

Lab 3

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```
options(repos = "https://mirrors.nics.utk.edu/cran/")
contrib.url("https://mirrors.nics.utk.edu/cran/")
```

```
## [1] "https://mirrors.nics.utk.edu/cran/src/contrib"
```

```
install.packages("palmerpenguins")
```

```
##
## The downloaded binary packages are in
## /var/folders/ph/k62cts0d4nd_l67yrv4q7v8m0000gn/T//Rtmp3j0YIW/downloaded_packages
```

```
library(palmerpenguins)
library(tidyr)
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v purrr      1.0.2
## v forcats    1.0.0      v readr      2.1.5
## v ggplot2    3.4.4      v stringr    1.5.1
## v lubridate  1.9.3      v tibble     3.2.1
## -- 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
```

```
data(package='palmerpenguins')
```

Data

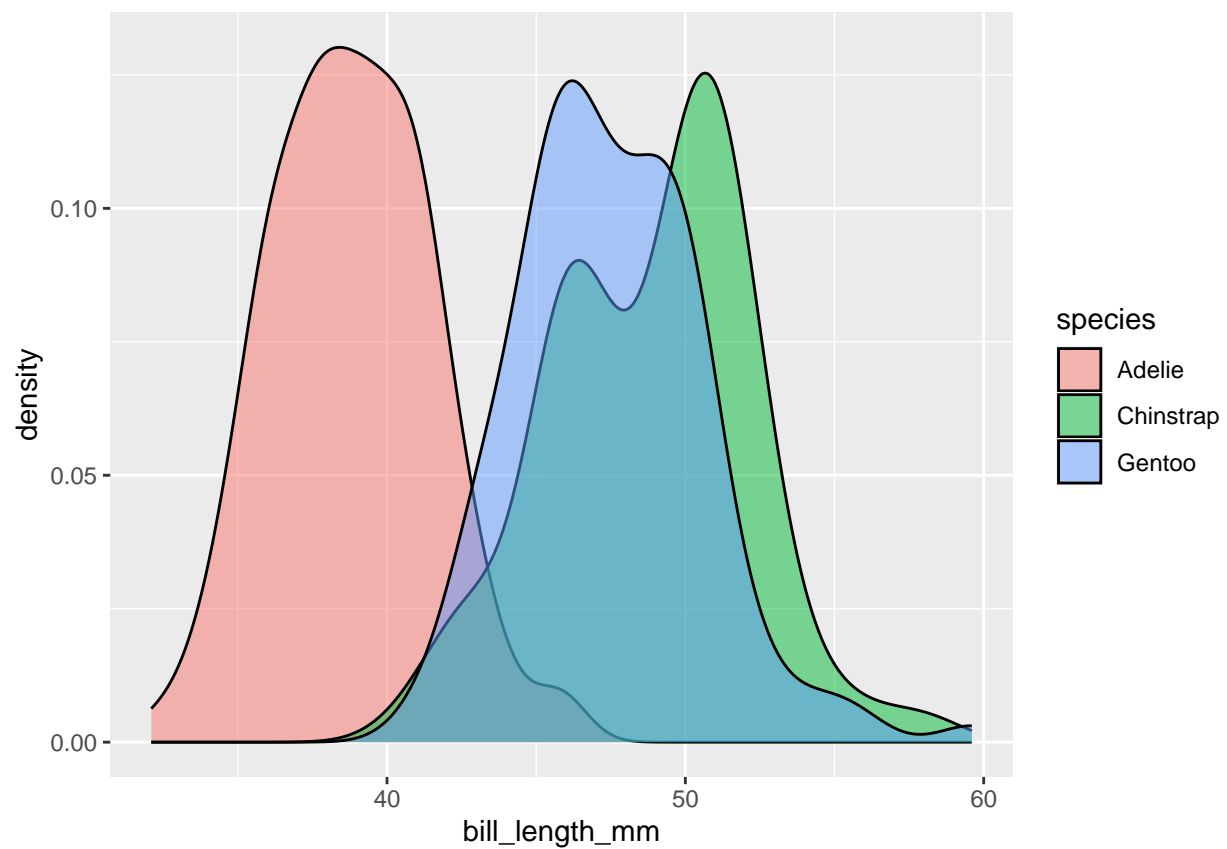
The data used in this lab represent the patterns of morphological traits in three different species of penguin. This data were collected and made available by Dr. Kristen Gorman and the Palmer Station, Antarctica LTER, and were compiled by Dr. Allison Horst and colleagues.



Single trait distribution

