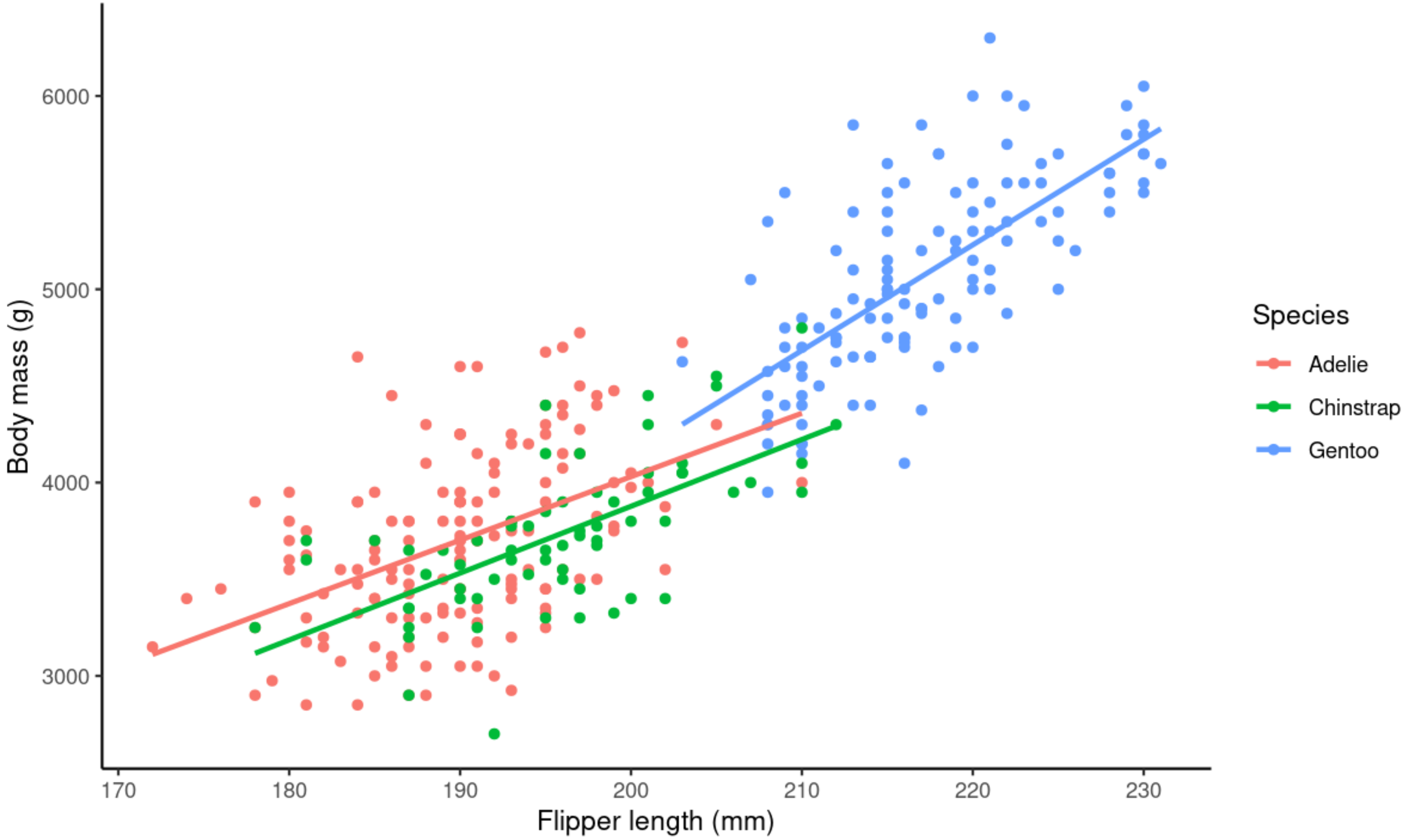
NRI 7350

Advanced Linear Models

Transformations,
Interactions, and
Post-hoc tests



Artwork by @allison_horst

Getting started (again)

Open RStudio

Open your NRI project

Open a **new** script for today:

File > New File > R Script

Make sure to load packages at the top:

```
library(tidyverse)
library(palmerpenguins)
library(car)
```

Side Note

Messages vs. Warnings vs. Errors

Messages and Warnings and Errors (Oh my!)

- Not all coloured text is a problem

- Messages are just helpful information

```
ggplot(data = drop_na(penguins), aes(x = body_mass_g, y = flipper_length_mm)) +
  stat_smooth()
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

Messages and Warnings and Errors (Oh my!)

- Not all coloured text is a problem
- Messages are just helpful information
- Warnings should be considered **FYIs**. They might be a problem, but not always
  - Your code will run, even with a warning
  - Warnings always start with **Warning:**

```
ggplot(data = penguins, aes(x = sex, y = body_mass_g)) +
  geom_boxplot()
```

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

Messages and Warnings and Errors (Oh my!)

- Not all coloured text is a problem
- Messages are just helpful information
- Warnings should be considered **FYIs**. They might be a problem, but not always
    - Your code will run, even with a warning
    - Warnings always start with **Warning:**
- Errors are always problems 😞
    - Your code will stop with an error
    - Errors always start with **Error:**

```
ggplot(data = Penguins, aes(x = sex, y = body_mass_g)) +
  geom_boxplot()
```

```
## Error in ggplot(data = Penguins, aes(x = sex, y = body_mass_g)): object 'Penguins' not found
```

Messages and Warnings and Errors (Oh my!)

- Not all coloured text is a problem
- Messages are just helpful information
- Warnings should be considered **FYIs**. They might be a problem, but not always
  - Your code will run, even with a warning
  - Warnings always start with **Warning:**
- Errors are always problems 😞
  - Your code will stop with an error
  - Errors always start with **Error:**

Messages < Warnings < Errors

```
ggplot(data = Penguins, aes(x = sex, y = body_mass_g)) +
  geom_boxplot()
```

```
## Error in ggplot(data = Penguins, aes(x = sex, y = body_mass_g)): object 'Penguins' not found
```

Data Transformations

Transformations

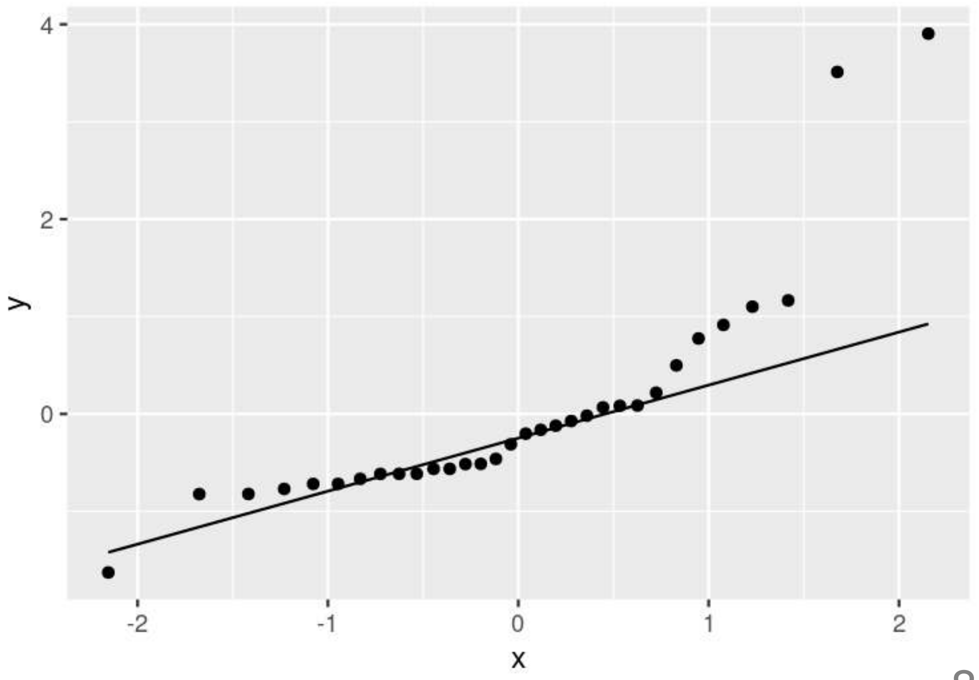
Non-normal residuals

```
m <- lm(sleep_cycle ~ bodywt, data = msleep)

d <- data.frame(residuals = residuals(m),
                std_residuals = rstudent(m),
                fitted = fitted(m),
                cooks = cooks.distance(m))

d <- mutate(d, obs = 1:n())
```

```
ggplot(data = d, aes(sample = std_residuals)) +
  stat_qq() +
  stat_qq_line()
```



Use a transformation!
Good for addressing non-normality of residuals,
and problems with variance

Transformations

Order of Operations

1. See the need (i.e. non-normal residuals, heteroscedacity, etc.)
2. Figure out which transformation
3. Apply the transformation
4. Check model assumptions
5. Try again as needed

Transformations: Common options

Table of transformations in R

```
data_trans <- mutate(data, y_trans = 1/y^2)

data_trans <- mutate(data, y_trans = 1/y)

data_trans <- mutate(data, y_trans = 1/sqrt(y))

data_trans <- mutate(data, y_trans = log(y))

data_trans <- mutate(data, y_trans = log10(y))

data_trans <- mutate(data, y_trans = sqrt(y))

data_trans <- mutate(data, y_trans = y^2)

data_trans <- mutate(data, y_trans = (y^lambda -
1)/lambda)

data_trans <- mutate(data, y_trans = asin(sqrt(y/100)))
```

Transformation	R Code
Inverse square	`1/y^2`
Reciprocal	`1/y`
Inverse square root	`1/sqrt(y)`
Naural log (ln)	`log(y)`
Log base 10	`log10(y)`
Square root	`sqrt(y)`
Square	`y^2`
Box Cox	`(y^lambda - 1) / lambda`
Arcsine-sqare-root	`asin(sqrt(y/100))`

`data_trans` is the NEW data frame, **`y_trans`** is your TRANSFORMED y-value

Transformations: How to choose?

- Based on what you know (often discipline specific standards for certain data types)
- Based on what you see (does it look exponential or logarithmic?)
- Based on trial and error (try different transformations and see how it goes)
- Based on Box-Cox lambda (λ)

Can EITHER

Apply λ through Box-Cox transformation

OR

Use it to indicate best transformation $\rightarrow$

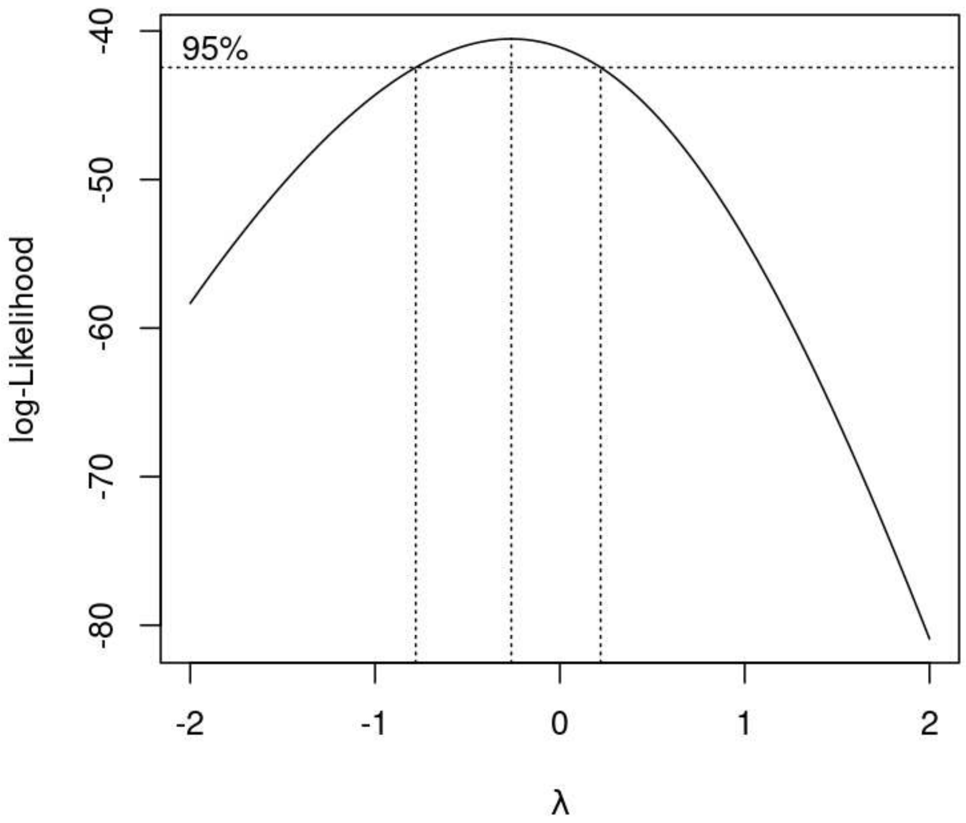
Best λ	Equation	Name
-2.5 to -1.5	$1/y^2$	inverse square
-1.5 to -0.75	$1/y$	reciprocal
-0.75 to -0.25	$1/\sqrt{y}$	inverse square root
-0.25 to 0.25	$\ln(y)$	natural log
0.25 to 0.75	$\sqrt{y}$	square root
0.75 to 1.5	y	none
1.5 to 2.5	y^2	square

Transformations: Box-Cox

Finding λ

- **Use a plot of λ**
  - **`boxcox()`** function from **`MASS`** package
  - Use **`boxcox()`** directly, otherwise **`MASS`** interferes with **`select()`**

