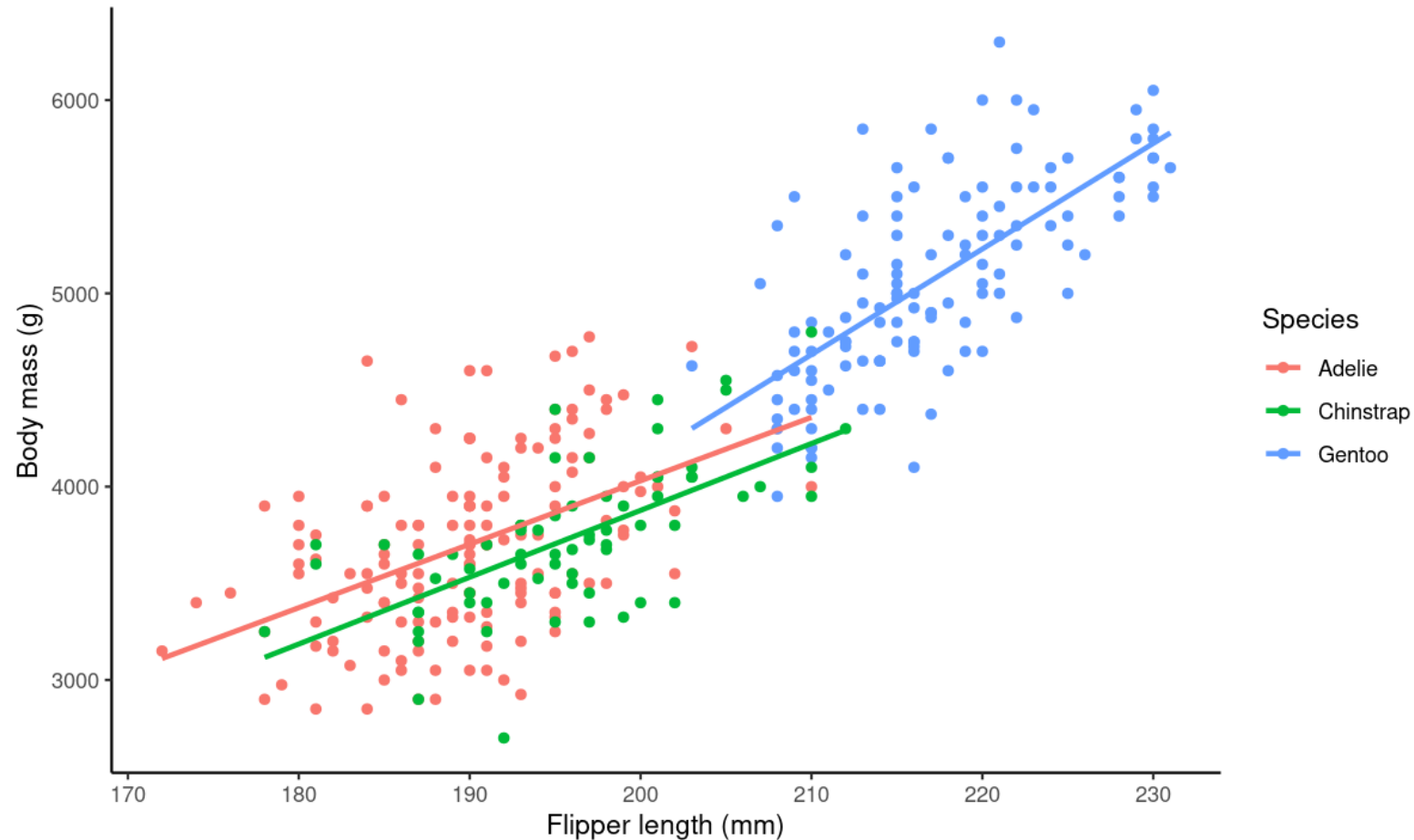


# Advanced Linear Models

Transformations,  
Interactions, and  
Post-hoc tests



# 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



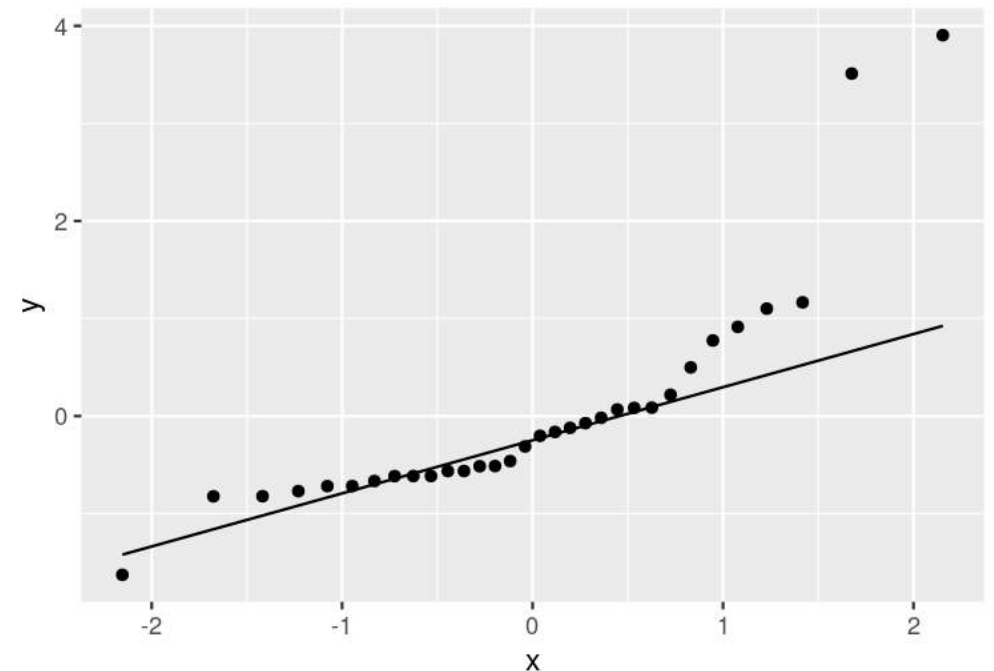
# Transformations

## 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	$1/\sqrt{y}$
Natural log (ln)	$\log(y)$
Log base 10	$\log_{10}(y)$
Square root	$\sqrt{y}$
Square	$y^2$
Box Cox	$(y^{\lambda} - 1) / \lambda$
Arcsine-square-root	$\text{asin}(\sqrt{y/100})$