```
penguins %>%
  ggplot() +
  geom_density(mapping = aes(x = bill_length_mm, fill=species), alpha=0.5)
```

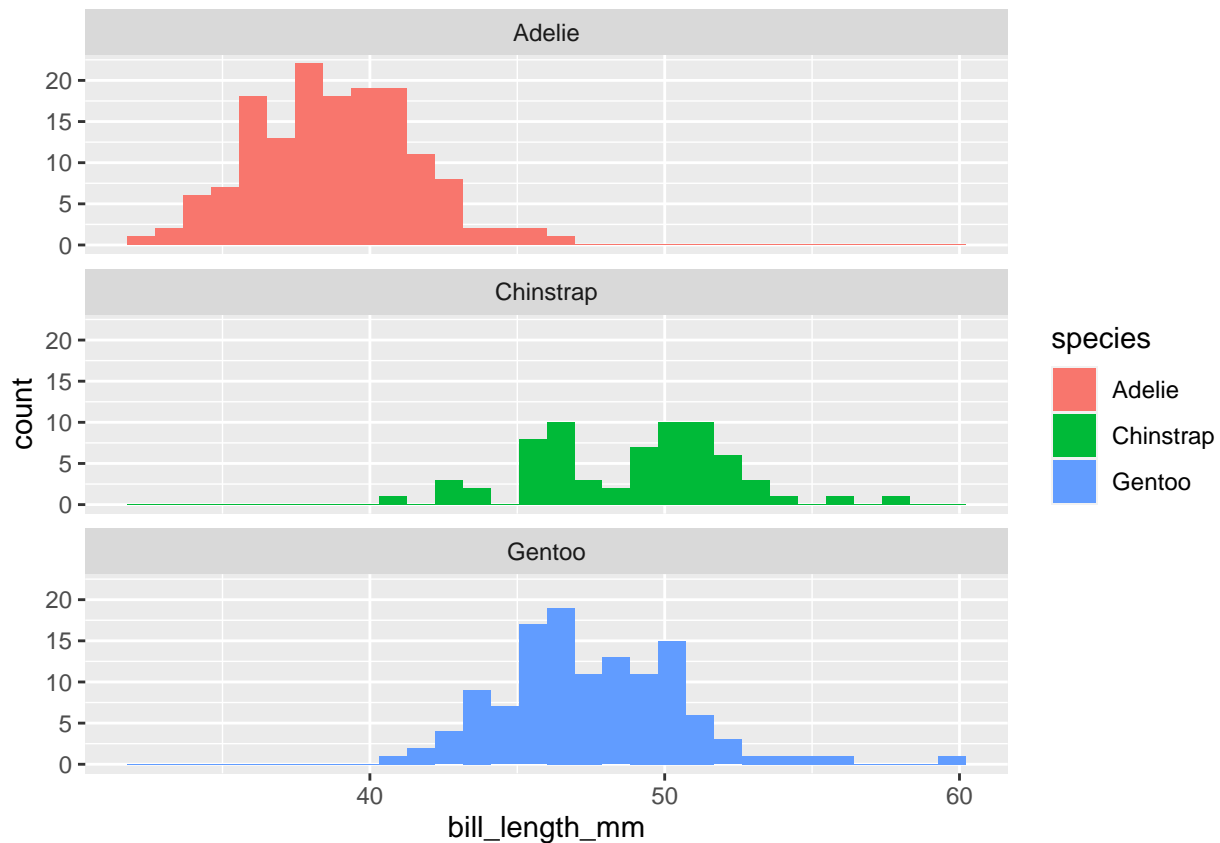
Warning: Removed 2 rows containing non-finite values ('stat_density()').