```
b <- MASS::boxcox(m)
```



Transformations: Box-Cox

Finding λ

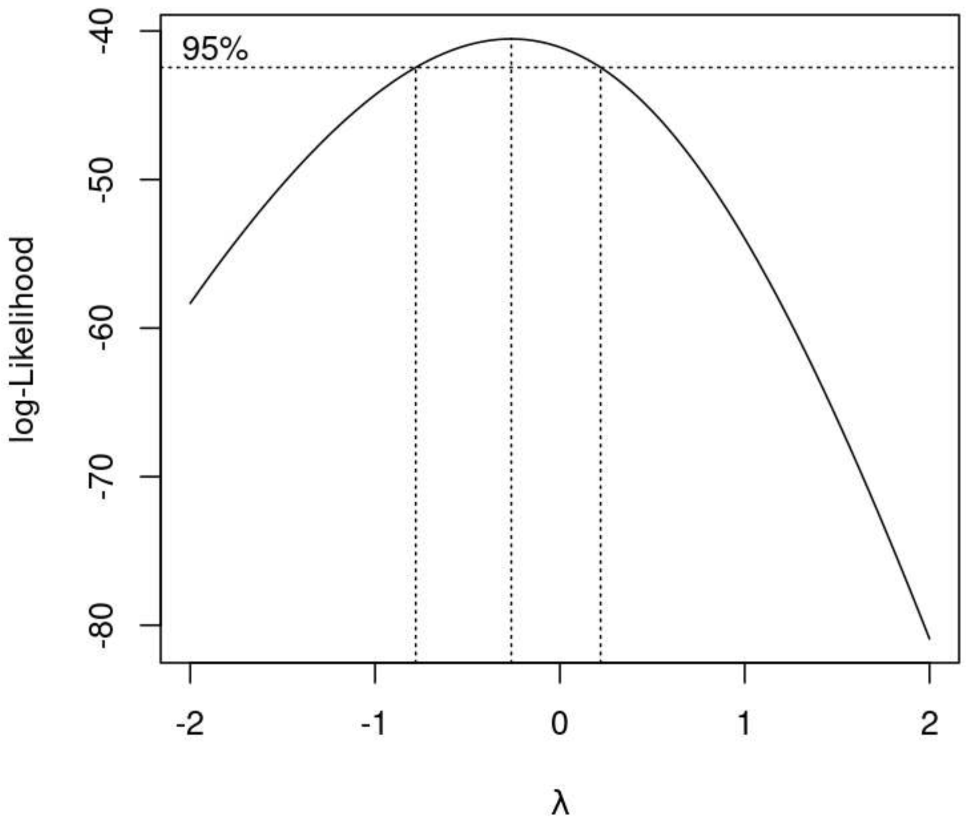
- **Use a plot of λ**
  - **`boxcox()`** function from **`MASS`** package
  - Use **`boxcox()`** directly, otherwise **`MASS`** interferes with **`select()`**

```
b <- MASS::boxcox(m)
```

- **Get the exact λ**

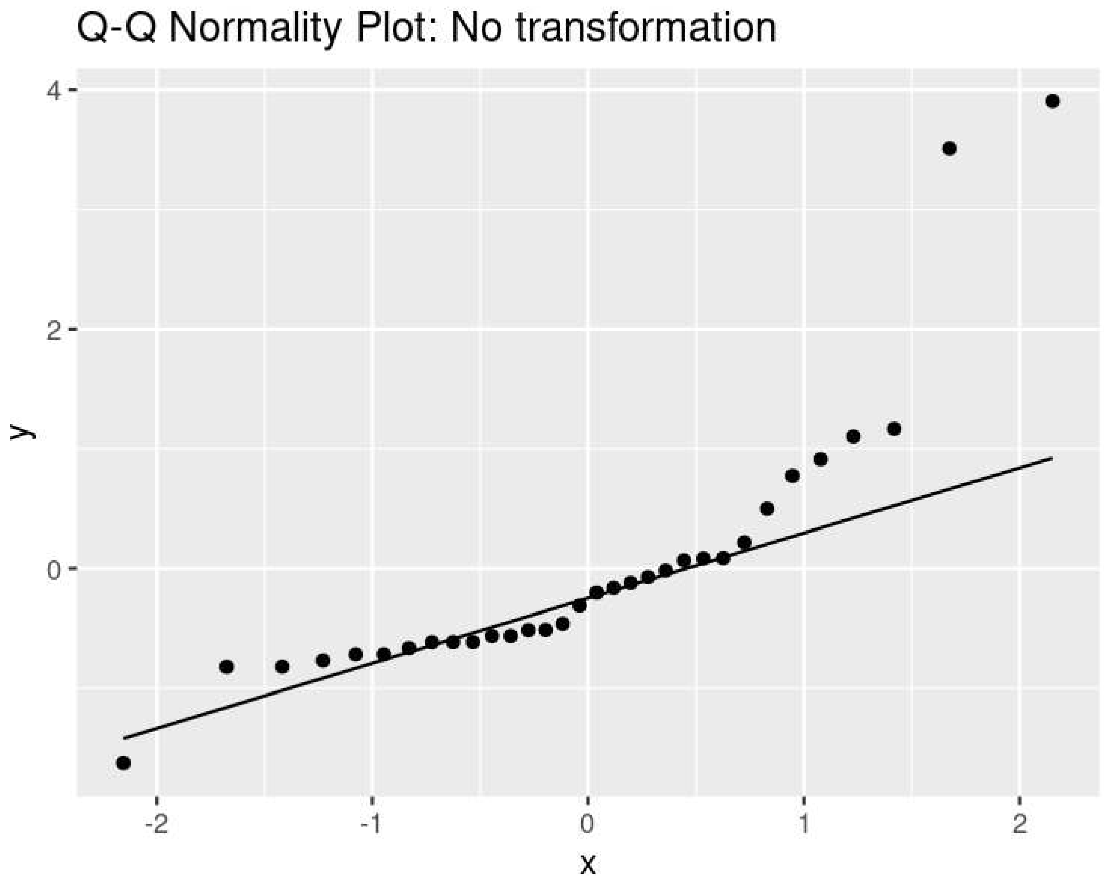
```
b$x[b$y == max(b$y)]
```

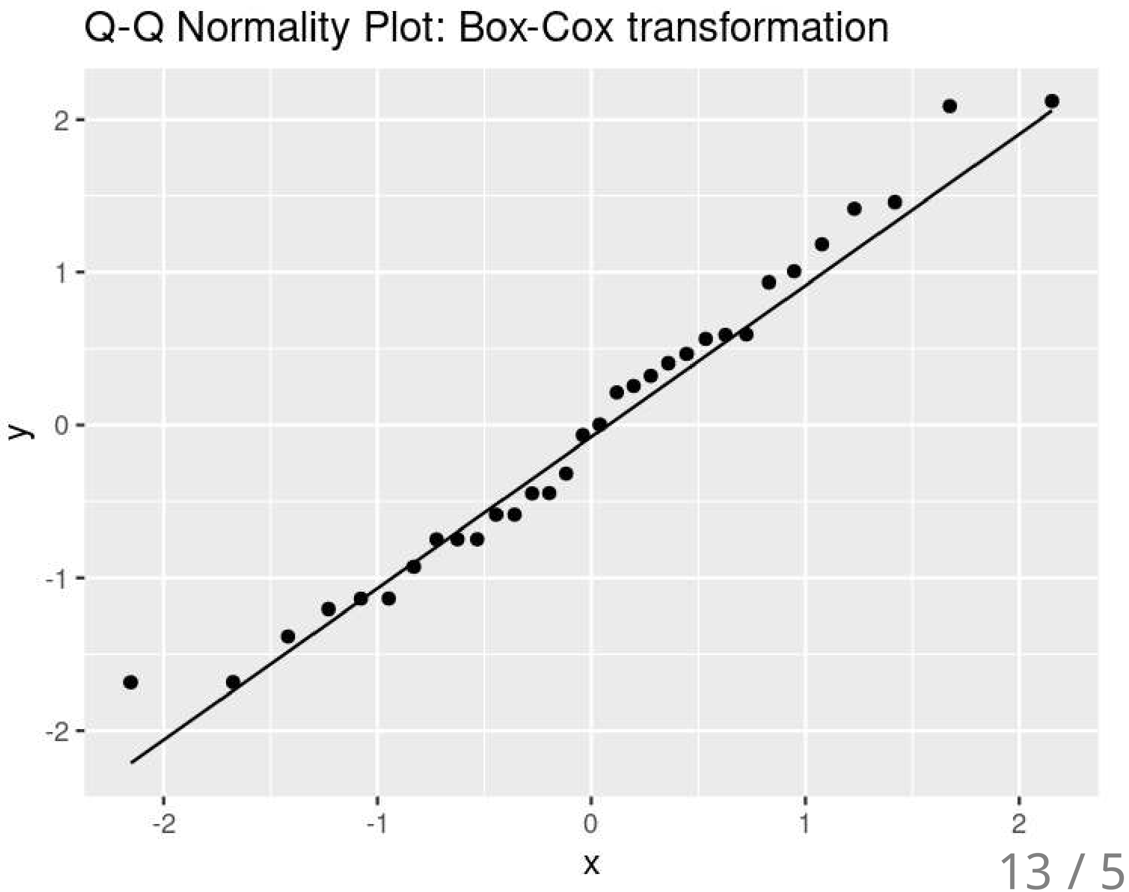
```
## [1] -0.2626263
```



Apply the transformation