**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 ( $\lambda$ )

**Can EITHER**  
**Apply  $\lambda$  through Box-Cox transformation**  
**OR**  
**Use it to indicate best transformation →**

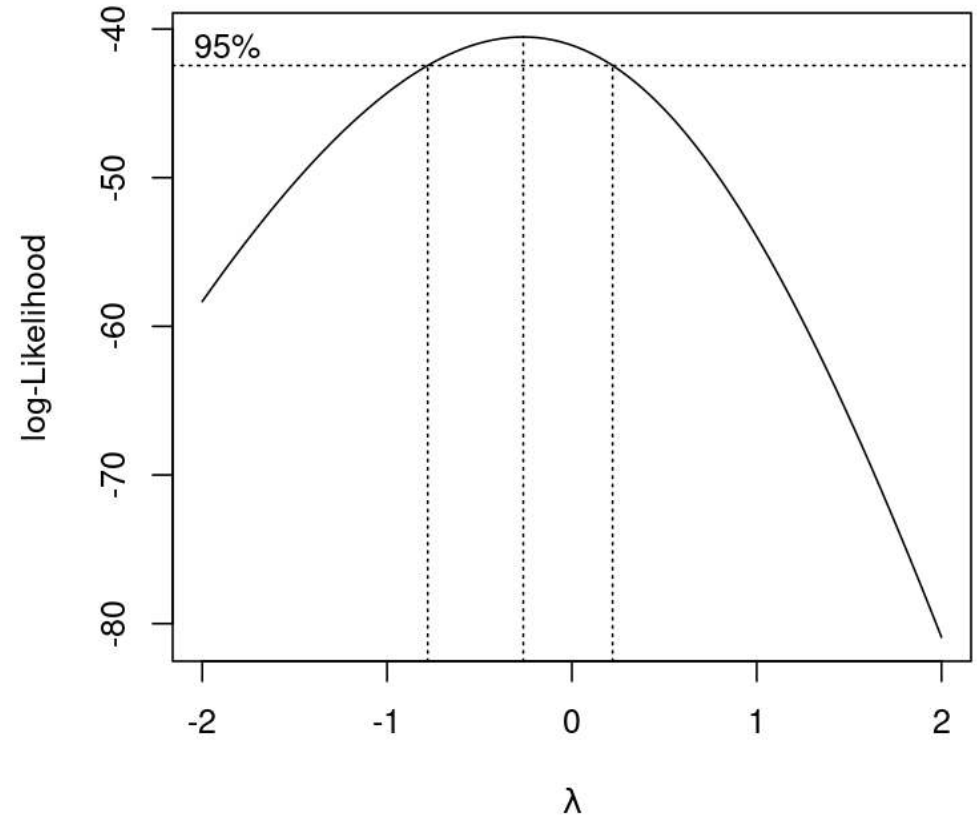
Best $\lambda$	Equation	Name
-2.5 to -1.5	$1/y^2$	inverse square
-1.5 to -0.75	$1/y$	reciprocal
-0.75 to -0.25	$1/\sqrt{y}$	inverse square root
-0.25 to 0.25	$\ln(y)$	natural log
0.25 to 0.75	$\sqrt{y}$	square root
0.75 to 1.5	$y$	none
1.5 to 2.5	$y^2$	square

