

PDF Project

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This is a tutorial on how to use R markdown for reproducible research.

Here we can type long passages or descriptions of our data without the need of “hashing” out our comments with the hashtag symbol. In our first example, we will be using the Toothgrowth dataset. In this experiment, Guinea pigs (literal) were given different amount of vitamin C to see the effects on the animal’s tooth growth.

To run code in a markdown file, we need to denote the section that is considered R code. We call these “code chunks”.

Below is a code chunk:

```
Toothdata <- ToothGrowth  
  
head(Toothdata)
```

```
##      len supp dose  
## 1  4.2   VC  0.5  
## 2 11.5   VC  0.5  
## 3  7.3   VC  0.5  
## 4  5.8   VC  0.5  
## 5  6.4   VC  0.5  
## 6 10.0   VC  0.5
```

As you can see, the from running the “play” button on the code chunk, the results are printed in line of the r markdown file.

```
fit <- lm(len ~ dose, data = Toothdata)  
  
b <- fit$coefficients  
  
plot(len ~ dose, data = Toothdata)  
  
abline(lm(len ~ dose, data = Toothdata))
```

The slope of the regression line is 9.7635714.

Section Headers

WE can also put sections and subsections in our R markdown file, similar to numbers or bulletpoints in a word document. This is done with the “#” that we previously used to denote text in an r script.

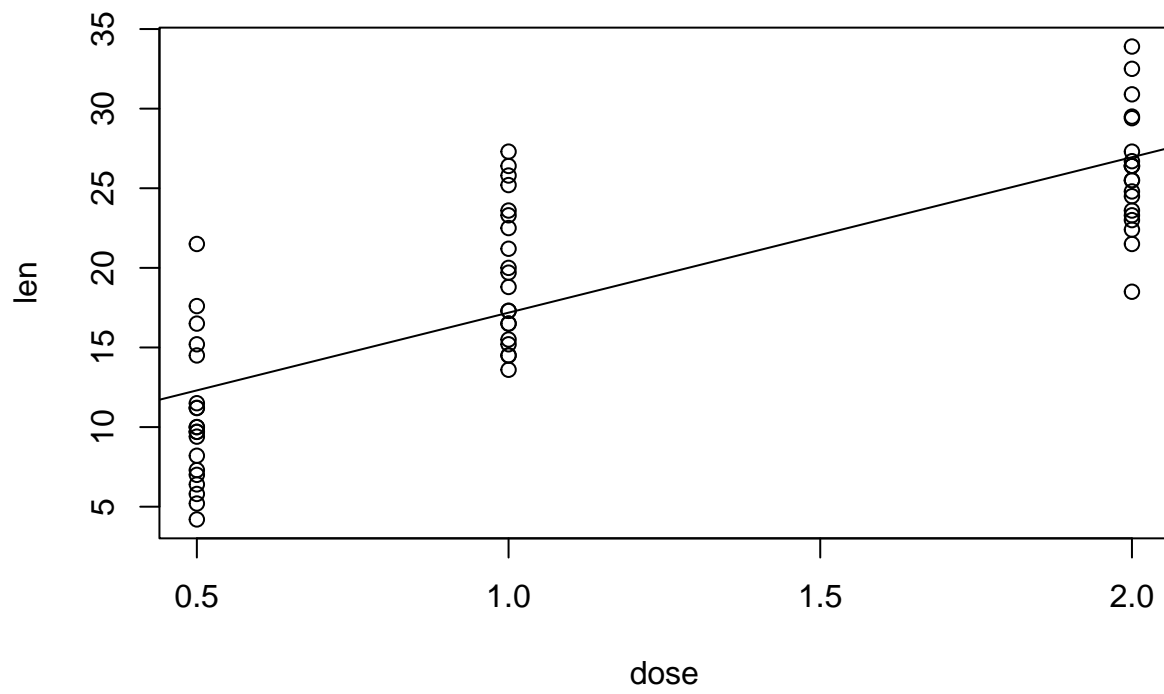


Figure 1: fig 1: Guinea Pig Tooth Growth

First level header

Second Level header

Third level header

Make sure that you a space after the hashtag, otherwise it won't work

We can also add bullet point-type marks in our r markdown file.

- one item
- one item
- One item
 - one more item
 - one more item
 - one more item
 - * one last item

it's important to note here that in R markdown, indentation matters!

1. First item
2. Second item
3. Third item

- Subitem 1
- Subitem 2
- Subitem 3

Block Quotes

We can put really nice quotes into the markdown document. We do this by using the “>” symbol.

“Genes are like the story, and DNA is the language that the story is written in.”
— Sam Kean

Hyperlinks

Hyperlinks can also be incorporated into these files. This is especially useful in HTML files, since they are in a web browser and will redirect the reader to the material that you are interested in showing them. Here we will use the link to R markdown's homepage for this example. Rmarkdown

Formulas

WE can also put nice formatted formulas into markdown using two dollar signs.

Hard-Weinberg Formula

$$p^2 + 2pq + q^2 = 1$$

And you can get really complex as well!

$$\Theta = \begin{pmatrix} \alpha & \beta \\ \gamma & \delta \end{pmatrix}$$

Code chunks

Code chunk options

There are also options for markdown file on how knitr interprets the code chunk. There are the following options: Eval (T or F): Whether or not to evaluate the code chunk

```
print("hello world!")
```

```
## [1] "hello world!"
```

```
print("I am testing the eval function")
```

Echo (T or F): Whether or not to show the code for the chunk, but results will still print.

Cache: If enabled, the same code chunk will not be evaluated the next time that the knitr is run. This is great for code that has long run times.

fig.width or fig.height: The (graphical device) size of the R plots in inches. The figures are first written to the knitr documents, then to files that are saved separately.

out.width or out.height: The output size of the R plot in the R document.

fig.cap: the words for the figure caption.

Table of Contents

We can also add a table of contents to our HTML Document. We do this by altering the YAML code (the weird code chunk at the very top of the document.) We can add this:

```
title: "HTML_TUTORIAL" author: "Pascal Onaho" date: "2024-05-15" output: html_document: toc: true toc_float: true
```

This will give us a very nice floating table of content on the right hand side of the document.

Tabs

You can also add TABS in our report. To do this, you need to specify each section that you want to become a tab by placing "{.tabset}" after the line. Every subsequent header will be a new tab.

Themes

You can also add themes to your HTML document that changes the highlighting colour and hyperlink colour of your HTML output. This can be nice aesthetically. To do this, you change your theme in the YAML to one of the following:

Cerulean Journal Flatly readable spacelab untied cosmo lumen paper sand stone simplex yeti null

You can also change the colour by specifying highlight: default tango payment kate monochrome espresso zenburn haddock textmate

Code folding

you can also use the code folding option to allow the reader toggle between displaying and hiding the code. This is done with: code_folding: hide

Summary

There are a ton of options and ways for one to customize their R code using HTML format. This is also a great way to display a “Portfolio” of your work if you are trying to market yourself to interested parties.