

Exercises

Exercise 7: Reproducible reports with R markdown

Read Chapter 8 to help you complete the questions in this exercise.

Before the session. This exercise needs the `rmarkdown`, `knitr` R packages, a LaTeX installation so that you can make PDF documents, and the `ggplot2` package, which you installed for Exercise 6. Work through **Setting up R markdown**, under the Setup menu above, before you come to the session. It takes about fifteen minutes and most of that is a download running by itself, but please don't leave it until the morning of the session. If you hit a real problem we'll help you at the start of the session, but we can't get everybody set up and still have time to cover everything in this exercise.

Up until now everything you've written has been R code. This exercise is about producing a *document* for somebody else to read (including you, or the future you), in which your writing, your code and your results and interpretation all live in the same R markdown file. Because they're in the same file they can't drift apart, which is what we mean by a reproducible report. Change the data, press one button, and every number, figure and table in the output file updates itself.

It's also the exercise that brings a lot of what you have learned so far on this course together. So, you'll be importing data, checking your data, transforming variables, drawing plots and summarising data into tables. You'll set these processes out in an order that best makes sense to your reader and describes what your data is, what you did to your data and why, and what you found.

That order is the point. A report is not just a pile of results, it's a reproducible account of your work.

The figures in this exercise use `ggplot2`, the way Exercise 6 did. If you'd rather draw them with base R then please do. That's one of the nice things about R. Nobody makes you work in one particular way, so use whichever you're quickest and most confident with. If you want to follow this exercise (and solutions exactly) then I recommend that you use `ggplot2`.

You'll build **one document** across the whole exercise, adding something to it at each question, so don't start a new file each time. There's a lot of new vocabulary here, so take it slowly and knit often. Knitting after every small change is the quickest way to see what each thing does and the quickest way to find out which change broke something.

1. Right, let's make a start. Open the RStudio Project you have been using for this course. Create a new R markdown document by going to **File -> New File -> R Markdown...** (see Section 8.4 of the Introduction to R book if you would like to read about this first).

The first time you do this, RStudio might tell you it needs to install some packages (although if you have followed the setup instructions this probably won't happen). Let it, and wait for it to finish.

In the dialogue box that appears, type **Cardiac study report** in the Title box, put your name in the Author box, choose **PDF** as the default output format, and click OK. RStudio opens a new document that's already full of example content about cars. That's normal, and we'll delete it in a moment.

Watch the output format, because HTML is selected for you and we want PDF.

New R Markdown

Document

Title: Cardiac study report

Author: Alex Douglas

Date: 2026-09-09

☐ Use current date when rendering document

Default Output Format:

☐ HTML
Recommended format for authoring (you can switch to PDF or Word output anytime).

