

# Dynamic Reports

TheRBootcamp, <http://therbootcamp.github.io> (<http://therbootcamp.github.io>)



Source: <https://www.rstudio.com/> (<https://www.rstudio.com/>)

## Slides



Here are the introduction slides for this practical on dynamic reports!

([https://therbootcamp.github.io/\\_sessions/D4S1\\_DynamicReports/DynamicReports.html](https://therbootcamp.github.io/_sessions/D4S1_DynamicReports/DynamicReports.html))

## Overview

In this practical you'll practice creating interactive reports using RMarkdown.

## Cheatsheet

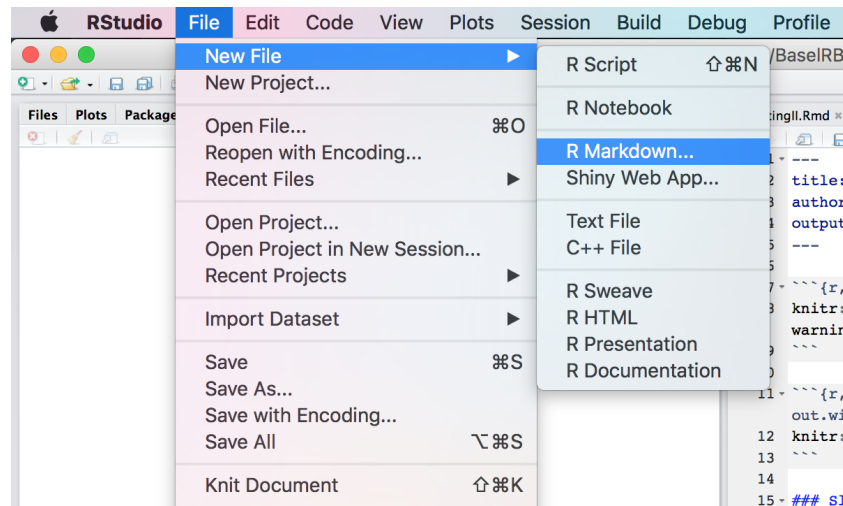
<div> <b>R Markdown</b> Reference Guide</div> <div>Learn more about R Markdown at <a href="http://rmarkdown.rstudio.com">rmarkdown.rstudio.com</a> Learn more about Interactive Docs at <a href="http://shiny.rstudio.com/articles">shiny.rstudio.com/articles</a></div> <div>Contents: 1. <b>Markdown Syntax</b> 2. Knitr chunk options 3. Pandoc options</div>	
Syntax	Becomes
Plain text	Plain text
End a line with two spaces to start a new paragraph.	End a line with two spaces to start a new paragraph.
<i>*italics*</i> and <i>_italics_</i>	<i>Italics and Italics</i>
<b>**bold**</b> and <b>__bold__</b>	<b>bold and bold</b>
superscript^2^	superscript <sup>2</sup>
~~strikethrough~~	<del>strikethrough</del>
[link] ( <a href="http://www.rstudio.com">www.rstudio.com</a> )	<a href="#">link</a>
# Header 1	<b>Header 1</b>
## Header 2	<b>Header 2</b>
### Header 3	<b>Header 3</b>
#### Header 4	<b>Header 4</b>
##### Header 5	<b>Header 5</b>
##### Header 6	<b>Header 6</b>
endash: --	endash: —
emdash: ---	emdash: —
ellipsis: ...	ellipsis: ...
inline equation: $A = \pi r^2$	inline equation: $A = \pi r^2$
image: ![] (path/to/smallorb.png)	image: 
horizontal rule (or slide break):	horizontal rule (or slide break):

<https://www.rstudio.com/wp-content/uploads/2015/03/rmarkdown-reference.pdf> (<https://www.rstudio.com/wp-content/uploads/2015/03/rmarkdown-reference.pdf>)