```
penguins %>%
  ggplot() +
  geom_histogram(mapping = aes(x = bill_length_mm, fill=species)) +
  facet_wrap(~species, nrow=3)
```

'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.

Warning: Removed 2 rows containing non-finite values ('stat_bin()').



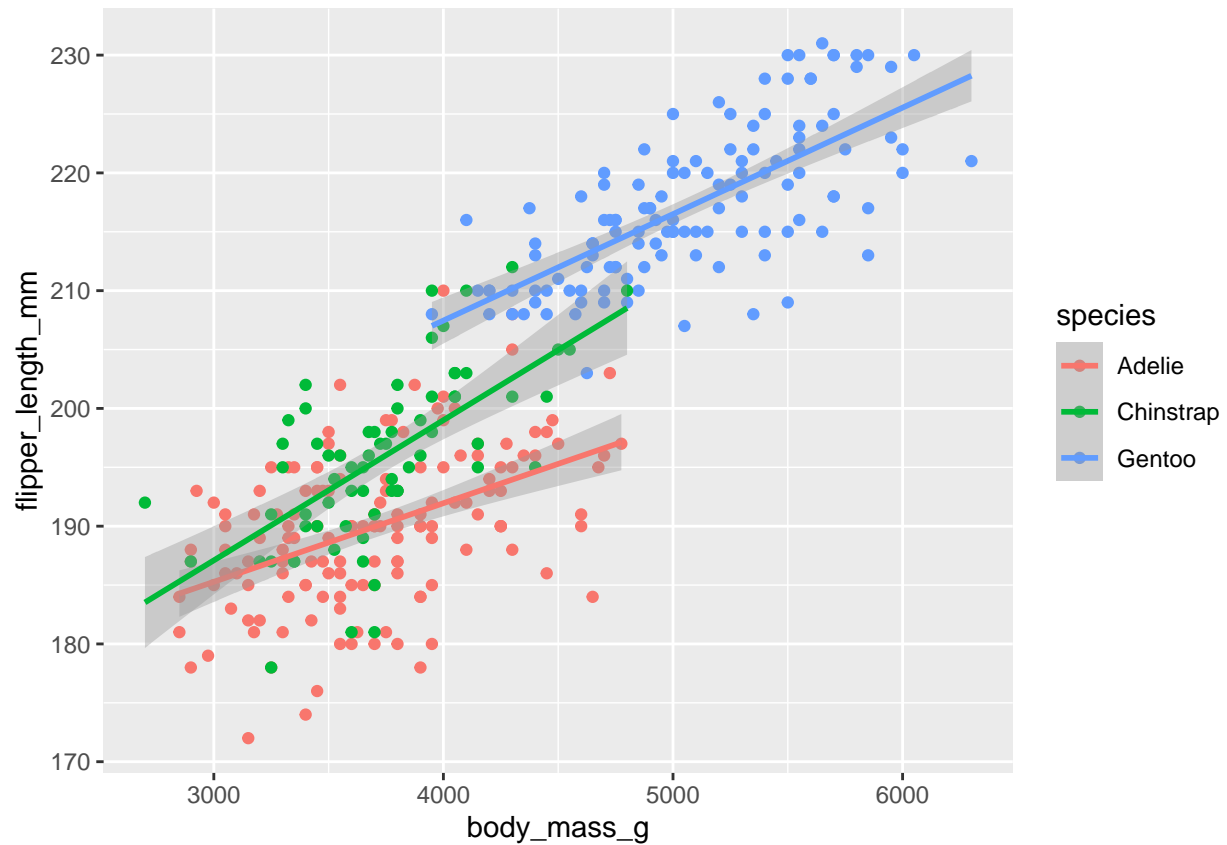
Relationship between multiple traits