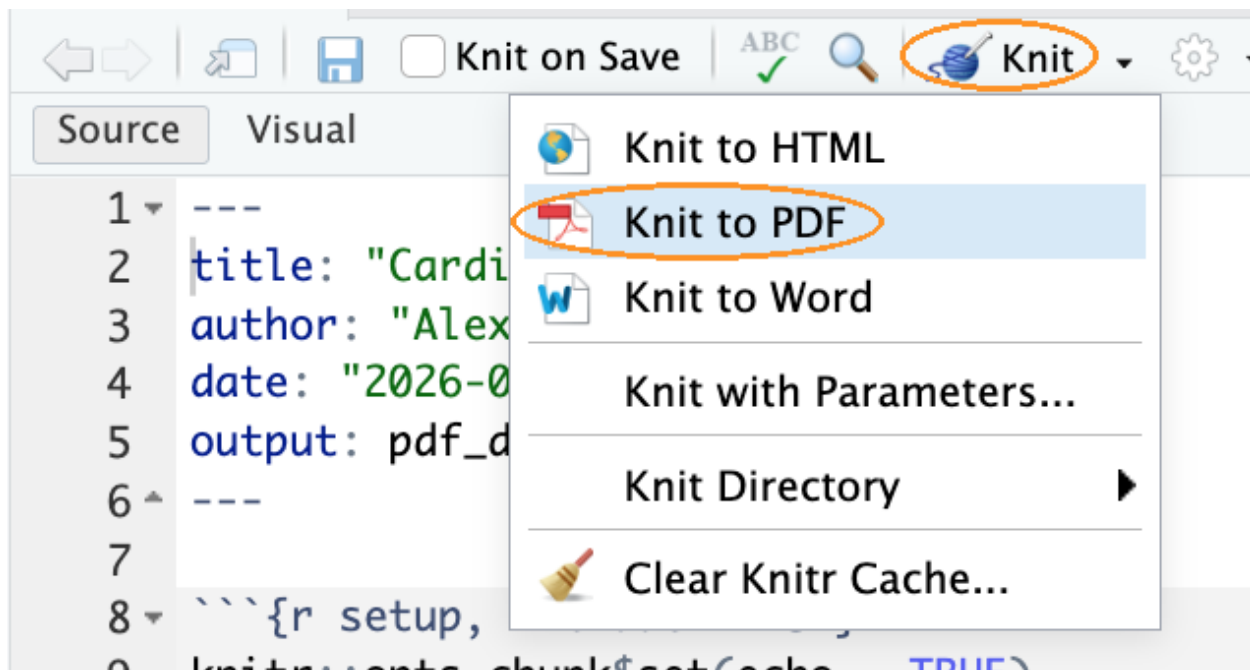
☒ PDF
PDF output requires TeX (MiKTeX on Windows, MacTeX 2013+ on OS X, TeX Live 2013+ on Linux).

☐ Word
Previewing Word documents requires an installation of MS Word (or Libre/Open Office on Linux).

Create Empty Document OK Cancel

Before you change anything at all, save the file into your Project directory as **cardiac_report.Rmd** (File -> **Save As...**), then click the **Knit** button at the top of the editor. You can also press Ctrl+Shift+K, or Cmd+Shift+K on a Mac.

The **Knit** button is the ball of wool. The menu hanging below it in the picture comes from the small black triangle beside the button, and you don't need it now, because you chose PDF in the dialogue box a moment ago and clicking **Knit** will give you one anyway. It's worth knowing it's there, and we come back to it in Q13.



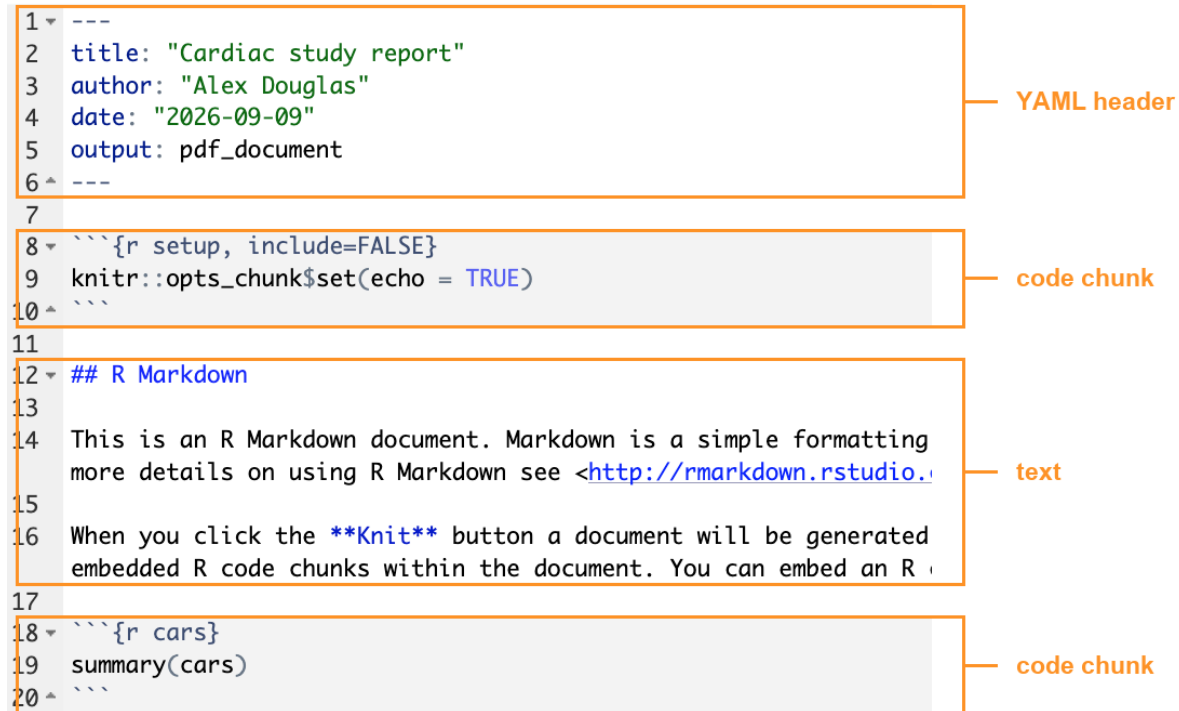
Do this before you understand any of it. If a PDF appears then your setup is working, and you can be confident that anything which goes wrong later is something you can fix.

