

BIOSCI738 Lab 1: Learning R markdown

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Exercise: write a section/paragraph of text that includes as many of the above as you can. You can even look for more syntax options on the Rmarkdown website

My work

Test paragraph

This is not my first time using R or Rmarkdown, however it has been about two years since I have used it, so **I have forgotten everything**. I know I will have to work *really* hard in this course but I am excited to learn!

As many people have told me...

“Learning how to code will help you alot in your career”

And if I get stressed then I can look at this cute picture of a puppy! Click here for photo.

Now that I know how to ~~cross out my mistakes~~ and format my work nicely, I am already on the right track! And I can highlight *important conclusions in my writing!*

Test equations

I have always found formatting equations in work difficult, so ~~hopfully~~ hopefully this will be easier. I will probably be using equations a lot in my research, for example: $Y = X_1 + X_2$

Lists!

Now I have written my paragraph, all I have left to do is

- Finish this lab by
 - Completing the other exercises
 - Knitting the document
 - Up loading the document

Following that I will:

1. Have a cup of tea to celebrate
2. Start cooking dinner
 - chop veges
 - cook rice
3. Combine into fried rice
4. Eat the fried rice

I also need to plan out when my next assignments are due so that I keep on track! The ones due closest are:

Assignment	Class	Due date
Seminar	735	15/3
Assignment 1	738	25/3
Policy submission	747	30/3
Research summary	761	30/3

Exercise: change the title of this document to something informative and specific to this lab. Add in your name and the date too. Done! :)

Exercise: Write a chunk of R code that carries out some basic manipulation on the palmerpenguins data. Include chunks that 1) both evaluates and prints the code, 2) only evaluates the code, and 3) only prints the code.

1) Evaluate and print code

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5      v purrr   0.3.4
## v tibble  3.1.6      v dplyr  1.0.8
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(palmerpenguins)
penguins_nafree <- penguins %>% drop_na()
filter(penguins_nafree, island == "Biscoe") %>%
  group_by(species) %>%
  summarise(avgerage_flipper_length= mean(flipper_length_mm))
```

```
## # A tibble: 2 x 2
##   species avgerage_flipper_length
##   <fct>      <dbl>
## 1 Adelie      189.
## 2 Gentoo      217.
```

```
filter(penguins_nafree, island == "Dream") %>%
  group_by(species) %>%
  summarise(avgerage_flipper_length= mean(flipper_length_mm))
```

```
## # A tibble: 2 x 2
##   species avgerage_flipper_length
##   <fct>      <dbl>
## 1 Adelie      190.
## 2 Chinstrap    196.
```

2) Only evaluate code

```
## # A tibble: 2 x 2
##   species avgerage_flipper_length
##   <fct>      <dbl>
## 1 Adelie      189.
## 2 Gentoo      217.
```

```
## # A tibble: 2 x 2
##   species avgerage_flipper_length
##   <fct>      <dbl>
## 1 Adelie      190.
## 2 Chinstrap    196.
```

3) Only print code

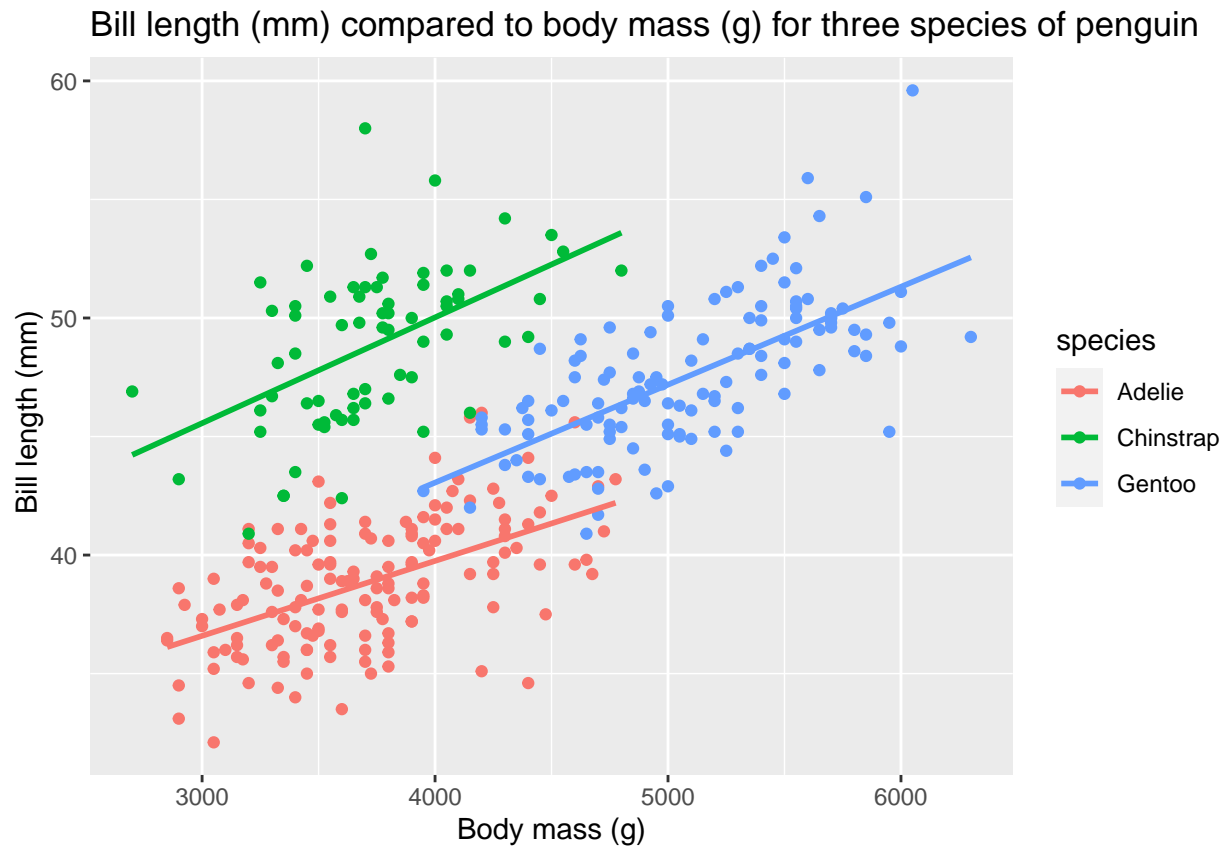
```
library(tidyverse)
library(palmerpenguins)
penguins_nafree <- penguins %>% drop_na()
filter(penguins_nafree, island == "Biscoe") %>%
  group_by(species) %>%
  summarise(avgerage_flipper_length= mean(flipper_length_mm))