```
penguins %>%
  ggplot(mapping = aes(x = body_mass_g, y=flipper_length_mm, color=species)) +
  geom_point() +
  geom_smooth(method="lm")
```

'geom_smooth()' using formula = 'y ~ x'

Warning: Removed 2 rows containing non-finite values ('stat_smooth()').

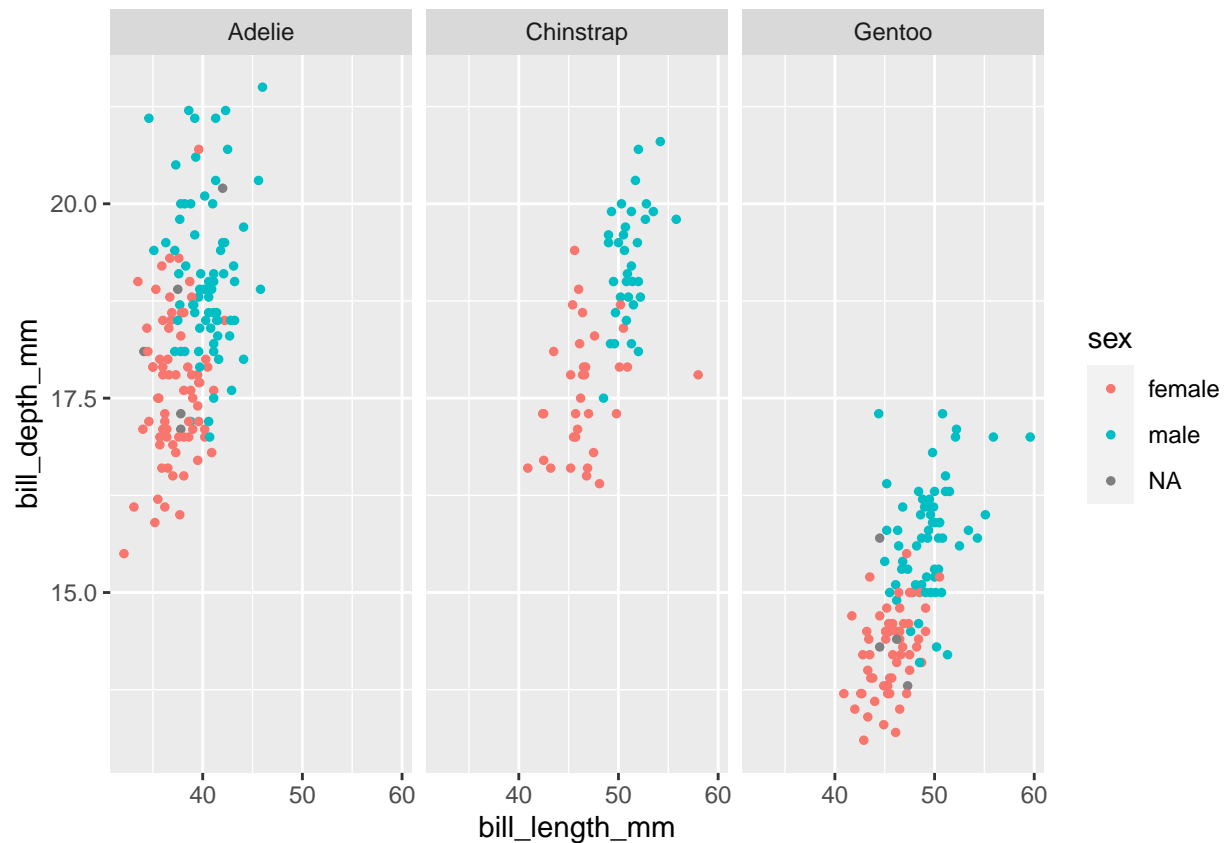
Warning: Removed 2 rows containing missing values ('geom_point()').



Sexual dimorphism