# Transformations: Box-Cox

## Finding $\lambda$

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

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



# Transformations: Box-Cox

## Finding $\lambda$

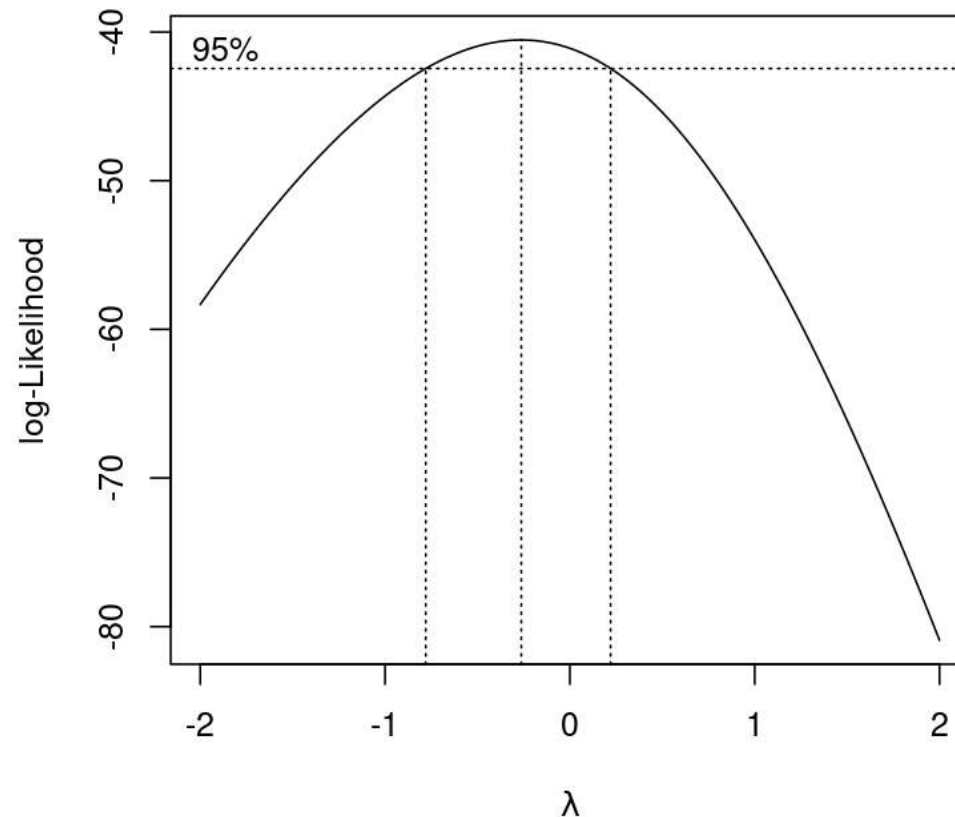
- Use a plot of  $\lambda$ 
  - `boxcox()` function from **MASS** package
  - Use `boxcox()` directly, otherwise **MASS** interferes with `select()`

