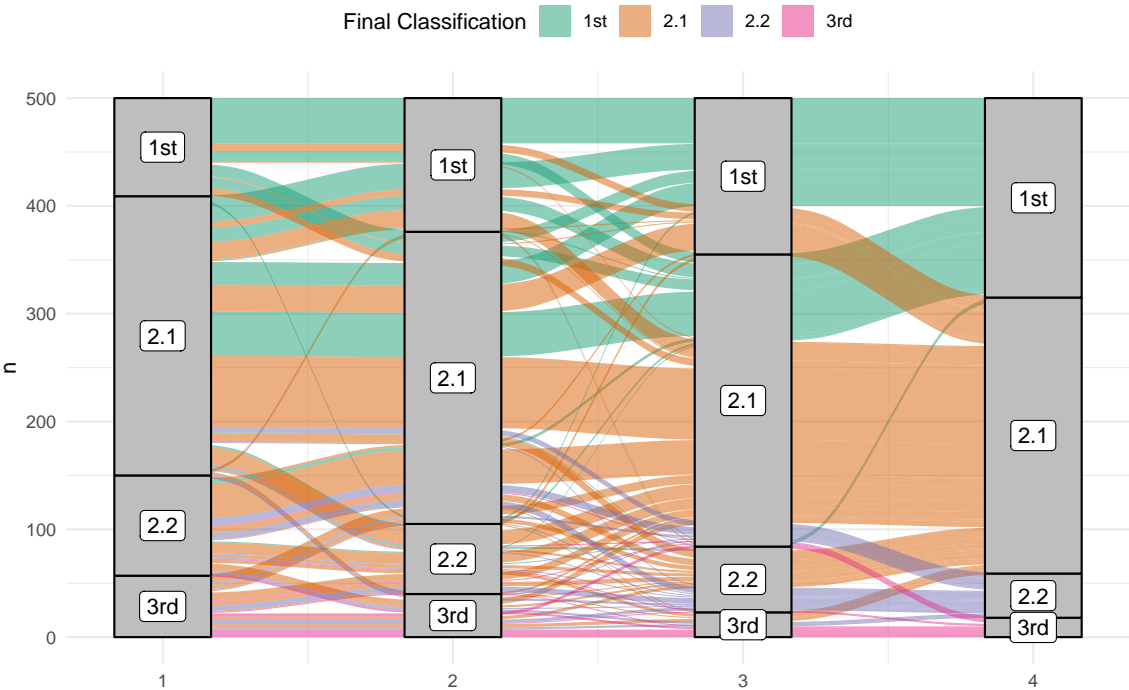
Figure 44. An alluvial plot showing the progression of student grades through the years.

Conclusion

In this tutorial we aimed to provide a practical introduction to common data visualisation techniques using R. Whilst a number of the plots produced in this tutorial can be created in point-and-click software, the underlying skill-set developed by making these visualisations is as powerful as it is extendable.

We hope that this tutorial serves as a jumping off point to encourage more researchers to adopt reproducible workflows and open-access software, in addition to beautiful data visualisations.

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- EN: Conceptualization; Visualization; Writing - original draft
- PM: Visualization; Writing - original draft
- WT: Visualization; Writing - original draft
- HP: Visualization; Writing - original draft
- LD: Software; Visualization; Writing - review & editing

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805   **Research Software.**   This tutorial uses the following open-source research software:
806 R Core Team (2021); Wickham et al. (2019); DeBruine (2021); Aust and Barth (2020),
807 Wickham (2016b), Pedersen (2020), Brunson (2020), Wilke (2021).

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