```
penguins %>%
  ggplot(mapping = aes(x = bill_length_mm, y=bill_depth_mm, color=sex)) +
  geom_point(size=1) +
  facet_wrap(~species)
```

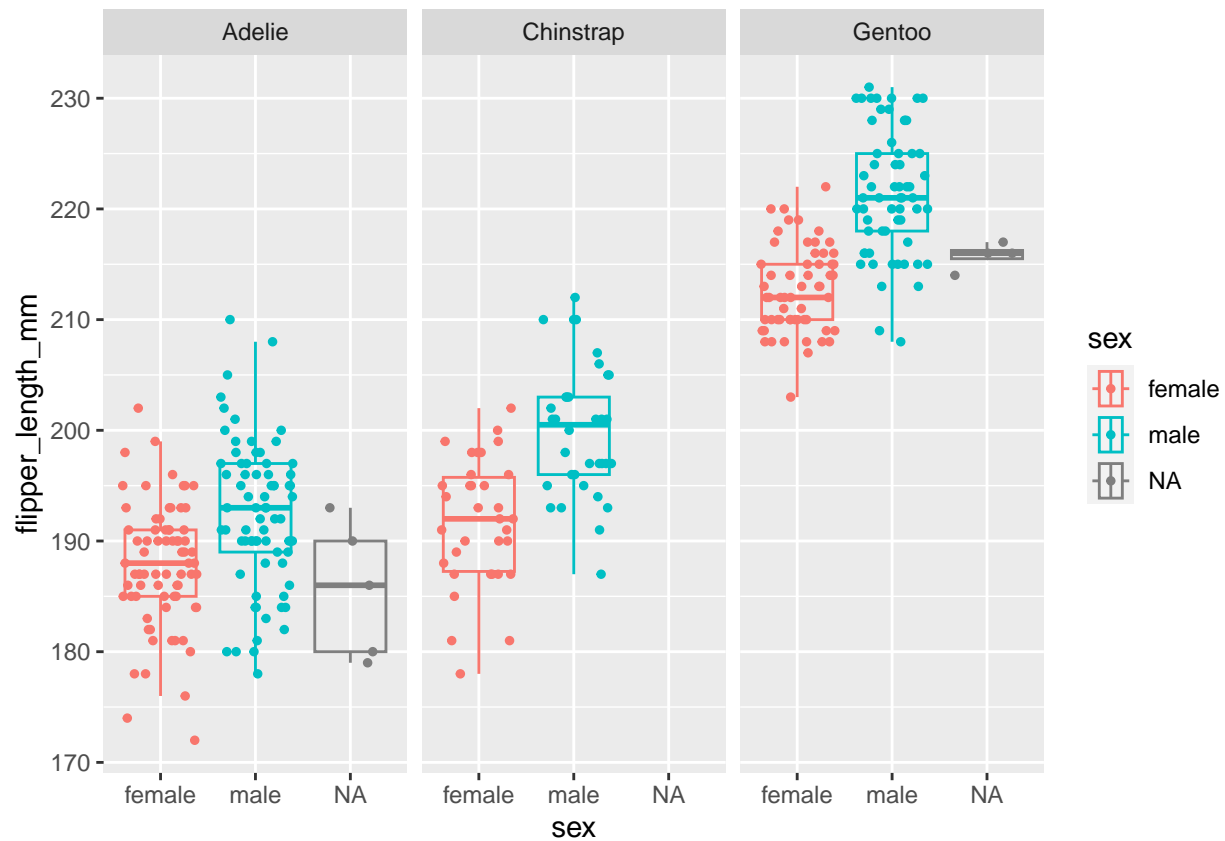
```
## Warning: Removed 2 rows containing missing values ('geom_point()').
```