2. An R markdown file has only three kinds of content, and everything else is a variation on them (Section 8.5 of the book takes each of them in turn):

- the **YAML header** at the very top, between the two lines of `---`, which controls the document as a whole
- **text**, written in a simple markup language called markdown
- **code chunks**, which look like this:

```
```{r}
mean(cardiac$age)
```
```

Here they are in the document RStudio has just made for you. The two code chunks show that a document alternates between text and code as often as it needs to, and that only the YAML header is in one piece at the top.



Find one of each in `cardiac_report.Rmd`, the file you are editing rather than the PDF it produced, so that you can recognise them when we start changing them. Then delete everything in `cardiac_report.Rmd` below the first code chunk, the one called `setup`, leaving the YAML header and that chunk in place. Knit again to check you have an empty but working document. This is your starting point.

While you're in that `setup` chunk, add `library(knitr)` and `library(ggplot2)` to it. You'll want a couple of functions from `knitr` later on and `ggplot2` for the figures, and the best place for a `library()` call is at the top of a document rather than buried in the middle of it. Do it now and you won't have to think about it again.

3. Now let's take control of the YAML header (see Section 8.5.1 of the book). Find the `output:` line, which currently says `pdf_document` on the same line as it, and turn it into the indented block shown below.

Two warnings (because this is where people lose ten minutes), indentation in YAML matters, so copy the spacing exactly and use spaces, never tabs.

Build it up rather than pasting it in one go. Put `pdf_document:` on its own line first, with `toc: true` indented underneath, and knit. Then add `number_sections: true` below that and knit again. Doing it one line at a time, and knitting after each, is how you see what each one actually does. Here is what you are aiming for:

```
---
title: "Cardiac study report"
author: "Your Name"
date: "2 November 2026"
output:
  pdf_document:
    toc: true
    number_sections: true
---
```

4. Most reports start by telling the reader what the data are, so that's where we'll start too. You already have a description of these data in **Exercise 3, Q4**. Copy the first 3 sentences of the data description into your document underneath the setup chunk, then use markdown to format it. There is no R code in this question.

- put a heading above it, written as `# Introduction`, and a second smaller heading below that, written as `## Data description`
- in the text, change **cohort study** in bold, by writing it as `**cohort study**`
- put *measurements* in italics the first time it appears, by writing it as `*measurements*`
- set four of the variables out as a bulleted list at the end, each line starting with a dash and a space. Use age, systolic blood pressure, HDL cholesterol and smoking status, since those are the four the rest of the report uses

OK, that's enough to be going on with. If you want to add a link, a numbered list, a quotation or a table, Section 8.5.2 of the book has the syntax for all of them, and there's a summary on the R markdown cheat sheet under `Help -> Cheat Sheets`.

Knit, and look at the R markdown file and the PDF side by side. Notice that the headings you wrote have appeared in the table of contents on their own, because of the `toc: true` you added in Q3.