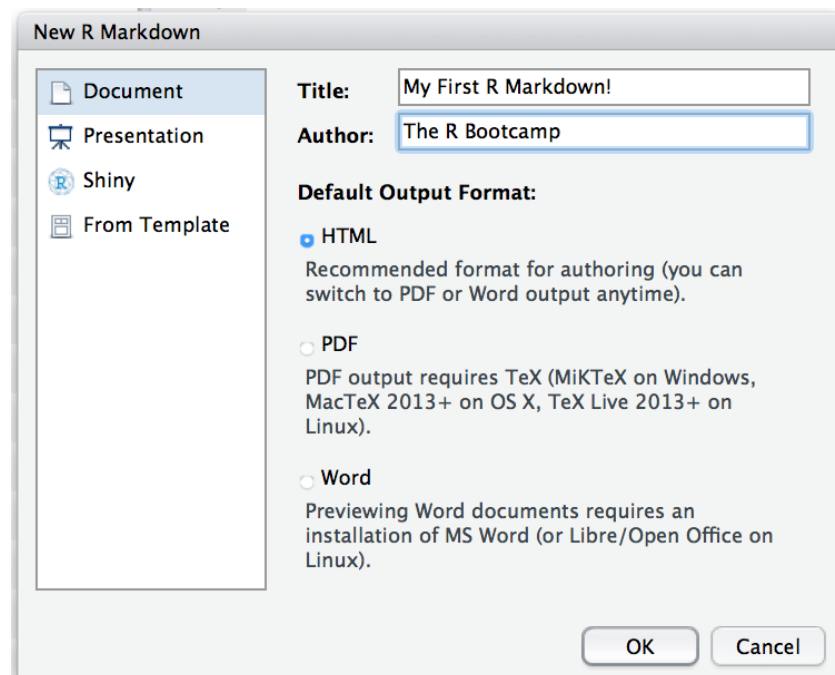
If you don't have it already, you can access the `Markdown` cheatsheet here <https://www.rstudio.com/wp-content/uploads/2015/03/rmarkdown-reference.pdf> (<https://www.rstudio.com/wp-content/uploads/2015/03/rmarkdown-reference.pdf>)

## Examples

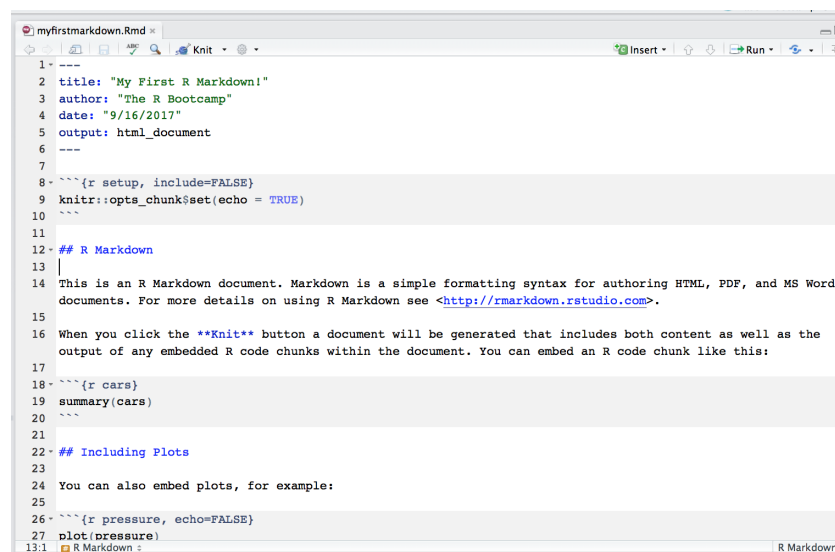
- Because R Markdown looks quite a bit different from standard R code, the best way to look at examples is to see a new R Markdown document in action. In RStudio, click File – New File – R Markdown



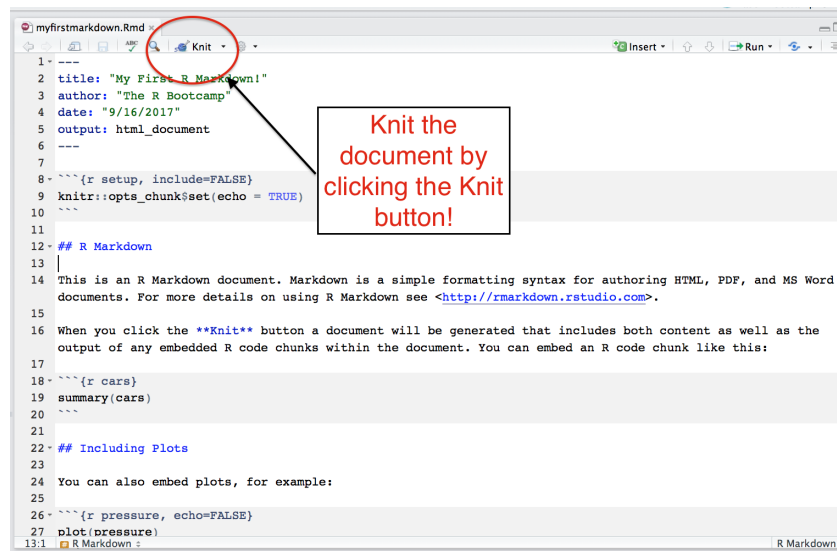
- Give the document a title and an author. For the output format, select HTML (the default). Click OK!