```
penguins %>%
  ggplot(mapping = aes(x=flipper_length_mm, y=sex, color=sex)) +
  geom_boxplot(outlier.alpha = 0, alpha=0) +
  geom_jitter(width = 0, size=1) +
  coord_flip() +
  facet_wrap(~species)
```

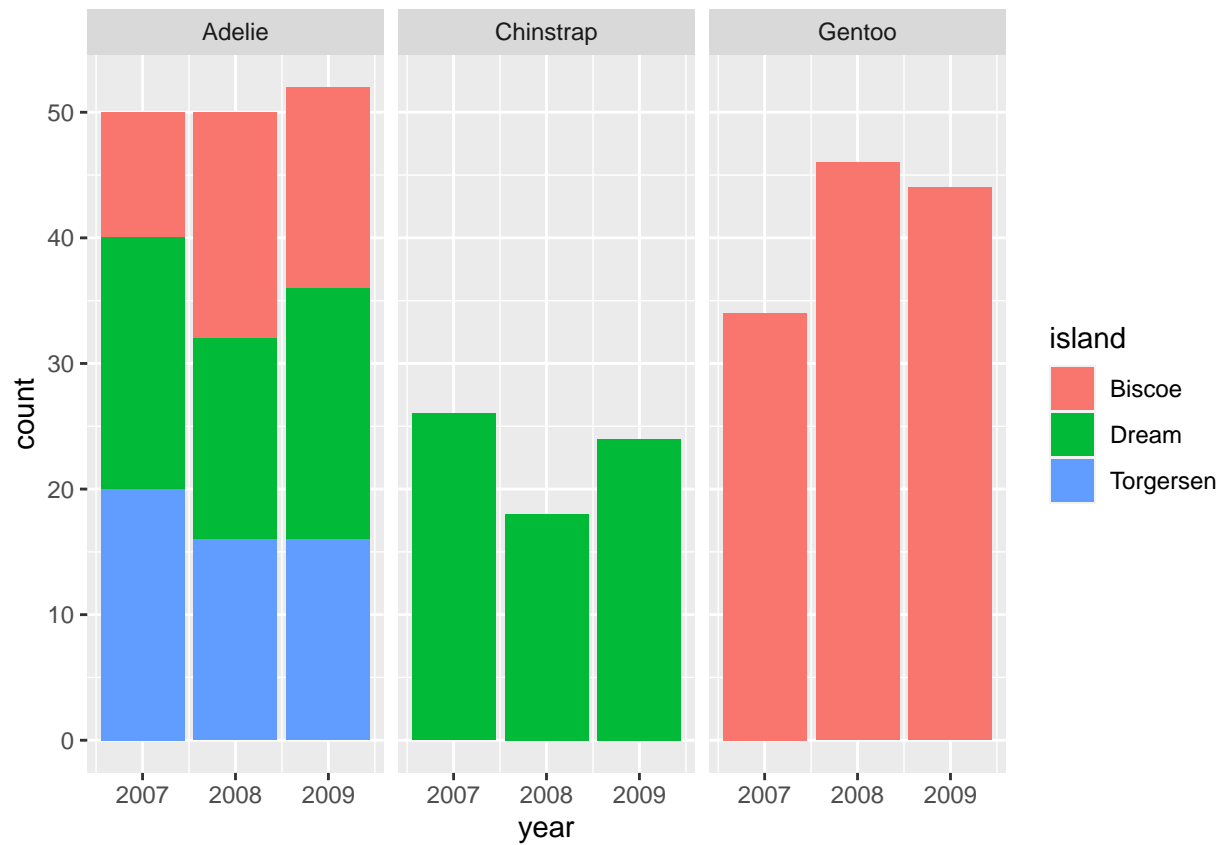
```
## Warning: Removed 2 rows containing non-finite values ('stat_boxplot()').
```

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

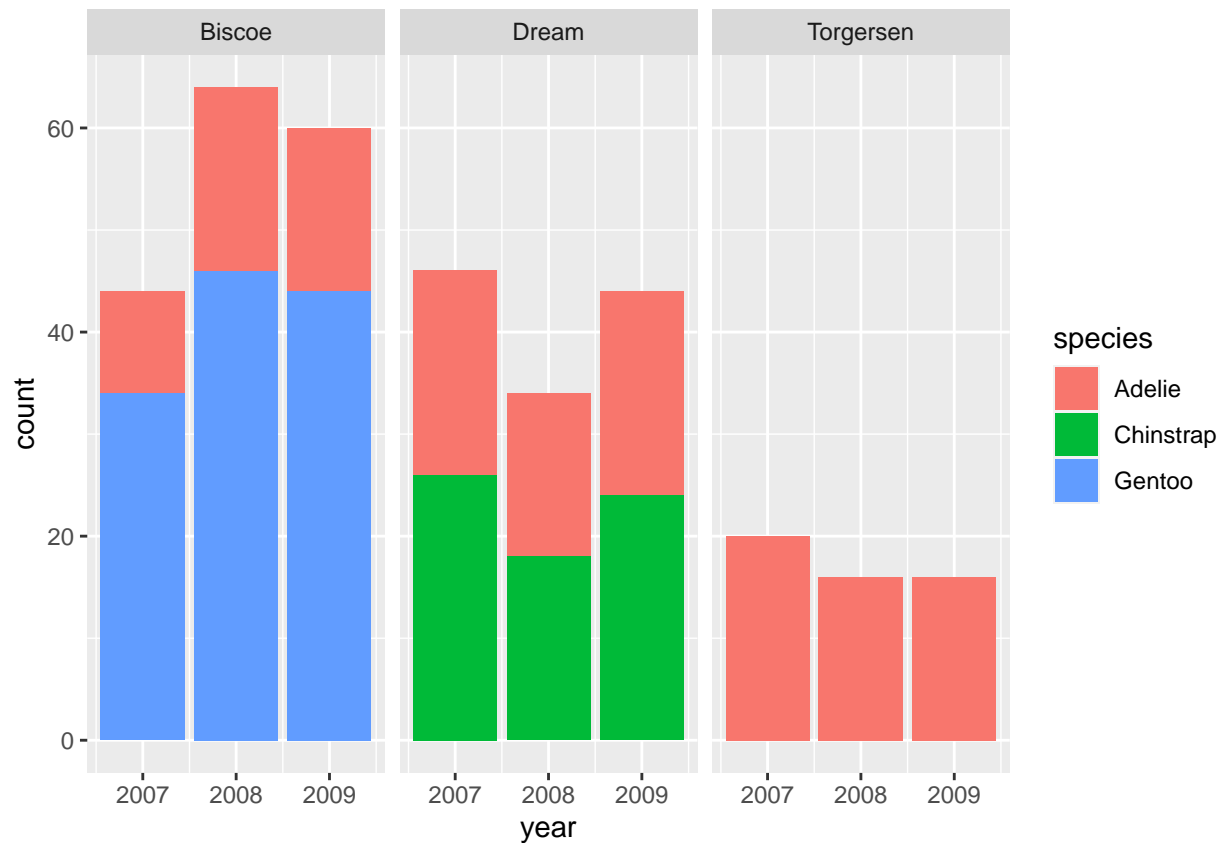


Free exploration