filter(penguins_nafree, island == "Dream") %>%
  group_by(species) %>%
  summarise(avgerage_flipper_length= mean(flipper_length_mm))
```

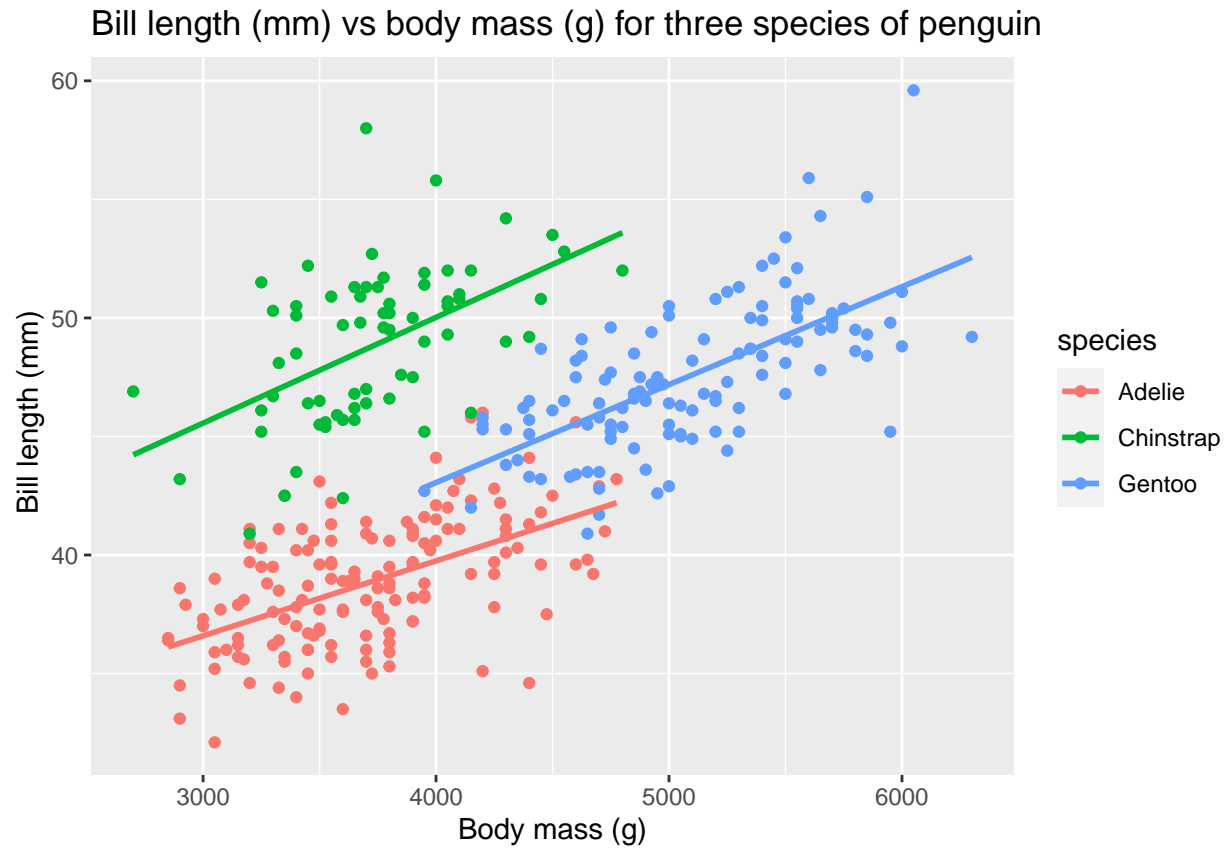
Exercise: Write a chunk of R code that creates a basic plot of the palmerpenguins data. Include chunks that 1) both prints the code and shows the plot, 2) only shows the plot, and 3) only shows the plot with a figure caption included.

1) Print code and show plot