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

- Get the exact  $\lambda$

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

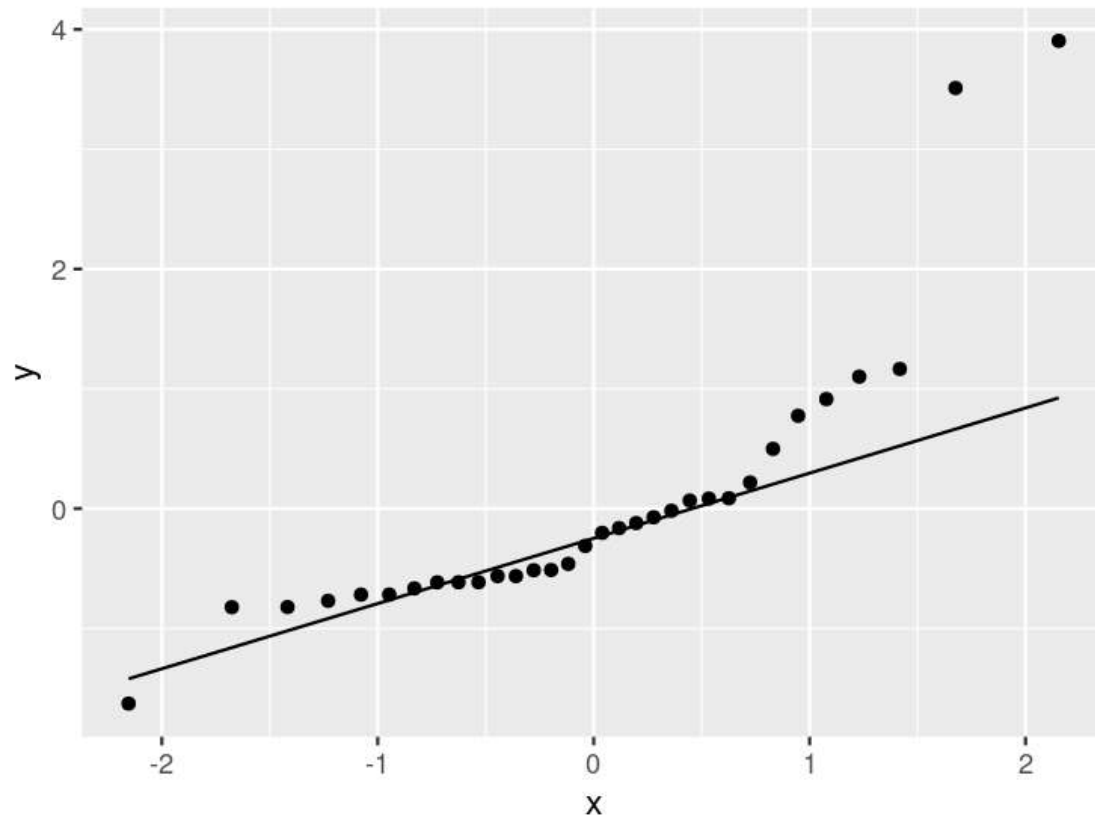
```
## [1] -0.2626263
```



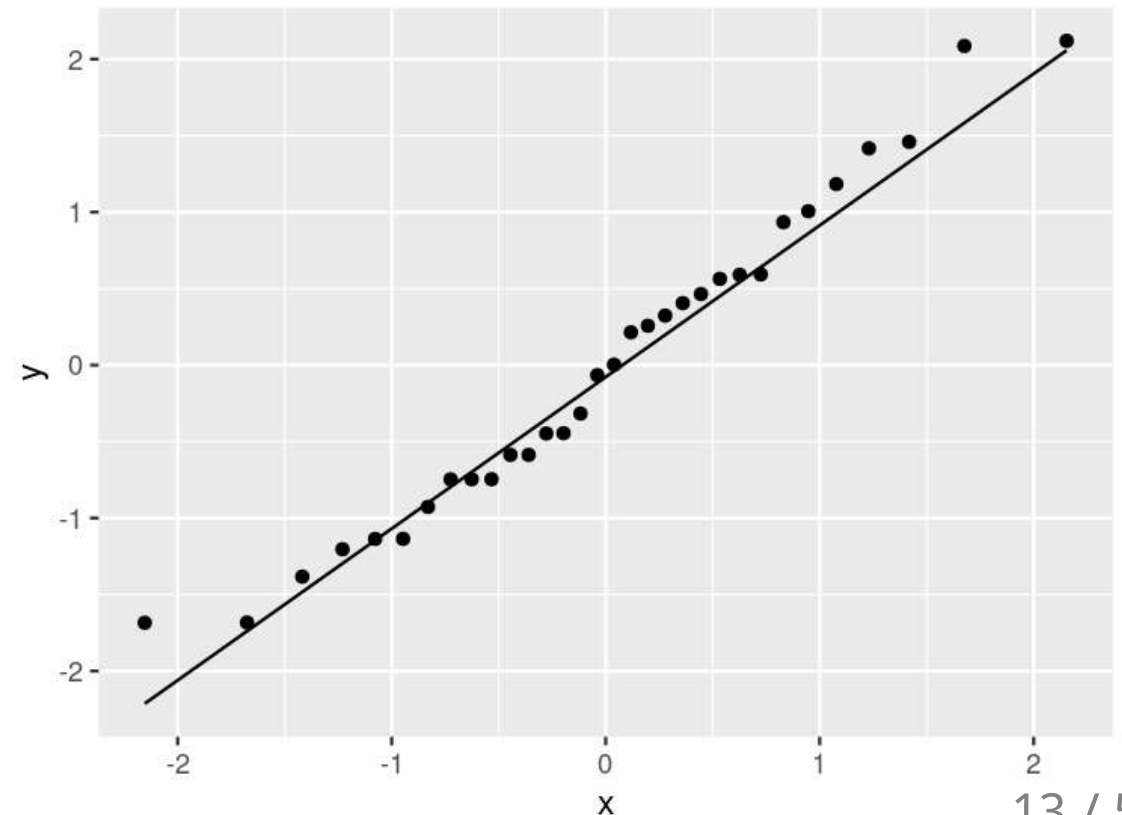
# Apply the transformation

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

Q-Q Normality Plot: No transformation



Q-Q Normality Plot: Box-Cox transformation