5. Next, let's deal with the data. There are a few small steps here, so take them one at a time.

- a) Insert a new code chunk (see Section 8.5.3 of the book) by going to `Code -> Insert Chunk`, or with the keyboard shortcut `Ctrl+Alt+I`, which is `Cmd+Alt+I` on a Mac. An empty chunk appears. There's nothing magic about the menu, so if you'd rather, just type ````${r}```` on a line of its own and ````` on another line below it. Anything you put between them is a chunk.
- b) Give the chunk a name by typing it straight after the `r`, so the first line reads ````${r import}`. Naming chunks costs nothing and makes them far easier to find when something goes wrong.
- c) Inside the chunk, import the `cardiacdata.txt` file exactly as you did in **Exercise 3, Q5**, with the `read.table()` function, writing out the `header`, `sep` and `stringsAsFactors` arguments, and assigning the result to `cardiac`.
- d) In the same chunk, add the two `factor()` lines from **Exercise 3, Q7** that create `Fsex` and `Fsmoking`. Hopefully you'll remember why, but just in case you've forgotten, the original `sex` and `smoking` variables are coded in the file as numbers, 1 and 2 for sex and 1, 2 and 3 for smoking, but they're really categories not numbers. The `factor()` function attaches a meaningful label to each code and leaves the original columns untouched (see `?factor` and Section 3.1 of the book for where factors sit among R's data types).

You'll need `Fsmoking` for the boxplot in Q7 and the table in Q8, and both of them read better with words in them rather than numbers.

- e) Now run the import chunk in the editor with the small green arrow at its top right corner of your R markdown document in RStudio. It's the rightmost of the three little buttons there. If you can't see it, `Code -> Run Region -> Run Current Chunk` does the same job, and so does `Ctrl+Alt+C`, or `Cmd+Alt+C` on a Mac.

Running the chunk puts `cardiac` into your Environment, so you can check the import has worked before you go any further and so the dataframe is there if you want to try something out in the console. It's worth getting into the habit of running a chunk before you rely on it.

Then knit the whole document by clicking on the knit button. Notice that knitting starts a completely fresh R session, so anything you made earlier in the console doesn't exist when the document knits. That's exactly what makes it reproducible, and it also means the chunk that imports the data has to come before any chunk that uses it.

6. OK, now we have the data imported, the next thing to do is validate the data by checking for mistakes or inconsistencies. So, in this question we'll not only perform the validation with R code but also explain what the validation shows and any decisions that we make along the way.

Add a new heading called **## Data validation** below the previous chunk, then build the section up underneath it in four pieces.

- a) One sentence directly under the heading saying how many patients are in the dataset. There are 163, and for now just type that straight in as an ordinary number. You'll come back to that sentence in Q9.
- b) Below it, insert a code chunk named **validation** holding the three lines from **Exercise 4, Q1** that set the impossible **bmi**, **triglyceride** and **hdlchol** values to **NA**. Remember that your report imports the raw file from scratch every time it knits, so if the cleaning isn't in the document then it won't happen.
- c) Beneath that chunk, write a short paragraph of two or three sentences saying which variables you changed and why you set them to **NA** rather than deleting those patients or correcting the numbers yourself.
- d) Lastly, the variable **alcohol**, which you'll remember from **Exercise 5, Q9** needed some work as well. A small number of patients drink a great deal more than the rest, which leaves the distribution with a long tail to the right, and you took the square root to pull that tail in. That's a data preparation step exactly like the cleaning above, so it belongs in this section too.

Add another chunk and name it **alcohol-transform**. In it, create the square root of **alcohol** as you did in **Exercise 5, Q9**, then draw a histogram of **alcohol**. Add a second chunk below it, named **alcohol-sqrt**, with a histogram of the square root. That way a reader gets the two one under the other and can see what the transformation did. Write a sentence or two underneath saying why you did it.

7. So, with the data in and tidied up, we can start showing the reader what's in it. Insert another chunk, name it **chol-plot**, and use it to draw a boxplot of HDL cholesterol by smoking status. It's the same plot you drew in **Exercise 5, Q11**, built with **ggplot2** this time, with **Fsmoking** along the x axis, **hdlchol** up the y axis and **geom_boxplot()** as the geom. You already have **Fsmoking** from your import chunk.

You'll get a fourth box, labelled **NA**, which is the seven patients whose smoking status wasn't recorded. Base R quietly left those out of the same plot back in Exercise 5, whereas **ggplot** puts them in front of you. Leave it as it is for transparency.