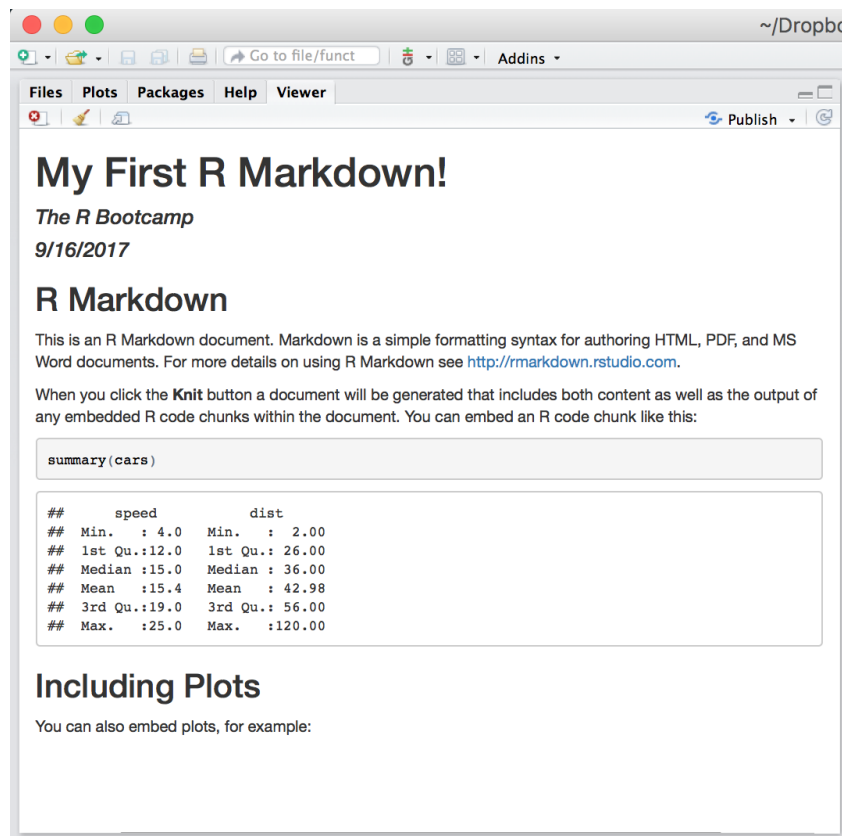
- A new file that looks like this should open up. This is your first R Markdown document!



- Before you do anything else, let's *knit* the R Markdown document to an HTML file. Click the *knit* button (or use the Command + Shift + K shortcut)



- Now you should see your final, HTML document! Scroll up and down the document and see how she looks!



## Tasks

1. Create a new R project called `dynamicreports.Rproj`. Add four folders `1_Data`, `2_Code`, `3_Materials`.
2. Go through the Examples above to create a new R Markdown document. Save the document under the name `speffanalysis.Rmd` in the root directory of your project (that is, next to the `dynamicreports.Rproj` file).
3. At the top of the `speffanalysis.Rmd` document, add a new R chunk. You can do this by clicking the "Insert" button at the top of the console, or by using the "Command + Option + i" shortcut.
4. In the chunk options, include `echo = FALSE`, `message = FALSE`, `warning = FALSE`. Inside of the chunk include the following code to set your global chunk options:

```
knitr::opts_chunk$set(fig.width = 6,      # Figure width (in)
                      fig.height = 6,     # Figure height (in)
                      echo = TRUE,        # Repeat code
                      eval = TRUE,        # Evaluate chunks
                      message = FALSE,    # Don't print messages
                      warning = FALSE,    # Don't print warnings
                      fig.align = 'center') # Center figures

options(digits = 2) # Round all output to 2 digits
```

4. Now create another chunk. Inside this chunk, write the comment `# Loading Packages -----`. Then, using the `library()` function, load the packages `tidyverse`, `knitr` and `speff2trial`.
5. Knit the document to make sure it worked! If you have any errors, try to figure out how to solve them!
6. For this practical we'll use the `ACTG175` dataset. This dataset originally comes from the `speff2trial` package. However, I saved a copy of the dataset as a text file at   
`"https://raw.githubusercontent.com/therbootcamp/therbootcamp.github.io/master/_sessions/_data/ACTG175.csv"`.  
 Open this link in a web-browser, and then save the `ACTG175.csv` file to the `1_Data` folder.
7. Create a new code chunk and put it under the previous one. We will use this chunk to load the `ACTG175.csv`. In this chunk, read the csv data with `read_csv()` and assign the result to the object `ACTG175`. Write appropriate comments in the chunk!
8. Knit the document! Diagnose and correct any errors!
9. Add the necessary text and markdown to your document to create the following two paragraphs. Pay attention to the header sizes, *italics* and `code` formats.