```
msleep_trans <- mutate(msleep, sleep_cycle = (sleep_cycle^(-0.26) - 1) / -0.26)
m_trans <- lm(sleep_cycle ~ bodywt, data = msleep_trans)
```



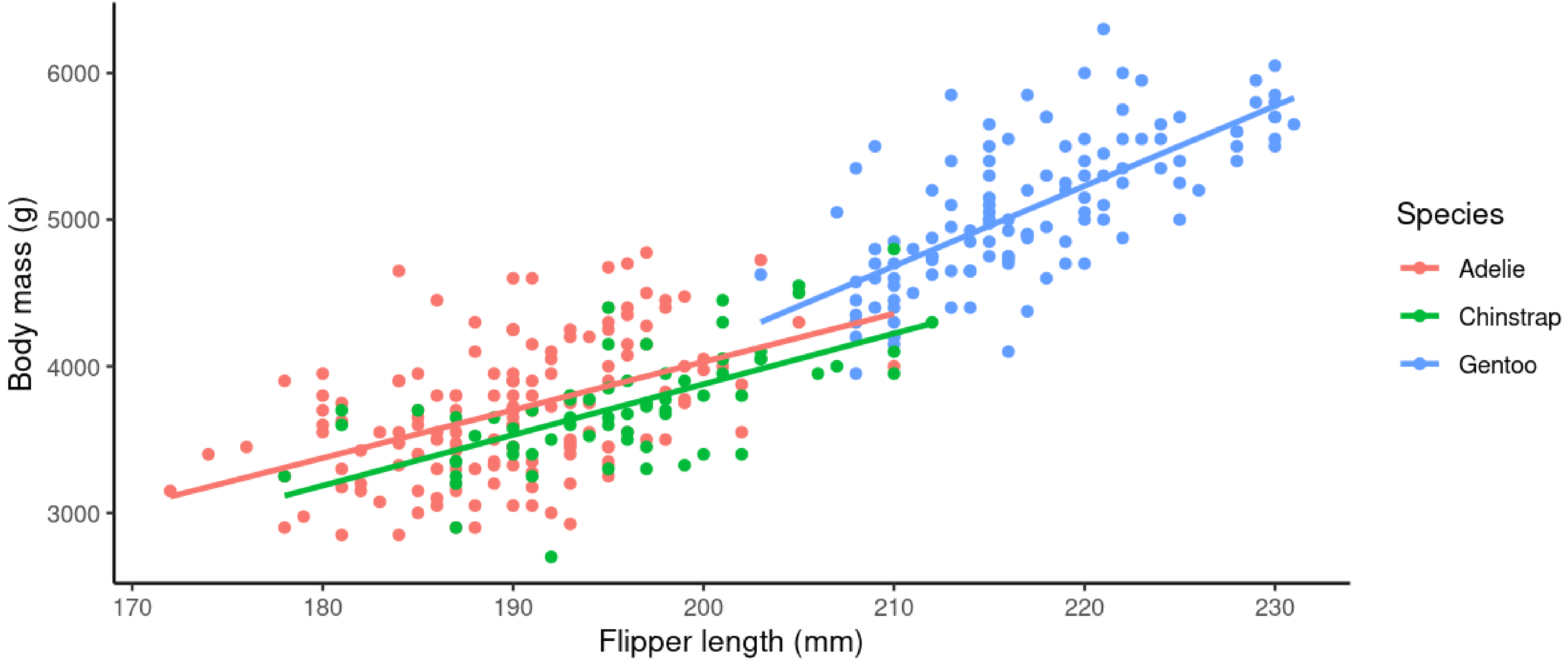


Interactions

Interaction between Flipper Length and Species

Does the effect of Flipper Length on Body Mass depend on Species?

(i.e. Are the slopes different?)

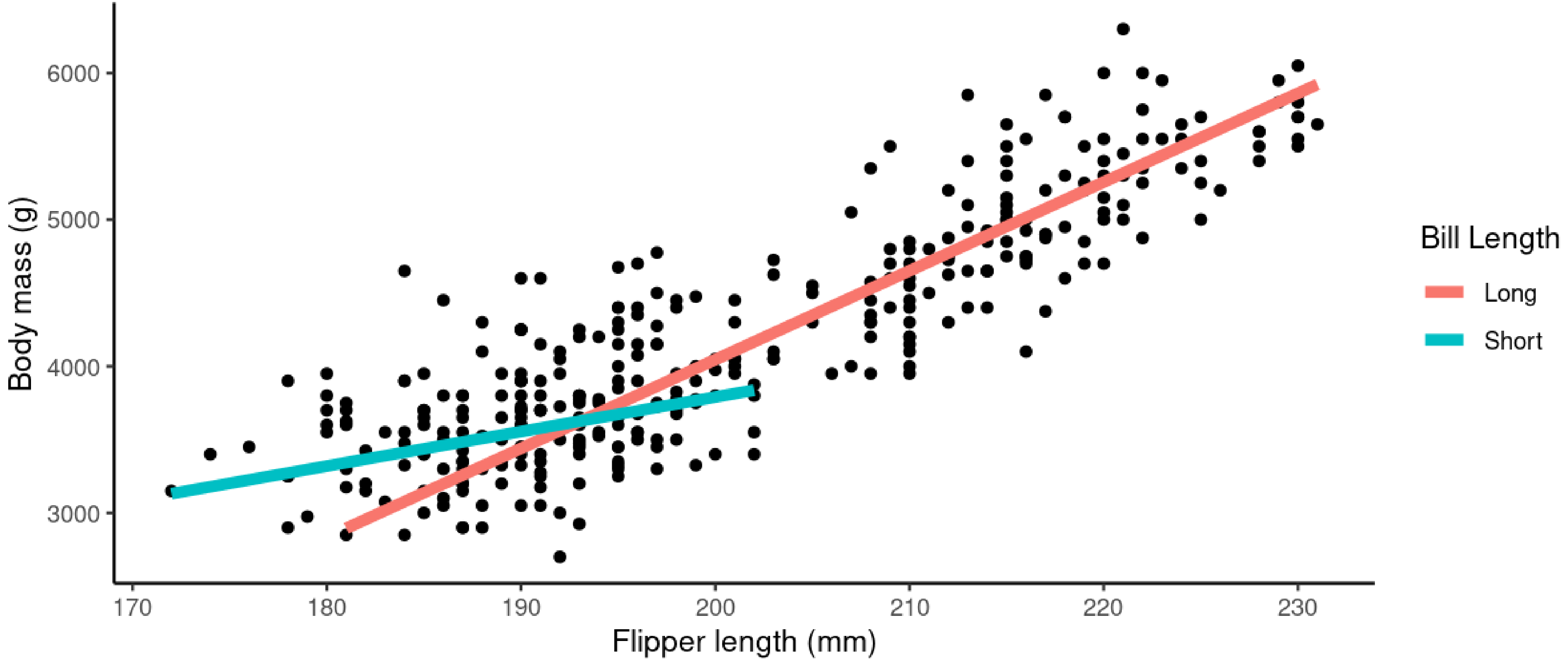


Interactions

Interaction between Flipper Length and Bill Length

Does the effect of Flipper Length on Body Mass depend on Bill Length?

(i.e. Does the slope of Flipper Length change with Bill Length?)



Interactions

Main Effects only +

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm, data = penguins)
```

Interactions

Main Effects only +

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm, data = penguins)
```

Main Effects and Interaction + :

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + flipper_length_mm:bill_length_mm,
        data = penguins)
```

Interactions

Main Effects only +

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm, data = penguins)
```

Main Effects and Interaction + :

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + flipper_length_mm:bill_length_mm,
        data = penguins)
```

Both Main Effects and Interaction * (shortcut)

```
m <- lm(body_mass_g ~ flipper_length_mm * bill_length_mm, data = penguins)
```

Interactions

Main Effects only `+`

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm, data = penguins)
```

Main Effects and Interaction `+` `:`

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + flipper_length_mm:bill_length_mm,
        data = penguins)
```

Both Main Effects and Interaction `*` (shortcut)

```
m <- lm(body_mass_g ~ flipper_length_mm * bill_length_mm, data = penguins)
```

> Don't forget your diagnostic plots!

Interactions

Main Effects only `+`

```
m <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm, data = penguins)
```

Main Effects and Interaction `+` `:`

```
m <- lm(body_mass_g ~ 
        data = penguin
```

```
l_length_mm,
```

Both Main Effects

```
m <- lm(body_mass_g ~
```

Your turn!
Create a model with your response variable by two of your *continuous* predictors including an interaction term.

Look at the output of `summary()`

Don't forget your diagnostic plots!

Interpreting Interactions

Including Correlation Tables

```
summary(m, correlation = TRUE)
```

```
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                  5090.5088  2925.3007   1.740 0.082740 .  
## flipper_length_mm              -7.3085    15.0321  -0.486 0.627145    
## bill_length_mm               -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm    1.1998     0.3224   3.721 0.000232 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 386.8 on 338 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.7694,    Adjusted R-squared:  0.7674 
## F-statistic: 375.9 on 3 and 338 DF,  p-value: < 2.2e-16
##
## Correlation of Coefficients:
##                                  (Intercept) flipper_length_mm bill_length_mm
## flipper_length_mm                -1.00                                     
## bill_length_mm                   -0.99        0.98                         
## flipper_length_mm:bill_length_mm  0.99       -0.99              -1.00      
```

Interpreting Interactions

Including Correlation Tables

```
summary(m, correlation = TRUE)
```

```
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 5090.5088  2925.3007   1.740 0.082740 .
## flipper_length_mm             -7.3085    15.0321  -0.486 0.627145
## bill_length_mm              -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm    1.1998     0.3224   3.721 0.000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 386.8 on 338 degrees of freedom
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##
## Correlation of Coefficients:
##                                  (Intercept) flipper_length_mm bill_length_mm
## flipper_length_mm                -1.00
## bill_length_mm                   -0.99        0.98
## flipper_length_mm:bill_length_mm  0.99       -0.99             -1.00
```

But for now we'll focus on the Estimates

Interpreting Interactions

```
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  5090.5088  2925.3007   1.740 0.082740 .
## flipper_length_mm              -7.3085    15.0321  -0.486 0.627145
## bill_length_mm               -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm  1.1998     0.3224   3.721 0.000232 ***
```

Effect of **Flipper Length** on Body Mass when Bill Length is 0 mm

Interpreting Interactions

```
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  5090.5088  2925.3007   1.740 0.082740 .
## flipper_length_mm              -7.3085    15.0321  -0.486 0.627145
## bill_length_mm               -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm  1.1998     0.3224   3.721 0.000232 ***
```

Effect of **Flipper Length** on Body Mass when Bill Length is 0 mm

When Bill Length is 0 mm, Body mass decreases by 7.31 g for each 1 mm increase in Flipper Length

Interpreting Interactions

```
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                 5090.5088  2925.3007   1.740 0.082740 .  
## flipper_length_mm             -7.3085    15.0321  -0.486 0.627145    
## bill_length_mm              -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm    1.1998     0.3224   3.721 0.000232 ***
```

Effect of **Flipper Length** on Body Mass when Bill Length is 0 mm

Not meaningful! Do we ever have a Bill Length of 0 mm?
Do not interpret

Interpreting Interactions

```
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 5090.5088  2925.3007   1.740 0.082740 .
## flipper_length_mm             -7.3085    15.0321  -0.486 0.627145
## bill_length_mm              -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm   1.1998     0.3224   3.721 0.000232 ***
```

Effect of **Bill Length** on Body Mass when Flipper Length is 0 mm

Interpreting Interactions

```
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  5090.5088  2925.3007   1.740 0.082740 .
## flipper_length_mm              -7.3085    15.0321  -0.486 0.627145
## bill_length_mm               -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm    1.1998     0.3224   3.721 0.000232 ***
```

Effect of **Bill Length** on Body Mass when Flipper Length is 0 mm

When Flipper Length is 0 mm, Body Mass decreases by 229.24 g for each 1 mm increase in Bill Length

Interpreting Interactions

```
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  5090.5088  2925.3007   1.740 0.082740 .
## flipper_length_mm              -7.3085    15.0321  -0.486 0.627145
## bill_length_mm               -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm   1.1998     0.3224   3.721 0.000232 ***
```

Effect of **Bill Length** on Body Mass when Flipper Length is 0 mm

Not meaningful! Do we ever have a Flipper Length of 0 mm?
Do not interpret

Interpreting Interactions

```
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 5090.5088  2925.3007   1.740 0.082740 .
## flipper_length_mm             -7.3085    15.0321  -0.486 0.627145
## bill_length_mm              -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm    1.1998     0.3224   3.721 0.000232 ***
```

Change in the effect of **Flipper Length** on Body Mass for every 1 mm change in **Bill Length**

Interpreting Interactions

```
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                   5090.5088  2925.3007   1.740 0.082740 .  
## flipper_length_mm               -7.3085    15.0321  -0.486 0.627145    
## bill_length_mm                -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm    1.1998     0.3224   3.721 0.000232 ***
```

Change in the effect of **Flipper Length** on Body Mass
for every 1 mm change in **Bill Length**

For every 1 mm increase in Bill Length,
the effect of a 1 mm increase in Flipper Length on Body Mass increases by 1.2 g
(i.e. the slope of the relationship between Body Mass and Flipper Length increases)

Interpreting Interactions

```
## Coefficients:
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      5090.5088  2925.3007   1.740 0
## flipper_length_mm                  -7.3085    15.0321  -0.486 0.
## bill_length_mm                   -229.2424    63.4334  -3.614 0.000347 ***
## flipper_length_mm:bill_length_mm    1.1998     0.3224   3.721 0.000232 ***
```

And **Vice Versa**!