```
library(ggplot2)
ggplot(penguins_nafree, aes(x = body_mass_g, y = bill_length_mm, color = species)) +
  geom_point() +
  geom_smooth(method = 'lm', se = FALSE) +
  ggtitle("Bill length (mm) compared to body mass (g) for three species of penguin") +
  ylab(" Bill length (mm)") +
  xlab("Body mass (g)")
```



2) Only show the plot



3) Only shows plot with figure caption included

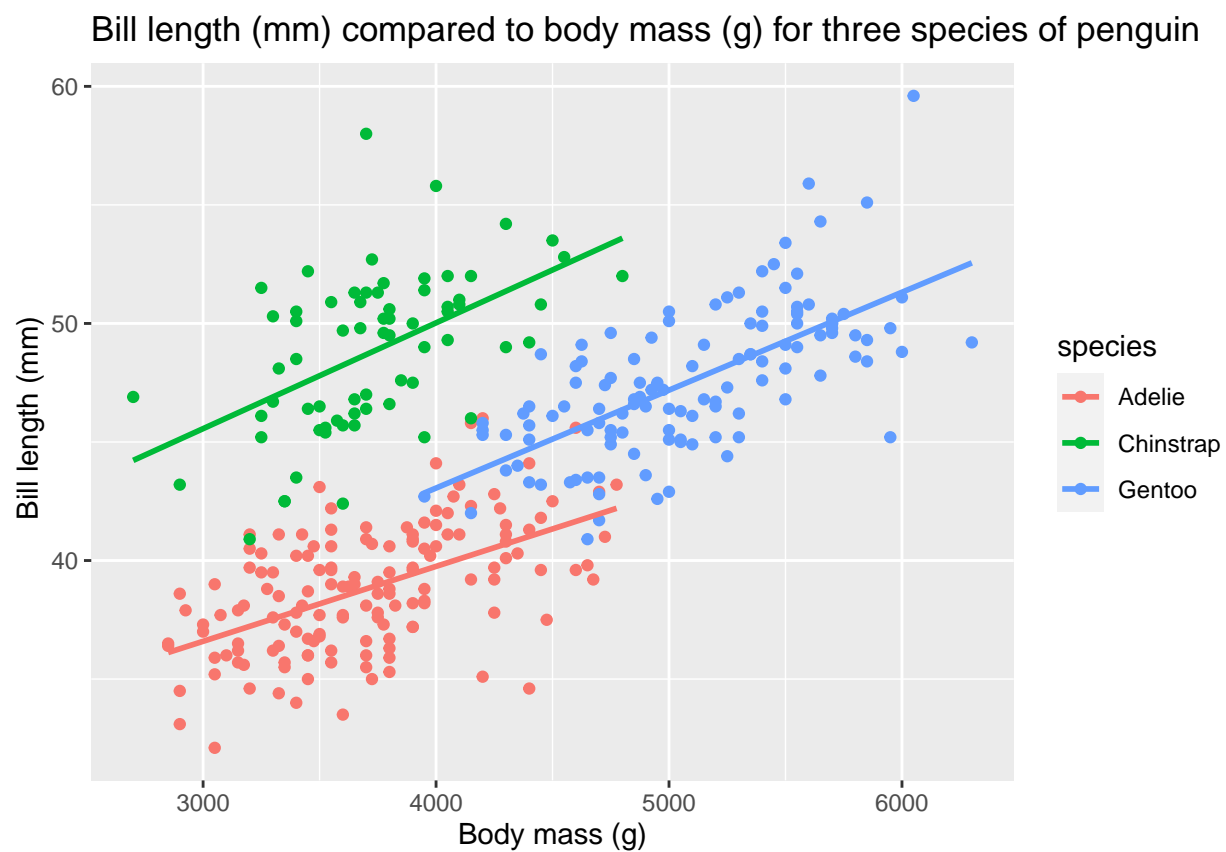


Figure 1: Graph created for BIOSCI 738 for Lab 1 showing the relationship between bill length (mm) and body mass (g) of Adelie, Chinstrap and Gentoo penguins, using the palmerpenguin data