

Penguins RMarkdown Sample

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Setting up the environment

Here is where we load the packages into the libraries:

```
library("ggplot2")

library("palmerpenguins")

library("tidyverse")

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

## v tibble 3.1.4      v dplyr 1.0.7
## v tidyr 1.1.4      v stringr 1.4.0
## v readr 2.0.2      v forcats 0.5.1
## v purrr 0.3.4

## -- Conflicts -----
tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
```

In this section we'll load the data frame into the file.

```
data(penguins)
```

This *view* function is optional to view the schema of the data frame.

```
view(penguins)
```

The *head* function is a great way to quickly preview the data frame in a tibble

```
head(penguins)
```

```
## # A tibble: 6 x 8
##   species island bill_length_mm bill_depth_mm flipper_length_~ body_mass_g
sex
##   <fct>   <fct>         <dbl>         <dbl>         <int>         <int>
<fct>
## 1 Adelie  Torge~           39.1           18.7           181           3750
male
## 2 Adelie  Torge~           39.5           17.4           186           3800
fema~
## 3 Adelie  Torge~           40.3            18           195           3250
fema~
## 4 Adelie  Torge~            NA            NA            NA            NA
```

```

<NA>
## 5 Adelie  Torge~          36.7          19.3          193          3450
fema~
## 6 Adelie  Torge~          39.3          20.6          190          3650
male
## # ... with 1 more variable: year <int>

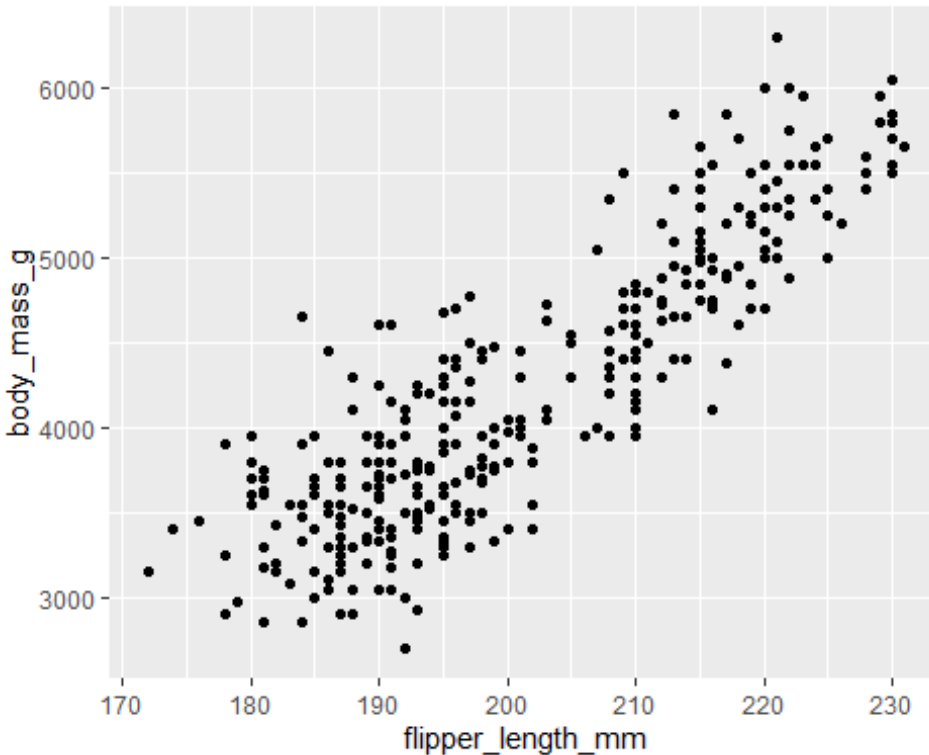
```

After a quick preview here is the code to render the plot for the data.

```

ggplot(data = penguins) +
  geom_point(mapping = aes(x = flipper_length_mm, y = body_mass_g))

```

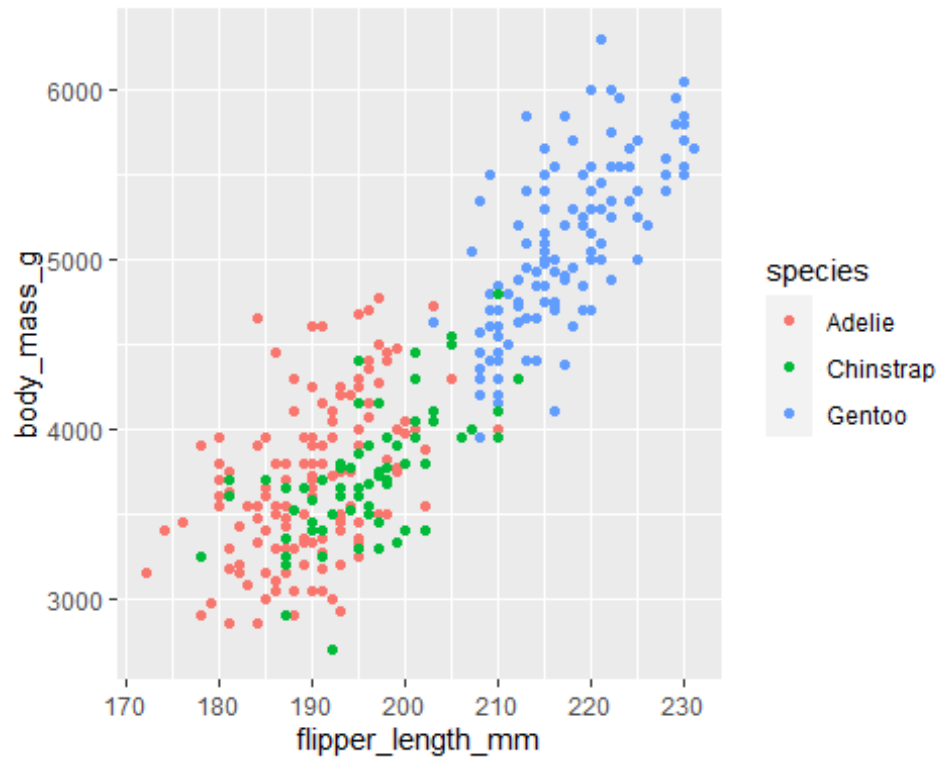


Here is a version with the points formatted by color for species:

```

ggplot(data = penguins) +
  geom_point(mapping = aes(x = flipper_length_mm, y = body_mass_g, color = species))

```



Lastly here are the species broken out into their own subplots:

```
ggplot(data = penguins) +  
  geom_point(mapping = aes(x = flipper_length_mm, y = body_mass_g, color =  
species)) +  
  facet_wrap(~species)
```