Change in the effect of **Flipper Length** on Body Mass
for every 1 mm change in **Bill Length**

For every 1 mm increase in Bill Length,
the effect of a 1 mm increase in Flipper Length on Body Mass increases by 1.2 g
(i.e. the slope of the relationship between Body Mass and Flipper Length increases)

Interpreting Interactions

Artwork by [@allison_horst](https://twitter.com/allison_horst)

Plotting Interactions

Create new data frame with extremes

```
penguins_new <- expand(penguins,
                       flipper_length_mm = c(min(flipper_length_mm, na.rm = TRUE),
                                             max(flipper_length_mm, na.rm = TRUE)),
                       bill_length_mm = c(min(bill_length_mm, na.rm = TRUE),
                                          max(bill_length_mm, na.rm = TRUE)))
```

Side Note: `tidyverse` functions

Create new data frame with extremes

```
penguins_new <- expand(penguins,
                       flipper_length_mm = c(min(flipper_length_mm, na.rm = TRUE),
                                             max(flipper_length_mm, na.rm = TRUE)),
                       bill_length_mm = c(min(bill_length_mm, na.rm = TRUE),
                                          max(bill_length_mm, na.rm = TRUE)))
```

`expand()`

- from **`tidyr`** package (part of the **`tidyverse`**)
- **`tidyverse`** functions always start with the **data**, followed by **other arguments**
- you can reference any **column** from '**data**'
- **`expand()`** creates a data frame with all possible combinations of **new columns**

Plotting Interactions

Create new data frame with extremes

```
penguins_new <- expand(penguins,
                       flipper_length_mm = c(min(flipper_length_mm, na.rm = TRUE),
                                             max(flipper_length_mm, na.rm = TRUE)),
                       bill_length_mm = c(min(bill_length_mm, na.rm = TRUE),
                                          max(bill_length_mm, na.rm = TRUE)))
```

Add predicted y values

- Use **`predict()`** function
  - **`predict()`** can be used on most statistical models
- Returns predicted **`body_mass_g`** values for new data

```
penguins_new <- mutate(penguins_new, body_mass_g = predict(m, newdata = penguins_new))
```

Plotting Interactions

Small data frame

- With values predicted from model
- Can plot this to illustrate interactions

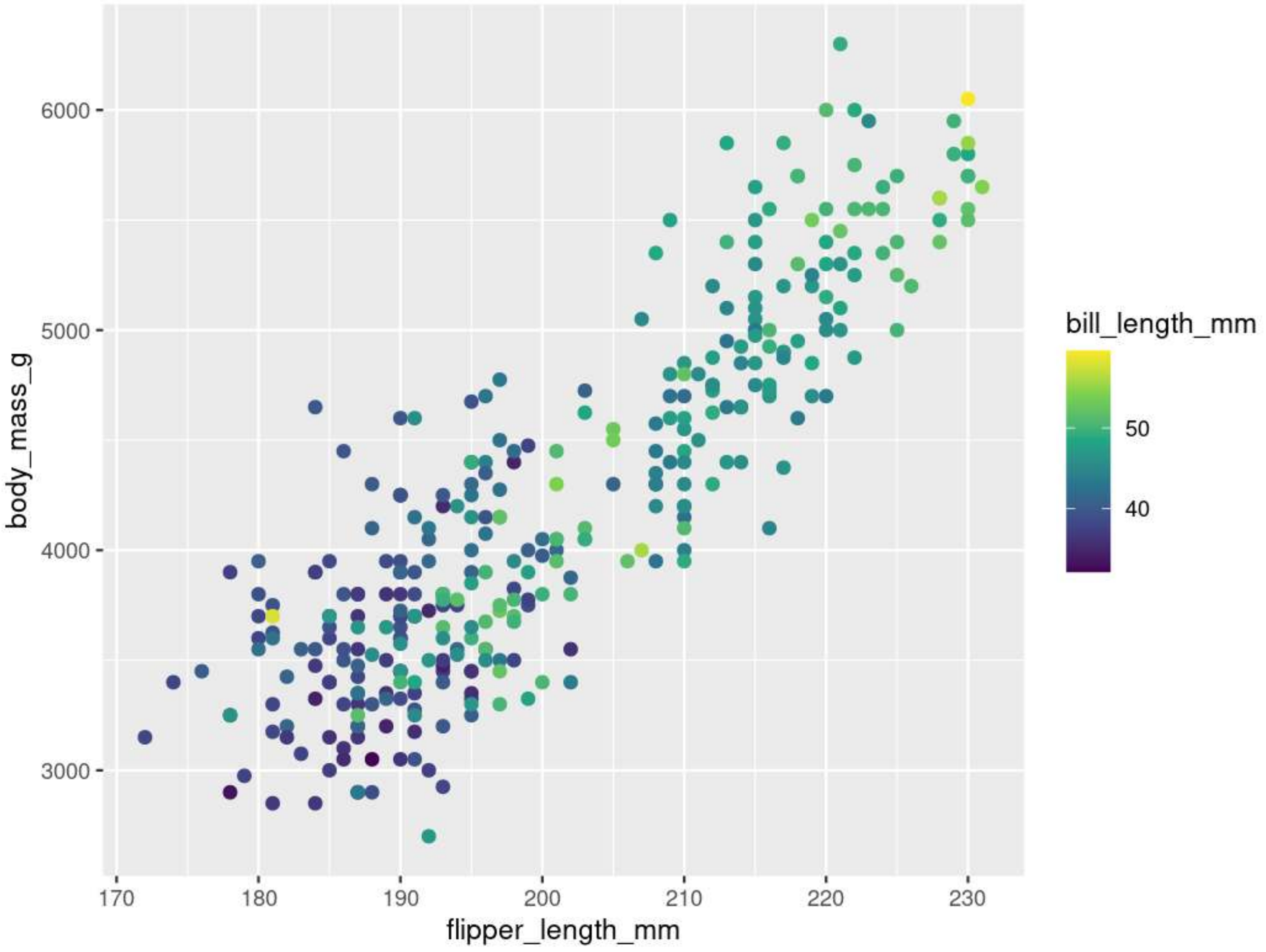
```
penguins_new
```

```
## # A tibble: 4 × 3
##   flipper_length_mm bill_length_mm body_mass_g
##               <int>          <dbl>       <dbl>
## 1               172           32.1       3099.
## 2               172           59.6       2470.
## 3               231           32.1       4941.
## 4               231           59.6       6258.
```

Plotting Interactions

Raw data (no model)

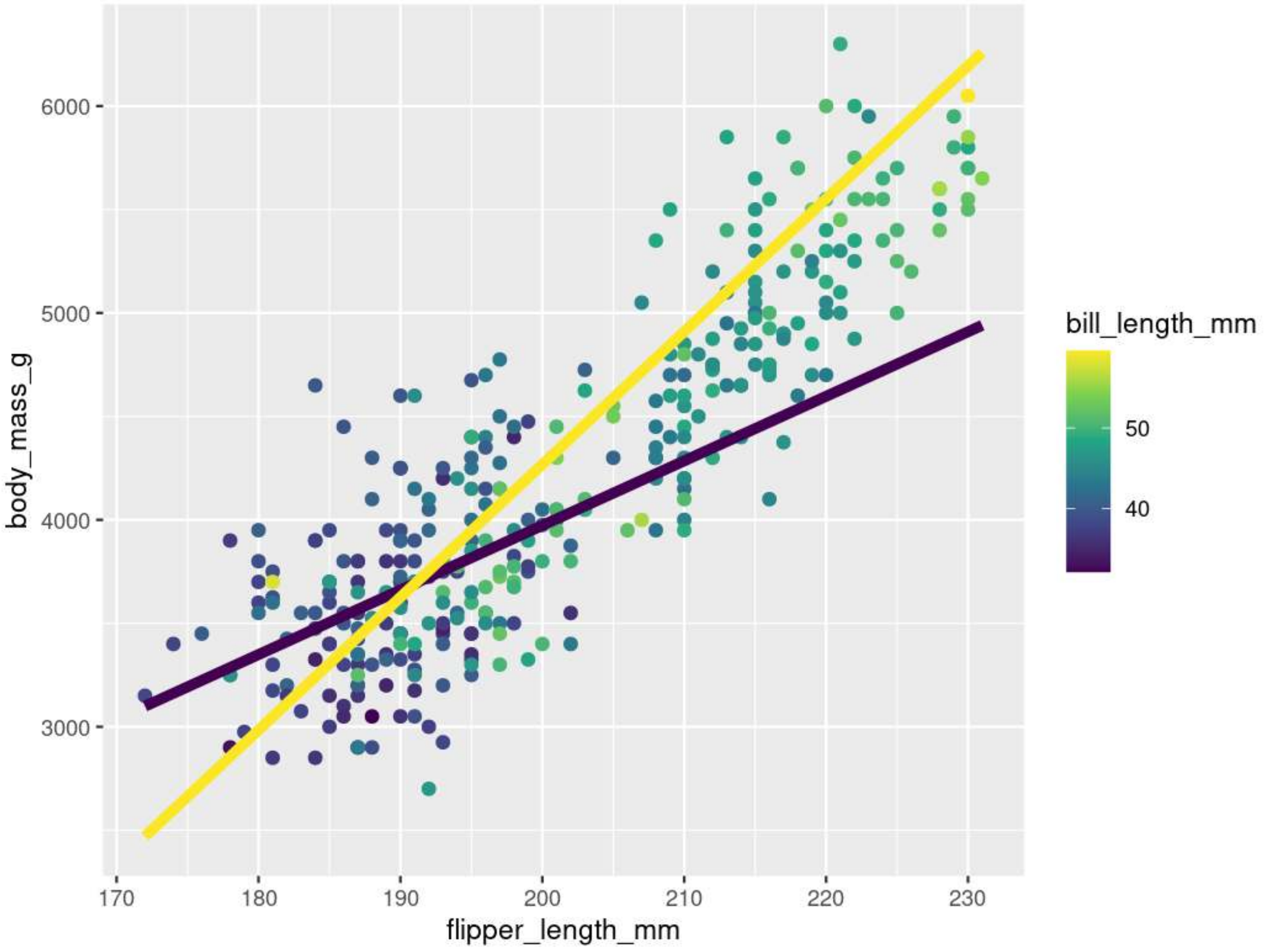
```
ggplot(data = penguins,
       aes(x = flipper_length_mm,
           y = body_mass_g,
           colour = bill_length_mm)) +
  geom_point(size = 2)
```