## Study

ACTG175 was a randomized clinical trial to compare monotherapy with *zidovudine* or *didanosine* with combination therapy with zidovudine and didanosine or zidovudine and *zalcitabine* in adults infected with the human immunodeficiency virus type I whose CD4 T cell counts were between 200 and 500 per cubic millimeter.

## Data

In R, the data is stored as `ACTG175`. The data originally come from the `speff2trial` package. However, for demonstration purposes, the analyses in this document are conducted from a copy of the dataset saved as text file `ACTG175.csv` on <http://therbootcamp.github.io>. The analyses in this document are based on this text file.

Write the necessary markdown to create this output!

10. Knit the document! Diagnose and correct any errors!
11. Add the appropriate combination of text, markdown, code chunks, and R code to add the following output to your document. To report the number of patients, use an in-line chunk to access the number directly from the data – that is, don't type 2139 directly! To create the table, create a new chunk, and inside that chunk, use the `kable()` function, with the appropriate arguments, to create the table.

# Analyses

The full dataset contains data from 2139 patients. For each patient, there are 26 observations (i.e., columns in the data). Table 1 shows the first 5 rows, and first 5 columns of the full dataset.

Table 1: First 5 rows and 5 columns of the full ACTG175 dataset

pidnum	age	wtkg	hemo	homo
10056	48	89.8128	0	0
10059	61	49.4424	0	0
10089	45	88.4520	0	1
10093	47	85.2768	0	1
10124	43	66.6792	0	1

12. Knit the document! Diagnose and correct any errors!

13. Write the necessary code to add the following output to your document. To do this, create a new chunk. In the chunk use `dplyr` code to create the summary table of data. Assign the result to the object `trial_summary`. Then, use `kable()` to render this dataframe as a table in the final document.

One of the primary measures was the number of days until a major negative event. Across all patients, the median number of days was 879.1. However, the results did differ between treatment arms. Summary statistics of the number of days, separated by each treatment arm, are presented in Table 2:

Summary statistics of the number of days until a major negative event for different treatment arms.

arms	N	Mean	Median	SD	Max
0	532	801	934	327	1231
1	522	916	1014	264	1224
2	524	906	1012	275	1231
3	561	893	1000	285	1230

Here is some code you might find helpful in creating this table!

```
# Helpful code to create the summary table!

trial_summary <- ACTG175 %>%
  group_by(arms) %>%
  summarise(
    N = n(),
    Mean = mean(days),
    Median = median(days),
    SD = sd(days),
    Max = max(days))
```

14. Knit the document! Diagnose and correct any errors!

15. Add the appropriate combination of text, markdown, code chunks, and R code to add the following output to your document. Be sure to include the figure caption (you can do this with the `fig.cap` argument to the chunk)

A plot showing the relationship between treatment arm and number of days until a major negative event are presented in Figure 2:

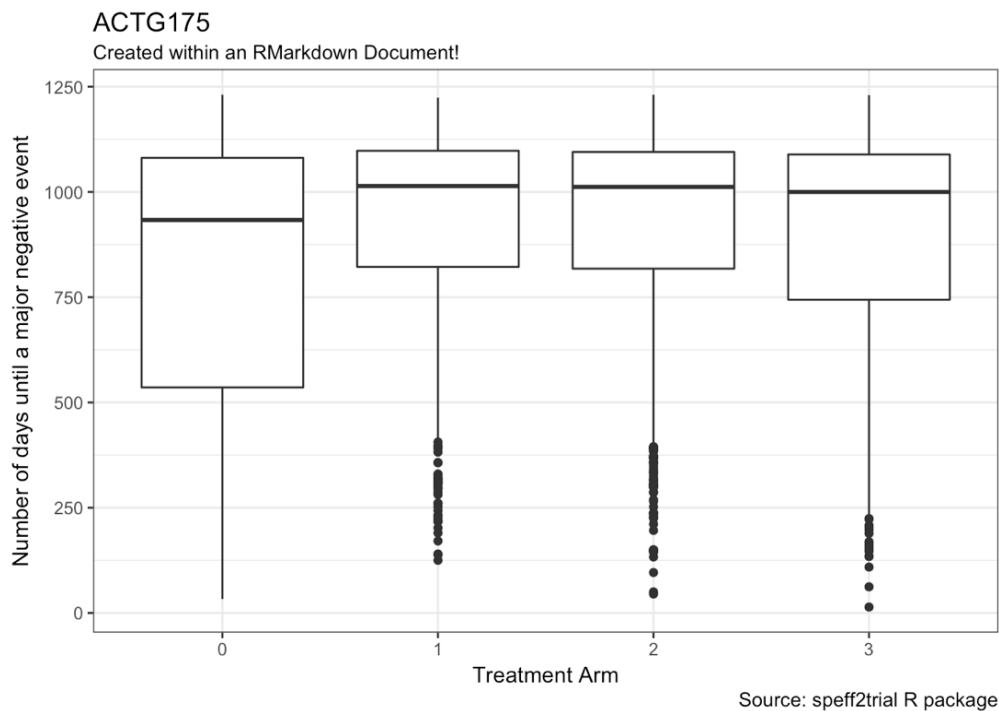


Figure 2: Number of days until a major negative event separated by treatment arm

This code might help you to create the plot:

```
# Boxplot code template

ggplot(data = XX,
       mapping = aes(x = factor(XX), y = XX)) +
  geom_boxplot() +
  labs(x = "Treatment Arm",
       y = "Number of days until a major negative event",
       title = "ACTG175",
       subtitle = "Created within an RMarkdown Document!",
       caption = "Source: speff2trial R package") +
  theme_bw()
```

16. Knit the document! Diagnose and correct any errors!

17. Add a new section called “Conclusions”. Write the main conclusions of your analyses in one or two sentences. Feel free to add some formatting and/or in-line chunks to your content!

18. You can easily publish an HTML document online to Rpubs.com for free. To do this, Knit your document. Then, click the blue “Publish” button. Go through the process of signing up for a free Rpubs account and get your document online!

## Slideshow

19. Now it's time to create a slideshow! To do this, we'll start with one of the templates in RStudio. Click File – New File – R Markdown. Then select “Presentation”. Give the presentation a title and your name as the author. Then click ok.

20. You should see a new .Rmd document open. Save the document in your main directory as `slideshow.Rmd`.

21. Knit the document to see the outline of the presentation!

*Note:* If you don't like the look of the default presentation, you can also try a Ninja presentation [click here for a demo](https://slides.yihui.name/xaringan/#1) (https://slides.yihui.name/xaringan/#1) from the `xaringan` package (that's what we use for all of our BaselRBootcamp slides). To install the `xaringan` package from GitHub, run the following code. Then open a new template with File – New File – R Markdown – From Template – Ninja Presentation.

22. Play around with the presentation a bit. Change the existing content a bit and add a few slides. Try adding an image (maybe this one: [https://actgnetwork.org/sites/default/files/https://actgnetwork.org/sites/default/files/.\\_image/ACTG\\_logo\\_2007\\_color.jpg](https://actgnetwork.org/sites/default/files/https://actgnetwork.org/sites/default/files/._image/ACTG_logo_2007_color.jpg)) by saving the image to your `3_Materials` folder, and then loading the image into your document with `include_graphics()`.

23. Now, try to customize the presentation to include all of main analyses, outputs, and plots you have in your `speffanalysis.Rmd` document! Of course, there won't be room for all of the text, so treat it like a normal presentation and put in what's important.

## Challenges

C1. A researcher wants to know if there is a correlation between patients' CD4 T cell count at baseline (`cd40`) and the number of days until a major negative event. Include this information as a new subsection (with a second level header) in your analyses. To do this, run the following chunk. Then, write a sentence with the main outputs from the test, using inline chunks to directly access the correlation and the p-value. For example, a sentence could be: "The correlation between CD4 T cell count at baseline and number of days until a major negative event was  $r = XX$ ,  $p = YY$ ".

```
# Correlation test between cd40 and days

cd4_cor <- cor.test(formula = ~ cd40 + days,
                    data = ACTG175)

cd4_cor_r <- cd4_cor$estimate # Get the correlation
cd4_cor_p <- cd4_cor$p.value  # Get the p-value
```

C2. In addition to the correlation test, include a relevant scatterplot showing the relationship between CDT4 T cell count at baseline and number of days until a major negative event.