

Week 7 Challenge

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2023-10-02

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

II. Code to edit and execute using the Code-along-6.Rmd file

```
# Loading the package and dataset
```

```
# Enter code here
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v dplyr      1.1.2      v readr      2.1.4
```

```
## v forcats   1.0.0      v stringr   1.5.0
```

```
## v ggplot2    3.4.3      v tibble    3.2.1
```

```
## v lubridate  1.9.2      v tidyr     1.3.0
```

```
## v purrr      1.0.2
```

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

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

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

```
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
penguins <- read_csv("penguins.csv")
```

```
## Rows: 344 Columns: 9
```

```
## -- Column specification -----
```

```
## Delimiter: ","
```

```
## chr (3): species, island, sex
```

```
## dbl (6): rowid, bill_length_mm, bill_depth_mm, flipper_length_mm, body_mass...
```

```
##
```

```
## i Use 'spec()' to retrieve the full column specification for this data.
```

```
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

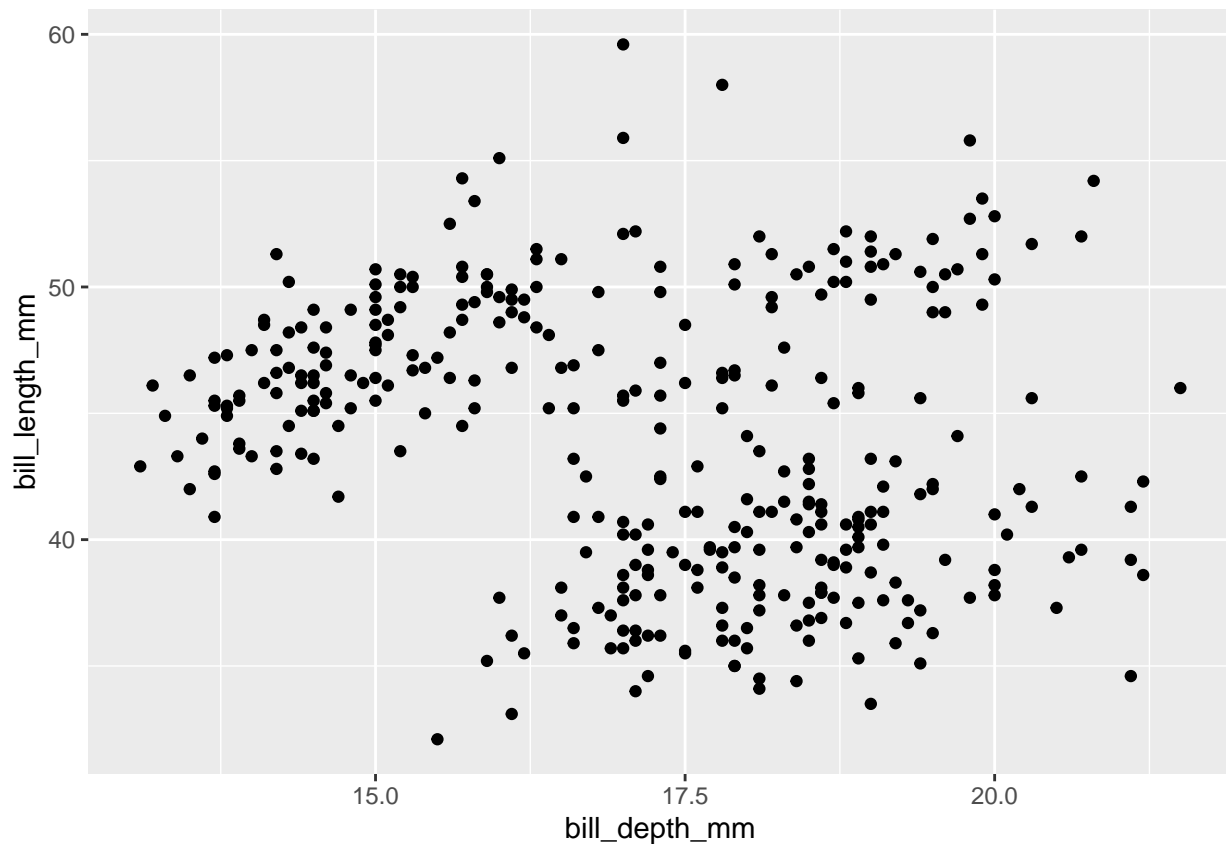
```
glimpse(penguins)
```

```
## Rows: 344
## Columns: 9
## $ rowid      <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1~
## $ species    <chr> "Adelie", "Adelie", "Adelie", "Adelie", "Adelie", "A~
## $ island     <chr> "Torgersen", "Torgersen", "Torgersen", "Torgersen", ~
## $ bill_length_mm <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34.1, ~
## $ bill_depth_mm <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18.1, ~
## $ flipper_length_mm <dbl> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186~
## $ body_mass_g <dbl> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, ~
## $ sex        <chr> "male", "female", "female", NA, "female", "male", "f~
## $ year       <dbl> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007~
```

```
# plotting a graph to interpret the relationship between bill length and bill depth
# Enter code here
```

```
ggplot(data=penguins,
       mapping = aes(x=bill_depth_mm,
                     y=bill_length_mm)) +
  geom_point()
```

```
## Warning: Removed 2 rows containing missing values ('geom_point()').
```



```
# plotting the same graph above but mapping species to the colour of each point
# Enter code here
ggplot(data=penguins,
       mapping = aes(x=bill_depth_mm,
                     y=bill_length_mm,
                     colour = species)) +
  geom_point()
```

Warning: Removed 2 rows containing missing values ('geom_point()').