Plotting Interactions

Raw data + Model interaction

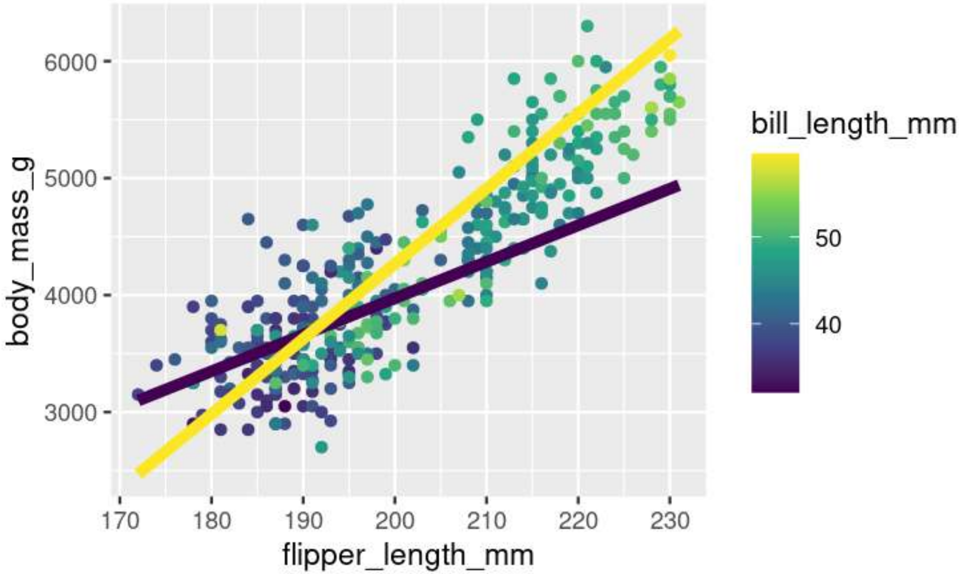
```
ggplot(data = penguins,
       aes(x = flipper_length_mm,
           y = body_mass_g,
           colour = bill_length_mm)) +
  geom_point(size = 2) +
  geom_line(data = penguins_new,
            aes(group = bill_length_mm),
            size = 2)
```



Plotting Interactions

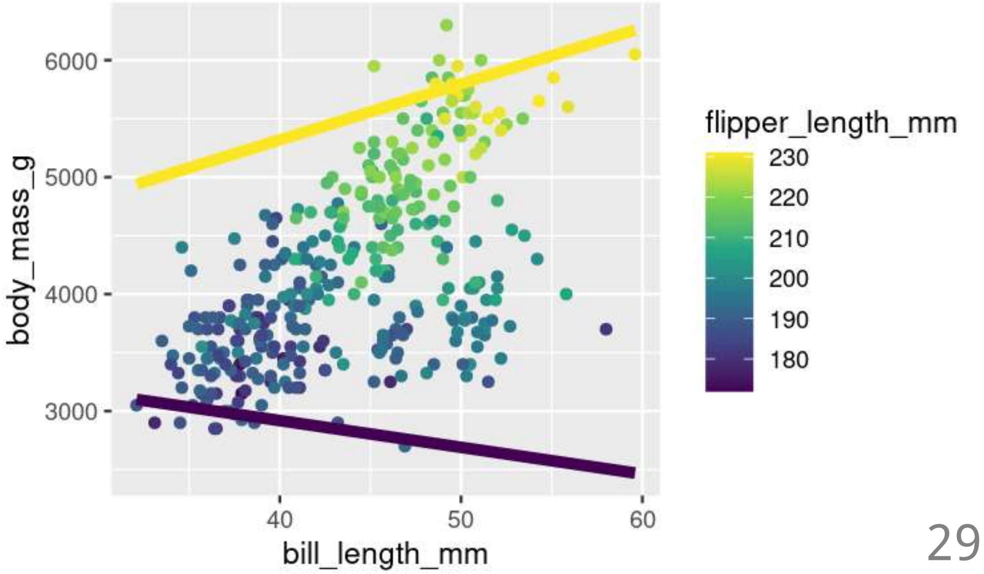
From a Flipper Length perspective

```
ggplot(data = penguins, aes(x = flipper_length_mm,
                            y = body_mass_g,
                            colour = bill_length_mm,
                            group = bill_length_mm))
+
  geom_point() +
  geom_line(data = penguins_new, size = 2)
```



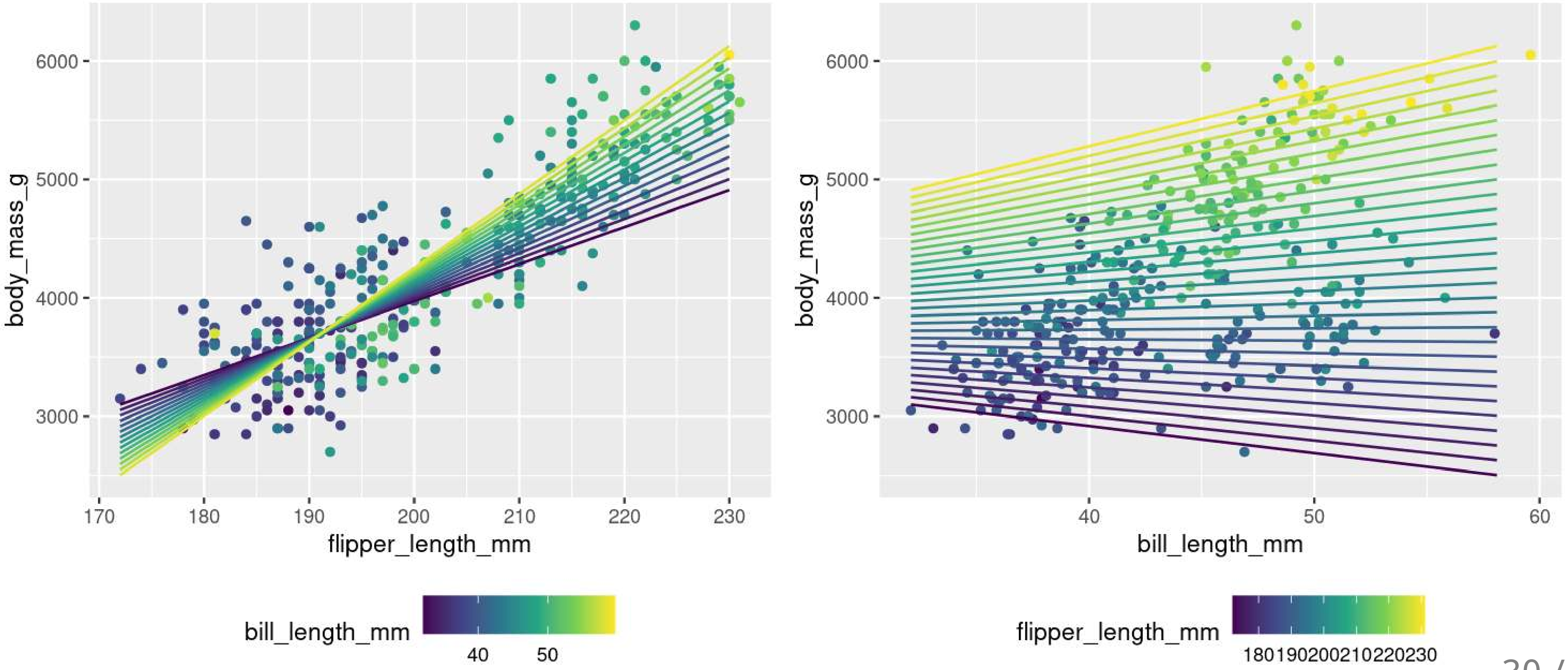
From a Bill Length perspective

```
ggplot(data = penguins, aes(x = bill_length_mm,
                            y = body_mass_g,
                            colour =
flipper_length_mm,
                            group =
flipper_length_mm))+
  geom_point() +
  geom_line(data = penguins_new, size = 2)
```



Visualizing Interactions

Not what you would present in a paper, but good to think about



ANOVAs and Post-Hoc Tests

Post-Hoc Tests

From last week...

```
m <- lm(body_mass_g ~ species + sex, data = penguins)
```

```
Anova(m, type = 3)
```