Now give the figure a caption. Chunk options go inside the curly braces, after the chunk name, separated by commas. The first line of your chunk should read:

```
```{r chol-plot, fig.cap = 'HDL cholesterol by smoking status.'}
...
```
```

Knit the document and notice that your caption is underneath the plot. Then add **fig.width = 4** to the same code chunk options, knit again, and see what happens to the size of the text relative to the plot.

While you're at it, go back to your two alcohol chunks from Q6 and give those figures a caption each, so every figure in the report has one.

There are many other chunk options for figures, controlling height, alignment, resolution and so on. You don't need them today. Section 8.5.4 of the book covers the ones you're most likely to need.

8. A figure visualises your data, but a reader will usually find tabulated summaries useful as well, so let's add a table to go alongside it (see Section 8.5.5 of the book).

Insert a chunk, name it `summary-table`, and recreate the `aggregate()` summary from **Exercise 4, Q4**, the mean of `age`, `systolic` and `tchol` for each smoking category. Assign it to an object called `smoke_summary`. Then, on the next line, write `smoke_summary` on its own. A chunk prints anything that isn't assigned to something, so that second line is what makes the summary appear in your document. Knit and see what you get.

It's the console output, monospaced and squeezed into a grey box, which is fine while you're working but not something you would want for a more general audience. The `kable()` function, from the `knitr` package you loaded in Q2, turns a dataframe into a properly formatted table instead, with the columns lined up and the variable names picked out as a header row. Change that second line from `smoke_summary` to `kable(smoke_summary)` and knit again. Finally add `digits = 1` and a `caption` to the `kable()` code to tidy it up.

9. Your report is now more or less complete, so the rest of the exercise is about tidying it up. Let's start with the sentence you wrote at the top of your data validation section in Q6, the one saying how many patients are in the dataset. You wrote 163 and a number written into your text that way can go out of date. If the data changes, or you correct something later, your writing stops matching your results.

R markdown fixes this with **inline code** (see Section 8.5.6 of the book). In the middle of an ordinary sentence you write a backtick, then the letter `r`, then some R code, then a closing backtick. When you knit, the answer of that code appears in your text in place of the whole thing:

```
The dataset contains `r nrow(cardiac)` patients.
```

which comes out as "The dataset contains 163 patients."

- a) Go back to that sentence and swap the number 163 for ``r nrow(cardiac)``. Knit and check it still says the same thing.
- b) Now add the mean age to the same sentence, worked out the same way with `mean()`.
- c) Now add a second sentence saying what age the youngest and oldest patients were, using `min()` and `max()` inside inline code. Knit and compare what you get with the age range given in the description of the data back in **Exercise 3, Q4**.

Every one of these numbers is worked out from the `cardiac` dataframe each time you knit, so none of them can drift out of step with the data the way a number you typed in would.

10. Now, let's think about who's going to read your report, because it decides how much of your working they should see. This one is a technical document, written for people who know R, so showing the code is appropriate and everything you've done so far is fine as it is. But you'll often write for readers who don't know R at all, a clinical team, a service manager, a patient group, and for them a wall of code is just something to scroll past on the way to the results.

You control this on a chunk by chunk basis with the `echo` chunk option (see Section 8.5.3 of the book, which lists the chunk options alongside it).

Add `echo = FALSE` to your `chol-plot` chunk and knit. The plot is still there, but the code that drew it is not. Take it off again afterwards, since we want the code visible in this report.

Code isn't the only thing that can end up in your document without you asking for it.

Messages are the chatty output R produces while it's doing something in the background, most often when you load a package with `library()`, and they can easily run to half a dozen lines.

Warnings are R telling you that something might not be right, and they tend to look a lot more alarming to a reader than they usually deserve to. You've met one already. When `ggplot` drew your boxplot it warned that it had removed four rows, which are the four patients with no HDL cholesterol value. It's expected, and it isn't anything a reader needs to see.

Both messages and warnings land in the middle of your writing. You switch them off in the same way as the code, with `message = FALSE` and `warning = FALSE`, either on a single chunk or on all of them at once by putting them inside the `knitr::opts_chunk$set()` call in your `setup` chunk right at the top of your document.