```
penguins %>%
  ggplot() +
  geom_bar(mapping = aes(x=year, fill=island)) +
  facet_wrap(~species)
```



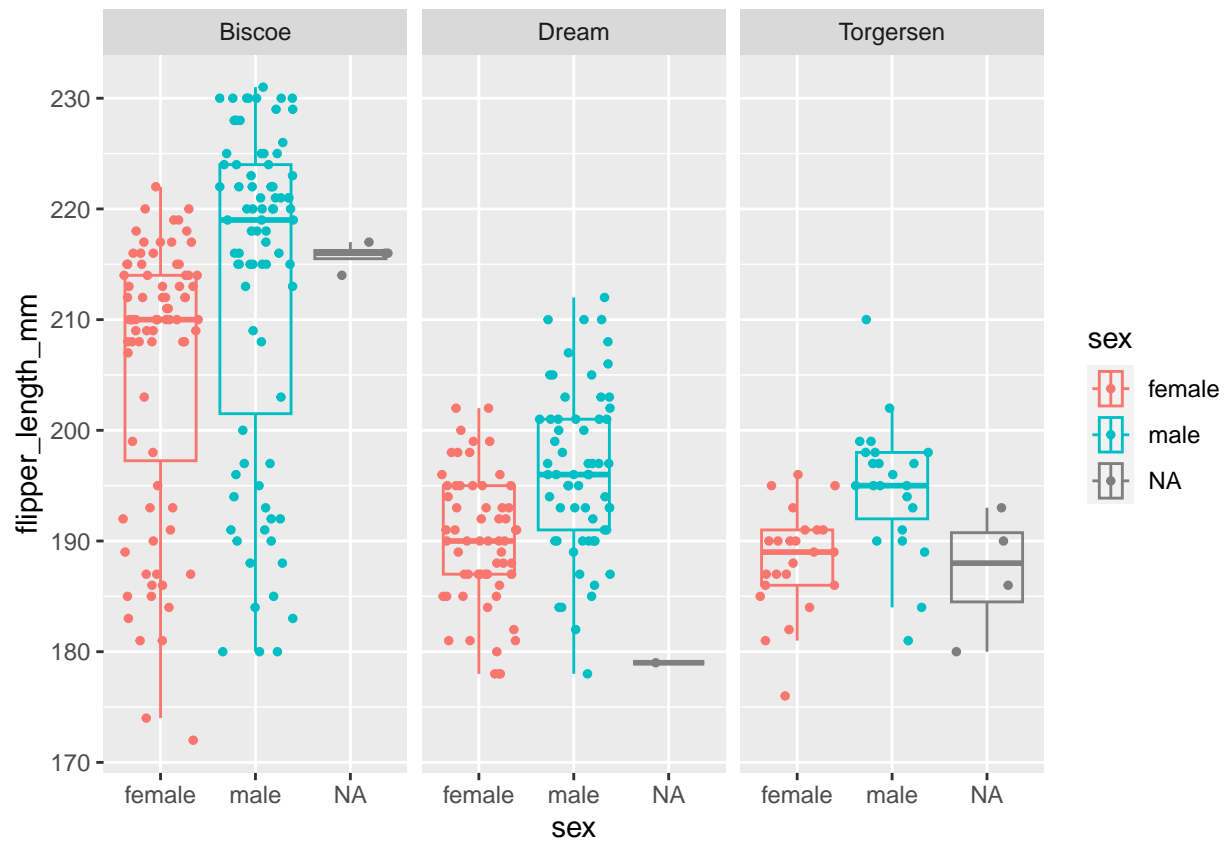
```
penguins %>%  
  ggplot() +  
  geom_bar(mapping = aes(x=year, fill=species)) +  
  facet_wrap(~island)
```



```
penguins %>%
  ggplot(mapping = aes(x=flipper_length_mm, y=sex, color=sex)) +
  geom_boxplot(outlier.alpha = 0, alpha=0) +
  geom_jitter(width = 0, size=1) +
  coord_flip() +
  facet_wrap(~island)
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_boxplot()').
```

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

```
penguins %>%
  ggplot(mapping = aes(x=bill_length_mm, y=sex, color=sex)) +
  geom_boxplot(outlier.alpha = 0, alpha=0) +
  geom_jitter(width = 0, size=1) +
  coord_flip() +
  facet_wrap(~species)
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_boxplot()').
```

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