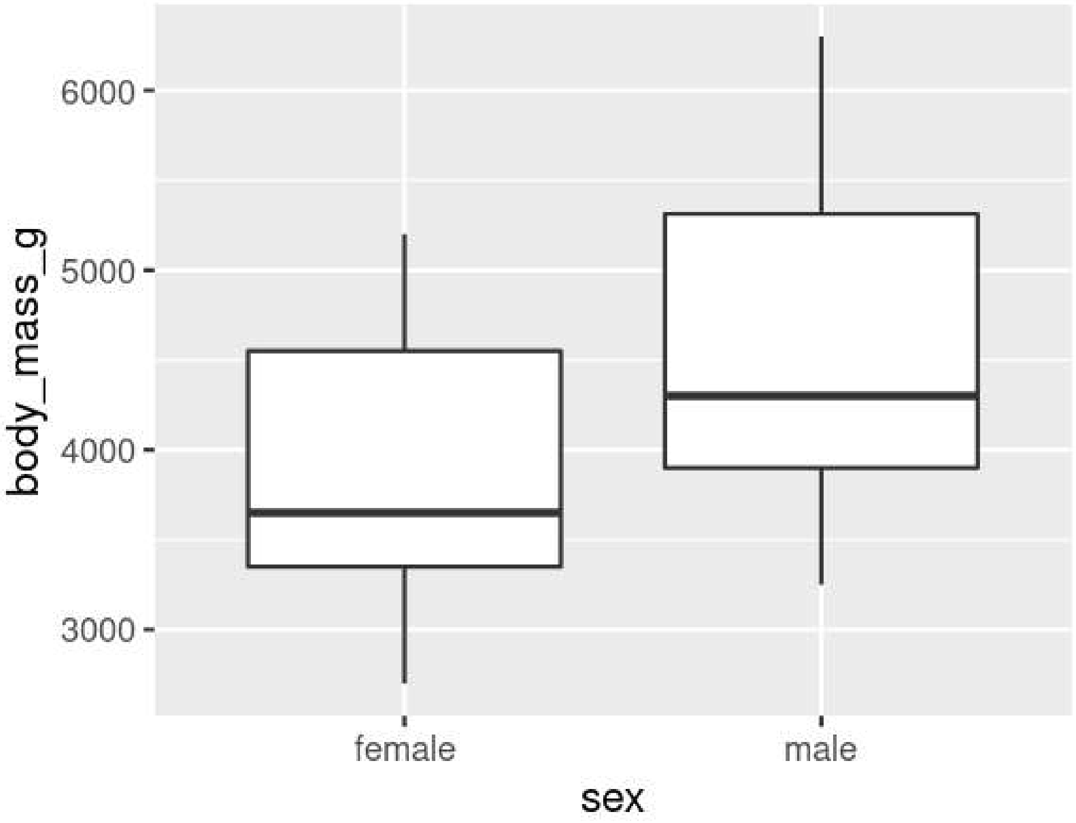
```
## Anova Table (Type III tests)
##
## Response: body_mass_g
##                 Sum Sq  Df  F value    Pr(>F)
## (Intercept) 1154266972   1 11514.96 < 2.2e-16 ***
## species      143401584   2   715.29 < 2.2e-16 ***
## sex           37090262   1   370.01 < 2.2e-16 ***
## Residuals     32979185 329
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

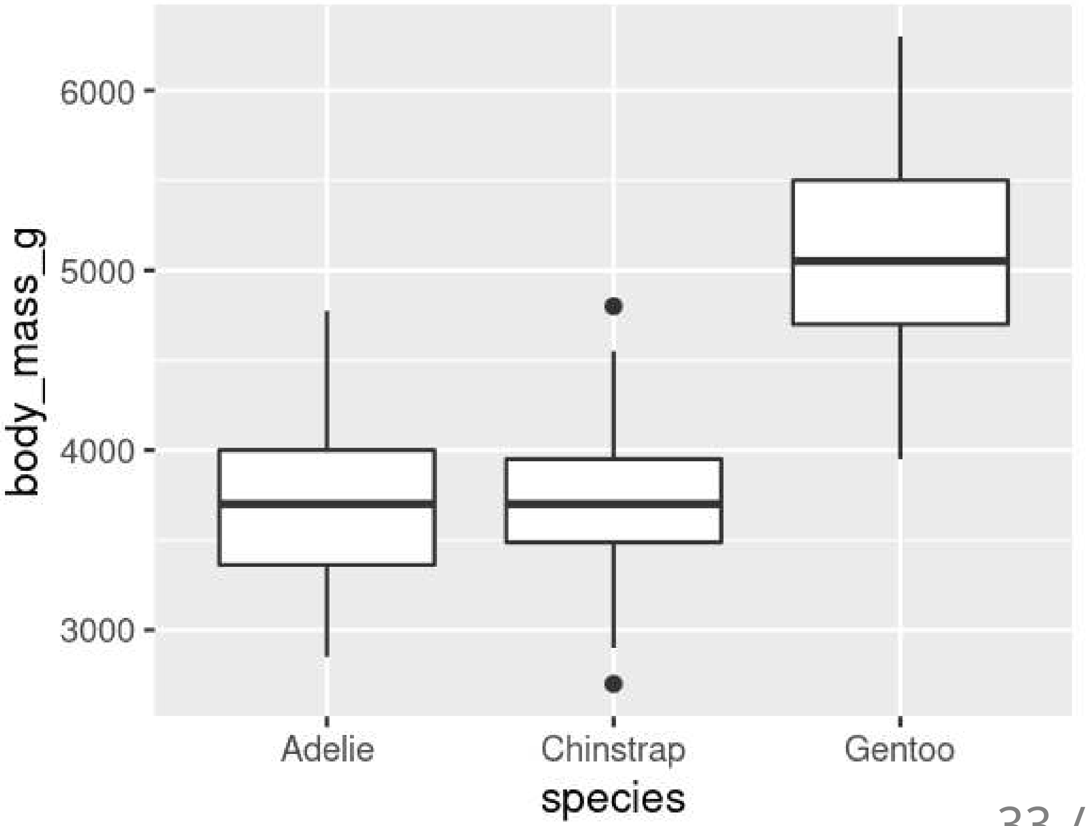
Differences within groups, but how are they different?

Post-Hoc Tests

- Males significantly bigger than females
- Only two groups, so we can use the figure

- Are Adelie and Chinstrap the same size?
- Looks like it, but no statistical support

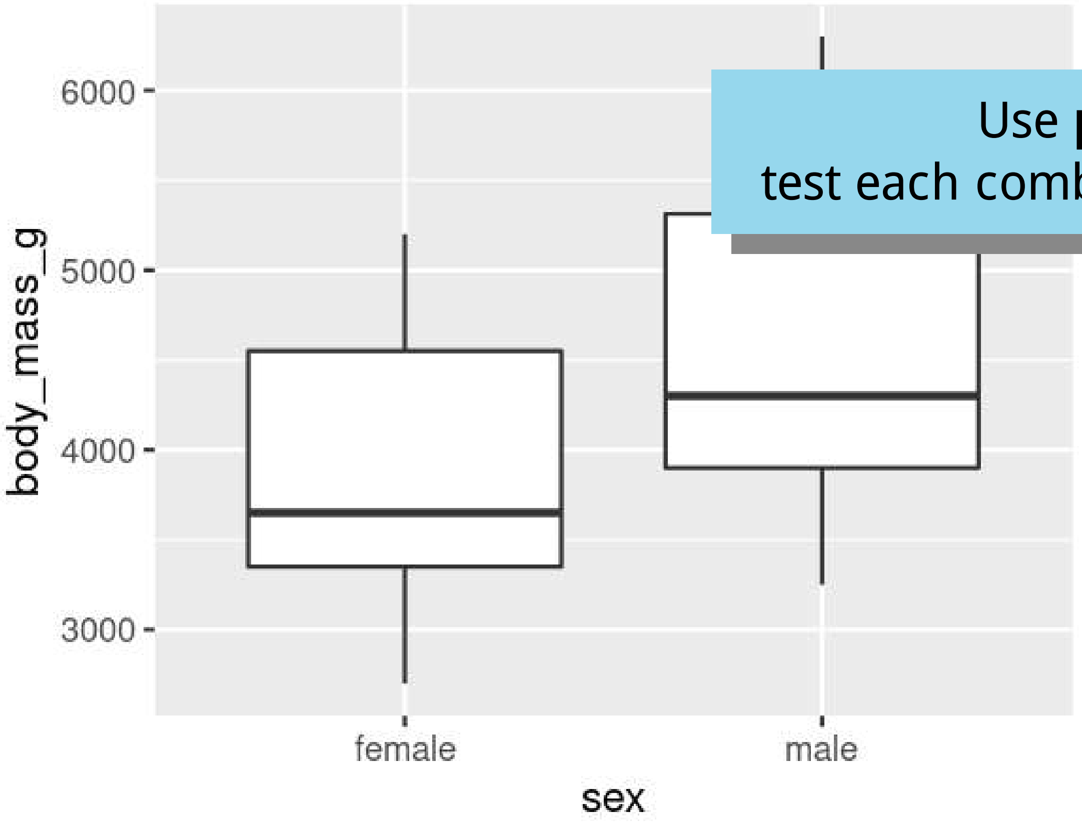


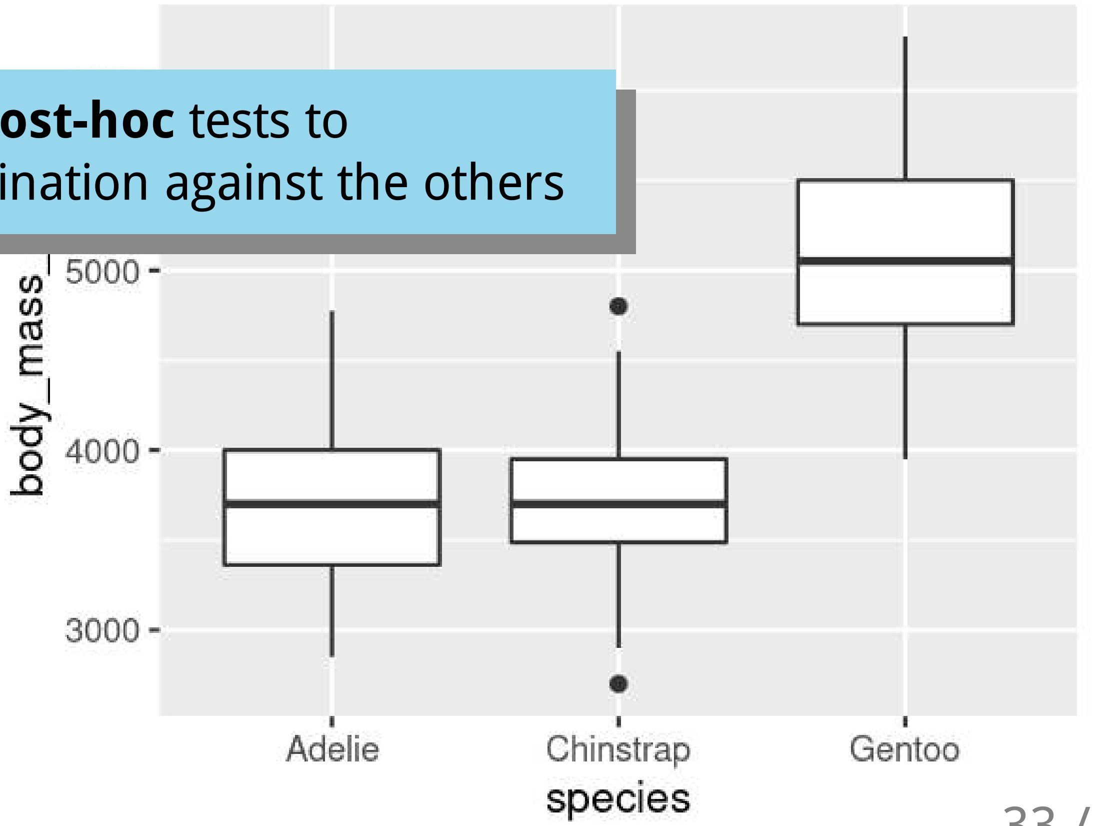


Post-Hoc Tests

- Males significantly bigger than females
- Only two groups, so we can use the figure

- Are Adelie and Chinstrap the same size?
- Looks like it, but no statistical support





Use **post-hoc** tests to
test each combination against the others

Estimated Marginal Means

`emmeans()` function from `emmeans` package

- Calculates **estimated marginal means** (least-squares means)
- Mean response of each factor, adjusting for other factors
- Can think of this as a predicted mean response if sample sizes were equal (and controlling for other parameters)

```
library(emmeans)
emm_sp <- emmeans(m, specs = "species")
emm_sp
```

```
##  species   emmean   SE  df lower.CL upper.CL
##  Adelie      3706 26.2 329     3655     3758
##  Chinstrap   3733 38.4 329     3658     3809
##  Gentoo      5084 29.0 329     5027     5141
##
## Results are averaged over the levels of: sex
## Confidence level used: 0.95
```

Post-Hoc Tests (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(emm_sp)
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap      -26.9 46.5 329  -0.579 0.8313
##  Adelie - Gentoo       -1377.9 39.1 329 -35.236 <.0001
##  Chinstrap - Gentoo    -1350.9 48.1 329 -28.067 <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: tukey method for comparing a family of 3
estimates
```

Post-Hoc Tests (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(emm_sp)
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap      -26.9 46.5 329  -0.579 0.8313
##  Adelie - Gentoo       -1377.9 39.1 329 -35.236 <.0001
##  Chinstrap - Gentoo    -1350.9 48.1 329 -28.067 <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: tukey method for comparing a family of 3
estimates
```

Differences in Body Mass

- Adelie penguins are **not** different from Chinstrap penguins (P value = 0.831)

Post-Hoc Tests (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(emm_sp)
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap     -26.9 46.5 329  -0.579 0.8313
##  Adelie - Gentoo      -1377.9 39.1 329 -35.236 <.0001
##  Chinstrap - Gentoo   -1350.9 48.1 329 -28.067 <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: tukey method for comparing a family of 3
estimates
```

Differences in Body Mass

- Adelie penguins are **not** different from Chinstrap penguins (P value = 0.831)
- Adelie penguins **are** on average 1377.9 g lighter than Gentoo penguins (P value = < 0.0001)

Post-Hoc Tests (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(emm_sp)
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap      -26.9 46.5 329  -0.579 0.8313
##  Adelie - Gentoo       -1377.9 39.1 329 -35.236 <.0001
##  Chinstrap - Gentoo    -1350.9 48.1 329 -28.067 <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: tukey method for comparing a family of 3
estimates
```

Differences in Body Mass

- Adelie penguins are **not** different from Chinstrap penguins (P value = 0.831)
- Adelie penguins **are** on average 1377.9 g lighter than Gentoo penguins (P value = < 0.0001)
- Chinstrap penguins **are** on average 1350.9 g lighter than Gentoo penguins (P value < 0.0001)

Post-Hoc Tests (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(emm_sp)
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap      -26.9 46.5 329  -0.579 0.8313
##  Adelie - Gentoo       -1377.9 39.1 329 -35.236 <.0001
##  Chinstrap - Gentoo    -1350.9 48.1 329 -28.067 <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: tukey method for comparing a family of 3
estimates
```