Be careful with `warning = FALSE` though. You're hiding warnings from your reader, not from yourself, so keep an eye on the ones that turn up while you work, because some of them matter.

11. Not every figure in a report will be one you constructed with R code. You might need a diagram, a photograph, a map, or a figure somebody else made (see Section 8.5.4 of the book again). Add the plot you exported in **Exercise 6, Q9**, `ex6_admissions.png`, to your report under a heading of its own. If you no longer have the file, download it here and save it into your `output` directory, the one you created in **Exercise 1, Q12**.

There are two ways of doing this, so let's try both.

- a) The quick way doesn't need a code chunk at all, just a line typed in among your text. It looks like this, and you replace the two parts in capitals with your own:

```
! [YOUR CAPTION] (PATH/TO/YOUR/FILE.png)
```

An exclamation mark, then square brackets, then round brackets, with no spaces anywhere between them. Knit and check the figure appears.

- b) The other way puts the file into a code chunk instead, using the `include_graphics()` function, which is another one from the `knitr` package you loaded in Q2. On its own that looks like more work for the same result, but it's more flexible. Because the figure is now coming out of a chunk, all the chunk options are available to it, so you can caption it with `fig.cap` exactly as you did in Q7 and set how much of the page width it takes up with `out.width`. Again, replace the parts in capitals:

```
```{r YOUR-CHUNK-NAME, out.width = "50%", fig.cap = 'YOUR CAPTION'}
include_graphics("PATH/TO/YOUR/FILE.png")
```
```

Try it, and have a play with the `out.width` percentage until the figure sits sensibly on the page.

- c) Now write two or three sentences underneath it. Say what the figure shows and what a reader should take away from it. A figure dropped into a report with nothing said about it leaves the reader to work out for themselves why it is there, which is your job rather than theirs.

One thing that catches everybody out. The path is relative to where the `.Rmd` file is, not to your working directory. If the image doesn't appear, the path is almost always the reason.

12. Right, one more thing to go in the report. It records what you did to your data, but it doesn't record what you did it *with*. R gets updated, packages get updated, and code that gives you one answer today can give you a slightly different one in a year or two.

The `sessionInfo()` function writes all of that down for you. It prints your R version, your operating system, and every package that was loaded when the document was knitted, along with its version number. See Section 1.10 of the book for more explanation. Add a heading at the very end of your report, `## Session information`, and a code chunk underneath it that calls `sessionInfo()`.

Knit and have a look at what comes out. It isn't pretty and nobody's going to read it the way they read the rest of the report, but if you or somebody else ever reruns this and gets a different answer, that list is the first place to look. It costs you two lines and it's what makes your report properly reproducible.

13. **Optional.** Last of all, if you have time, here's one of the nicer things about R markdown. The same file will give you a completely different kind of document without you rewriting anything.

In your YAML header, change `pdf_document` to `html_document` and knit. You'll get a html file instead which you can open in your browser. This has been built from exactly the same text, code and figures. Change the header back to `pdf_document` before you finish.

You don't have to edit the YAML to do this. Click the small black triangle next to the **Knit** button and you can pick a format straight from the menu, the one in the picture back in Q1, which overrides whatever your YAML header says for that one knit. It's quicker for a look, but the YAML is where you set what your document actually is.

Two things we haven't covered

The visual editor. RStudio can show an R markdown document formatted as you type, more like a word processor, hiding the markdown syntax. Look for the pair of buttons marked **Source** and **Visual** at the top left of the editor toolbar, just above your document, and click **Visual**. The keyboard shortcut is `Ctrl+Shift+F4`, or `Cmd+Shift+F4` on a Mac. It's genuinely useful, especially for tables and links. We've left it until now on purpose, so that you learn what the markdown underneath actually looks like first, because when something goes wrong it's the markdown you have to fix.

Quarto. Quarto is the successor to R markdown. It does the same job, works with languages other than R, and its syntax is so close that nearly everything in this exercise transfers unchanged. If you carry on using R after this course you'll meet it. Start at quarto.org.

End of Exercise 7