Differences in Body Mass

- Adelie penguins are **not** different from Chinstrap penguins (P value = 0.831)
- Adelie penguins **are** on average 1377.9 g lighter than Gentoo penguins (P value = < 0.0001)
- Chinstrap penguins **are** on average 1350.9 g lighter than Gentoo penguins (P value < 0.0001)

Therefore, on average
Gentoo penguins are the largest
Adelie and Chinstrap penguins are the same size

Post-Hoc Tests (Dunnett's)

With `contrast()` function from `emmeans` package

- Dunnett's comparison is a type of contrast
- Each level compared to control
- Use `method = "trt.vs.ctrl"` OR `method = "dunnett"`

```
contrast(emm_sp, method = "dunnett")
```

```
##  contrast           estimate   SE  df t.ratio p.value
##  Chinstrap - Adelie     26.9 46.5 329   0.579  0.7753
##  Gentoo - Adelie      1377.9 39.1 329  35.236  <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: dunnettx method for 2 tests
```

Post-Hoc Tests (Dunnett's)

With `contrast()` function from `emmeans` package

- Dunnett's comparison is a type of contrast
- Each level compared to control
- Use `method = "trt.vs.ctrl"` OR `method = "dunnett"`

```
contrast(emm_sp, method = "dunnett")
```

```
##  contrast           estimate   SE  df t.ratio p.value
##  Chinstrap - Adelie     26.9 46.5 329   0.579  0.7753
##  Gentoo - Adelie      1377.9 39.1 329  35.236  <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: dunnettx method for 2 tests
```

Look familiar?

Post-Hoc Tests (Dunnett's)

Dunnett's treatment vs. control contrasts with `summary()` table

```r
summary(m)
```

```
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       3372.39      31.43 107.308   <2e-16 ***
## speciesChinstrap    26.92      46.48   0.579    0.563
## speciesGentoo     1377.86      39.10  35.236   <2e-16 ***
## sexmale            667.56      34.70  19.236   <2e-16 ***
```

Dunnett's treatment vs. control contrasts with emmeans

```r
contrast(emm_sp, method = "dunnett", adjust = "none")
```

```
##  contrast           estimate   SE  df t.ratio
p.value
##  Chinstrap - Adelie     26.9 46.5 329   0.579
0.5628
##  Gentoo - Adelie      1377.9 39.1 329 35.236
<.0001
##
```

```r
contrast(emmeans(m, specs = "sex"), method =
"dunnett",
         adjust = "none")
```

```
##  contrast      estimate   SE  df t.ratio p.value
##  male - female      668 34.7 329 19.236  <.0001
##
## Results are averaged over the levels of: species
```

Post-Hoc Tests and P-Value adjustments

No adjustment, too liberal?

```
pairs(emm_sp, adjust = "none")
```

```
##  contrast            estimate   SE  df t.ratio
p.value
##  Adelie - Chinstrap     -26.9 46.5 329  -0.579
0.5628
##  Adelie - Gentoo      -1377.9 39.1 329 -35.236
<.0001
##  Chinstrap - Gentoo   -1350.9 48.1 329 -28.067
<.0001
##
## Results are averaged over the levels of: sex
```

Extremely conservative*

```
pairs(emm_sp, adjust = "bonferroni")
```

```
##  contrast            estimate   SE  df t.ratio
p.value
##  Adelie - Chinstrap     -26.9 46.5 329  -0.579
1.0000
##  Adelie - Gentoo      -1377.9 39.1 329 -35.236
<.0001
##  Chinstrap - Gentoo   -1350.9 48.1 329 -28.067
<.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: bonferroni method for 3 tests
```

In these examples, little difference, but can make a HUGE difference in other analyses

* Don't use "Bonferroni, [see this article]

Post-Hoc Tests and P-Value adjustments

Middle of the road: Benjamini Hochberg (FDR, False Discovery Rate)*

```
pairs(emm_sp, adjust = "fdr")
```

```
##  contrast            estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap     -26.9 46.5 329  -0.579 0.5628
##  Adelie - Gentoo      -1377.9 39.1 329 -35.236 <.0001
##  Chinstrap - Gentoo   -1350.9 48.1 329 -28.067 <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: fdr method for 3 tests
```

* See this article

Post-Hoc Tests and P-Value adjustments

Middle of the road: Benjamini Hochberg (FDR, False Discovery Rate)*

```
pairs(emm_sp, adjust = "fdr")
```

```
##  contrast            estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap     -26.9 46.5 329  -0.579 0.5628
##  Adelie - Gentoo      -1377.9 39.1 329 -35.236 <.0001
##  Chinstrap - Gentoo   -1350.9 48.1 329 -28.067 <.0001
##
## Results are averaged over the levels of: sex
## P value adjustment: fdr method for 3 tests
```

No one best method

What is your question? Are you more concerned about Type 1 or Type 2 error?

* See this article

Post-Hoc Tests

Test options

Argument	P-Value Adjustment
`none`	No P-Value Adjustment (essentially Fisher's LSD)
`tukey`	Tukey's HSD (Honestly significant difference), uses the Studentized range distribution with the number of means in the family.
`fdr`	Benjamini-Hochberg Test or False Discovery Rate Test
`bonferroni`	Bonferroni Correction
`scheffe`	Computes p values from F distribution
`mvt`	Adjusted p values based on the joint normal or t distribution of the linear function
`holm`	Holm Test
`hochberg`	Hochberg Test
`hommel`	Hommel Test

Post-Hoc Tests with Interactions

Model: 2-way ANOVA

```r
m <- lm(body_mass_g ~ species * sex, data = penguins)
```

Estimated Marginal Means

```r
library(emmeans)
m_emms <- emmeans(m, specs = c("species", "sex"))
m_emms
```

```
##  species   sex    emmean   SE  df lower.CL upper.CL
##  Adelie    female   3369 36.2 327     3298     3440
##  Chinstrap female   3527 53.1 327     3423     3632
##  Gentoo    female   4680 40.6 327     4600     4760
##  Adelie    male     4043 36.2 327     3972     4115
##  Chinstrap male     3939 53.1 327     3835     4043
##  Gentoo    male     5485 39.6 327     5407     5563
##
## Confidence level used: 0.95
```

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(m_emms, adjust = "fdr")
```

```
##  contrast                              estimate   SE  df t.ratio p.value
##  Adelie female - Chinstrap female          -158 64.2 327  -2.465 0.0152
##  Adelie female - Gentoo female            -1311 54.4 327 -24.088 <.0001
##  Adelie female - Adelie male               -675 51.2 327 -13.174 <.0001
##  Adelie female - Chinstrap male            -570 64.2 327  -8.875 <.0001
##  Adelie female - Gentoo male              -2116 53.7 327 -39.425 <.0001
##  Chinstrap female - Gentoo female         -1153 66.8 327 -17.246 <.0001
##  Chinstrap female - Adelie male            -516 64.2 327  -8.037 <.0001
##  Chinstrap female - Chinstrap male         -412 75.0 327  -5.487 <.0001
##  Chinstrap female - Gentoo male           -1958 66.2 327 -29.564 <.0001
##  Gentoo female - Adelie male                636 54.4 327  11.691 <.0001
##  Gentoo female - Chinstrap male             741 66.8 327  11.085 <.0001
##  Gentoo female - Gentoo male               -805 56.7 327 -14.188 <.0001
##  Adelie male - Chinstrap male               105 64.2 327   1.627 0.1047
##  Adelie male - Gentoo male                -1441 53.7 327 -26.855 <.0001
##  Chinstrap male - Gentoo male             -1546 66.2 327 -23.345 <.0001
##
## P value adjustment: fdr method for 15 tests
```

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(m_emms, adjust = "fdr")
```

```
##  contrast                             estimate   SE  df t.ratio p.value
##  Adelie female - Chinstrap female         -158 64.2 327  -2.465 0.0152
##  Adelie female - Gentoo female           -1311 54.4 327 -24.088 <.0001
##  Adelie female - Adelie male              -675 51.2 327 -13.174 <.0001
##  Adelie female - Chinstrap male           -570 64.2 327  -8.875 <.0001
##  Adelie female - Gentoo male             -2116 53.7 327 -39.425 <.0001
##  Chinstrap female - Gentoo female        -1153 66.8 327 -17.246 <.0001
##  Chinstrap female - Adelie male           -516 64.2 327  -8.037 <.0001
##  Chinstrap female - Chinstrap male        -412 75.0 327  -5.487 <.0001
##  Chinstrap female - Gentoo male          -1958 66.2 327 -29.564 <.0001
##  Gentoo female - Adelie male               636 54.4 327  11.691 <.0001
##  Gentoo female - Chinstrap male            741 66.8 327  11.085 <.0001
##  Gentoo female - Gentoo male              -805 56.7 327 -14.188 <.0001
##  Adelie male - Chinstrap male              105 64.2 327   1.627 0.1047
##  Adelie male - Gentoo male               -1441 53.7 327 -26.855 <.0001
##  Chinstrap male - Gentoo male            -1546 66.2 327 -23.345 <.0001
##
## P value adjustment: fdr method for 15 tests
```

Differences in Body Mass

- Female Adelie penguins **are** on average 158 g smaller than female Chinstrap penguins (P value = 0.015)

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(m_emms, adjust = "fdr")
```

Differences in Body Mass

- Female Adelie penguins **are** on average 158 g smaller than female Chinstrap penguins (P value = 0.015)

- Male Adelie penguins are **not** different from male Chinstrap penguins (P value = 0.105)

```
##  contrast                            estimate   SE  df t.ratio p.value
##  Adelie female - Chinstrap female        -158 64.2 327  -2.465 0.0152
##  Adelie female - Gentoo female          -1311 54.4 327 -24.088 <.0001
##  Adelie female - Adelie male             -675 51.2 327 -13.174 <.0001
##  Adelie female - Chinstrap male          -570 64.2 327  -8.875 <.0001
##  Adelie female - Gentoo male            -2116 53.7 327 -39.425 <.0001
##  Chinstrap female - Gentoo female       -1153 66.8 327 -17.246 <.0001
##  Chinstrap female - Adelie male          -516 64.2 327  -8.037 <.0001
##  Chinstrap female - Chinstrap male       -412 75.0 327  -5.487 <.0001
##  Chinstrap female - Gentoo male         -1958 66.2 327 -29.564 <.0001
##  Gentoo female - Adelie male              636 54.4 327  11.691 <.0001
##  Gentoo female - Chinstrap male           741 66.8 327  11.085 <.0001
##  Gentoo female - Gentoo male             -805 56.7 327 -14.188 <.0001
##  Adelie male - Chinstrap male             105 64.2 327   1.627 0.1047
##  Adelie male - Gentoo male              -1441 53.7 327 -26.855 <.0001
##  Chinstrap male - Gentoo male           -1546 66.2 327 -23.345 <.0001
##
## P value adjustment: fdr method for 15 tests
```

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare each combination

```
pairs(m_emms, adjust = "fdr")
```

Differences in Body Mass

- Female Adelie penguins **are** on average 158 g smaller than female Chinstrap penguins (P value = 0.015)

- Male Adelie penguins are **not** different from male Chinstrap penguins (P value = 0.105)

- Female Adelie penguins **are** on average 675 g lighter than male Adelie penguins (P value = 0)

```
##  contrast                          estimate   SE  df t.ratio p.value
##  Adelie female - Chinstrap female      -158 64.2 327  -2.465 0.0152
##  Adelie female - Gentoo female        -1311 54.4 327 -24.088 <.0001
##  Adelie female - Adelie male           -675 51.2 327 -13.174 <.0001
##  Adelie female - Chinstrap male        -570 64.2 327  -8.875 <.0001
##  Adelie female - Gentoo male          -2116 53.7 327 -39.425 <.0001
##  Chinstrap female - Gentoo female     -1153 66.8 327 -17.246 <.0001
##  Chinstrap female - Adelie male        -516 64.2 327  -8.037 <.0001
##  Chinstrap female - Chinstrap male     -412 75.0 327  -5.487 <.0001
##  Chinstrap female - Gentoo male       -1958 66.2 327 -29.564 <.0001
##  Gentoo female - Adelie male            636 54.4 327  11.691 <.0001
##  Gentoo female - Chinstrap male         741 66.8 327  11.085 <.0001
##  Gentoo female - Gentoo male           -805 56.7 327 -14.188 <.0001
##  Adelie male - Chinstrap male           105 64.2 327   1.627 0.1047
##  Adelie male - Gentoo male            -1441 53.7 327 -26.855 <.0001
##  Chinstrap male - Gentoo male         -1546 66.2 327 -23.345 <.0001
##
## P value adjustment: fdr method for 15 tests
```

Post-Hoc Tests with Interactions

Model: ANCOVA

```
m <- lm(body_mass_g ~ flipper_length_mm * species, data = penguins)
```

Estimated Marginal Means

- Here use **`emtrends()`** function from **`emmeans`** package

```
m_emms <- emtrends(m, specs = "species", var = "flipper_length_mm")
m_emms
```

```
##  species   flipper_length_mm.trend   SE  df lower.CL upper.CL
##  Adelie                       32.8 4.63 336     23.7     41.9
##  Chinstrap                    34.6 6.35 336     22.1     47.1
##  Gentoo                       54.6 5.17 336     44.4     64.8
##
## Confidence level used: 0.95
```

These are the effects of Flipper Length on Body Mass in each Species.

On average...

- Adelie: Body Mass increases by 32.8 g for each 1 mm increase in Flipper Length.
- Chinstrap: Body Mass increases by 34.6 g for each 1 mm increase in Flipper Length.
- Gentoo: Body Mass increases by 54.6 g for each 1 mm increase in Flipper Length.

Post-Hoc Tests with Interactions

Model: ANCOVA

```
m <- lm(body_mass_g ~ flipper_length_mm * species, data = penguins)
```

Estimated Marginal Means

- Here use **`emtrends()`** function from **`emmeans`** package

```
m_emms <- emtrends(m, specs = "species", var = "flipper_length_mm")
m_emms
```

```
##  species   flipper_length_mm.trend   SE  df lower.CL upper.CL
##  Adelie                       32.8 4.63 336     23.7     41.9
##  Chinstrap                    34.6 6.35 336     22.1     47.1
##  Gentoo                       54.6 5.17 336     44.4     64.8
##
## Confidence level used: 0.95
```

These are the effects of Flipper Length on Body Mass in each Species.

On average...

- Adelie: Body Mass increases by 32.8 g for each 1 mm increase in Flipper Length.
- Chinstrap: Body Mass increases by 34.6 g for each 1 mm increase in Flipper Length.
- Gentoo: Body Mass increases by 54.6 g for each 1 mm increase in Flipper Length.

But are these different from one another?

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare among species

```r
pairs(m_emms, adjust = "fdr")
```

```
##  contrast              estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap       -1.74 7.86 336 -0.222  0.8247
##  Adelie - Gentoo         -21.79 6.94 336 -3.139  0.0055
##  Chinstrap - Gentoo      -20.05 8.19 336 -2.448  0.0223
##
## P value adjustment: fdr method for 3 tests
```

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare among species

```
pairs(m_emms, adjust = "fdr")
```

```
##  contrast              estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap       -1.74 7.86 336 -0.222  0.8247
##  Adelie - Gentoo         -21.79 6.94 336 -3.139  0.0055
##  Chinstrap - Gentoo      -20.05 8.19 336 -2.448  0.0223
##
## P value adjustment: fdr method for 3 tests
```

Differences in the effect of Flipper Length on Body Mass

- The effect of Flipper Length on Body Mass is **not** different between Adelie and Chinstrap penguins (P value = 0.825)

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare among species

```r
pairs(m_emms, adjust = "fdr")
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap      -1.74 7.86 336 -0.222  0.8247
##  Adelie - Gentoo        -21.79 6.94 336 -3.139  0.0055
##  Chinstrap - Gentoo     -20.05 8.19 336 -2.448  0.0223
##
## P value adjustment: fdr method for 3 tests
```

Differences in the effect of Flipper Length on Body Mass

- The effect of Flipper Length on Body Mass is **not** different between Adelie and Chinstrap penguins (P value = 0.825)
- The effect of Flipper Length on Body Mass **is significantly less** in Adelie than in Gentoo penguins (Body Mass increases 21.8 g less per 1mm increase in Flipper Length; P value = 0.006)

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare among species

```
pairs(m_emms, adjust = "fdr")
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap     -1.74 7.86 336 -0.222  0.8247
##  Adelie - Gentoo       -21.79 6.94 336 -3.139  0.0055
##  Chinstrap - Gentoo    -20.05 8.19 336 -2.448  0.0223
##
## P value adjustment: fdr method for 3 tests
```

Differences in the effect of Flipper Length on Body Mass

- The effect of Flipper Length on Body Mass is **not** different between Adelie and Chinstrap penguins (P value = 0.825)
- The effect of Flipper Length on Body Mass **is significantly less** in Adelie than in Gentoo penguins (Body Mass increases 21.8 g less per 1mm increase in Flipper Length; P value = 0.006)
- The effect of Flipper Length on Body Mass **is significantly less** in Chinstrap than in Gentoo penguins (Body Mass increases 20 g less per 1mm increase in Flipper Length; P value = 0.022)

Post-Hoc Tests with Interactions (All pair-wise)

`pairs()` function from `emmeans` packages

- Compare among species

```
pairs(m_emms, adjust = "fdr")
```

```
##  contrast             estimate   SE  df t.ratio p.value
##  Adelie - Chinstrap      -1.74 7.86 336 -0.222  0.8247
##  Adelie - Gentoo        -21.79 6.94 336 -3.139  0.0055
##  Chinstrap - Gentoo     -20.05 8.19 336 -2.448  0.0223
##
## P value adjustment: fdr method for 3 tests
```

Best way is to use a figure at the same time!

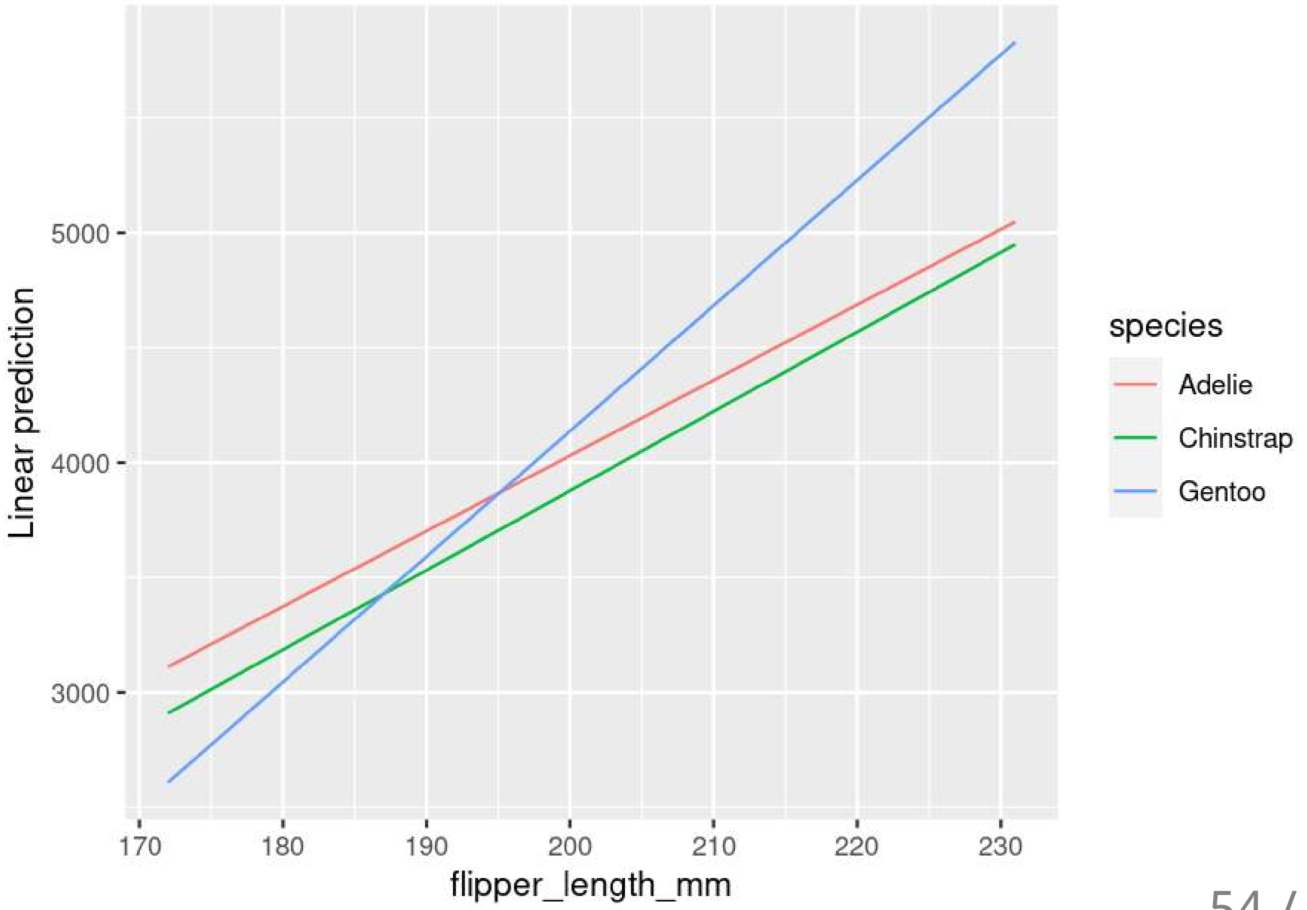
Differences in the ef

- The effect of Flipper Length on Body Mass is **not** different between Adelie and Chinstrap penguins (P value = 0.825)
- The effect of Flipper Length on Body Mass **is significantly less** in Adelie than in Gentoo penguins (Body Mass increases 21.8 g less per 1mm increase in Flipper Length; P value = 0.006)
- The effect of Flipper Length on Body Mass **is significantly less** in Chinstrap than in Gentoo penguins (Body Mass increases 20 g less per 1mm increase in Flipper Length; P value = 0.022)

Visualizing Interactions

```
emmip(m, species ~ flipper_length_mm, cov.reduce = range)
```

- Here, **Linear prediction** = **y** = **Body Mass**
- Adelie and Chinstrap penguins have similar effects (i.e. slopes are **not** significantly different)
- Gentoo has a larger effect (i.e. slope **is** significantly larger) than either Adelie or Chinstrap penguins



Homework (Practice)*

Consider bill depth your response variable and species and year your predictor variables

1. Convert year to a categorical variable and remove Gentoo penguins

```
penguins_sub <- mutate(penguins, year = factor(year))
penguins_sub <- filter(penguins_sub, species != "Gentoo")
```

2. Create a figure comparing bill depth to species and year. Think about how to best tease apart the relationships.
3. Model the relationship between bill depth and the interaction between species and year.
4. Check diagnostics
5. How does the relationship of species and bill depth change among years?

* Not to be handed in, answers posted in these slides next week