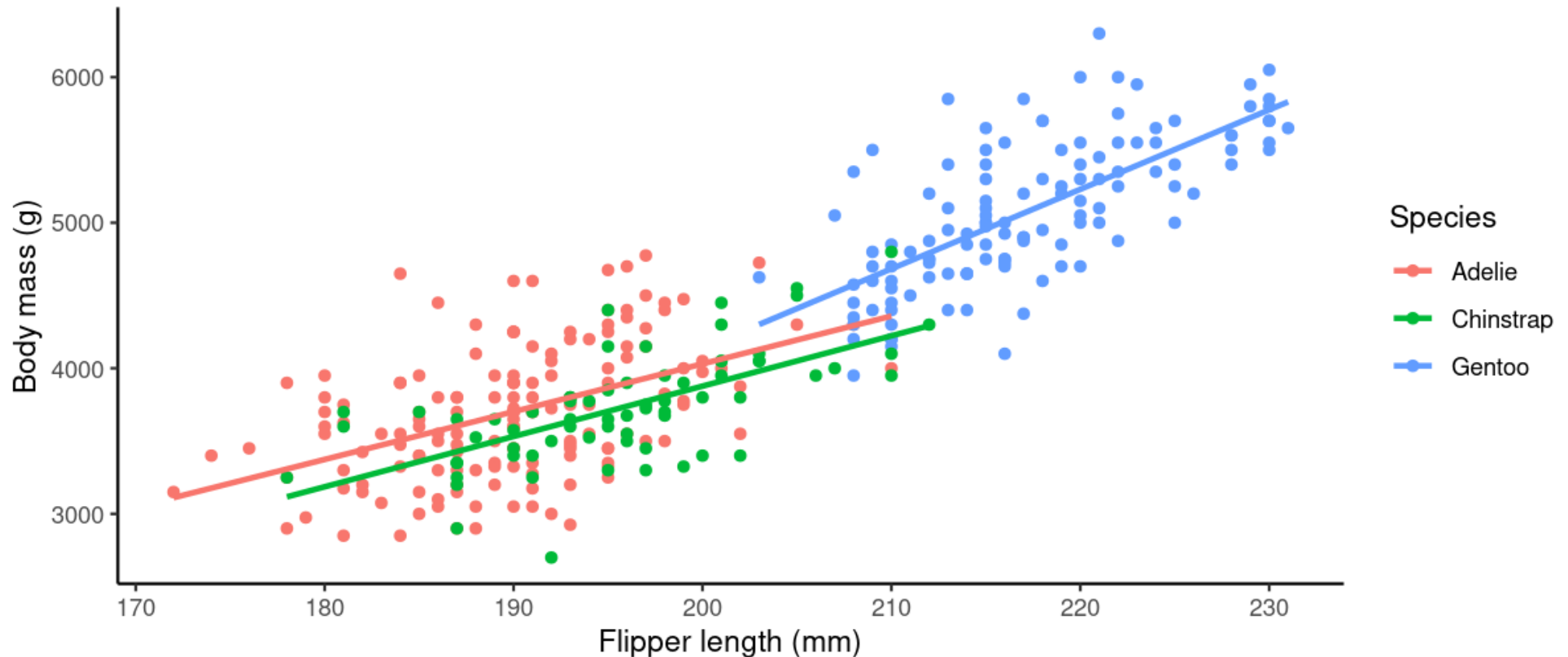
# Interactions



# 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?)

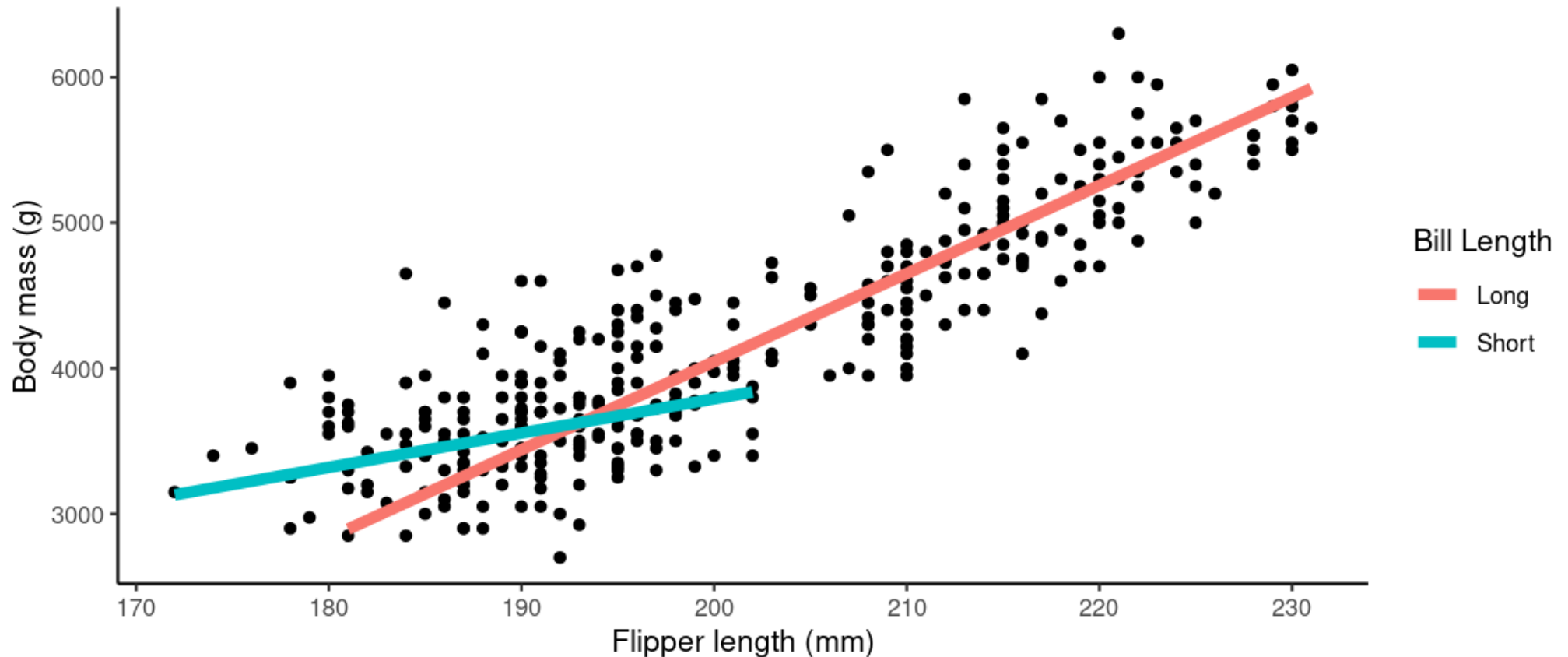


# Interactions

## 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
```

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

```
l_length_mm,
```

## Both Main Effects

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

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
## (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
##
```

But for now we'll focus on  
the Estimates

```
## 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

```
## 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 0.090
## flipper_length_mm -7.3085    15.0321   -0.486 0.628
## 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



OH WTF.

# 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

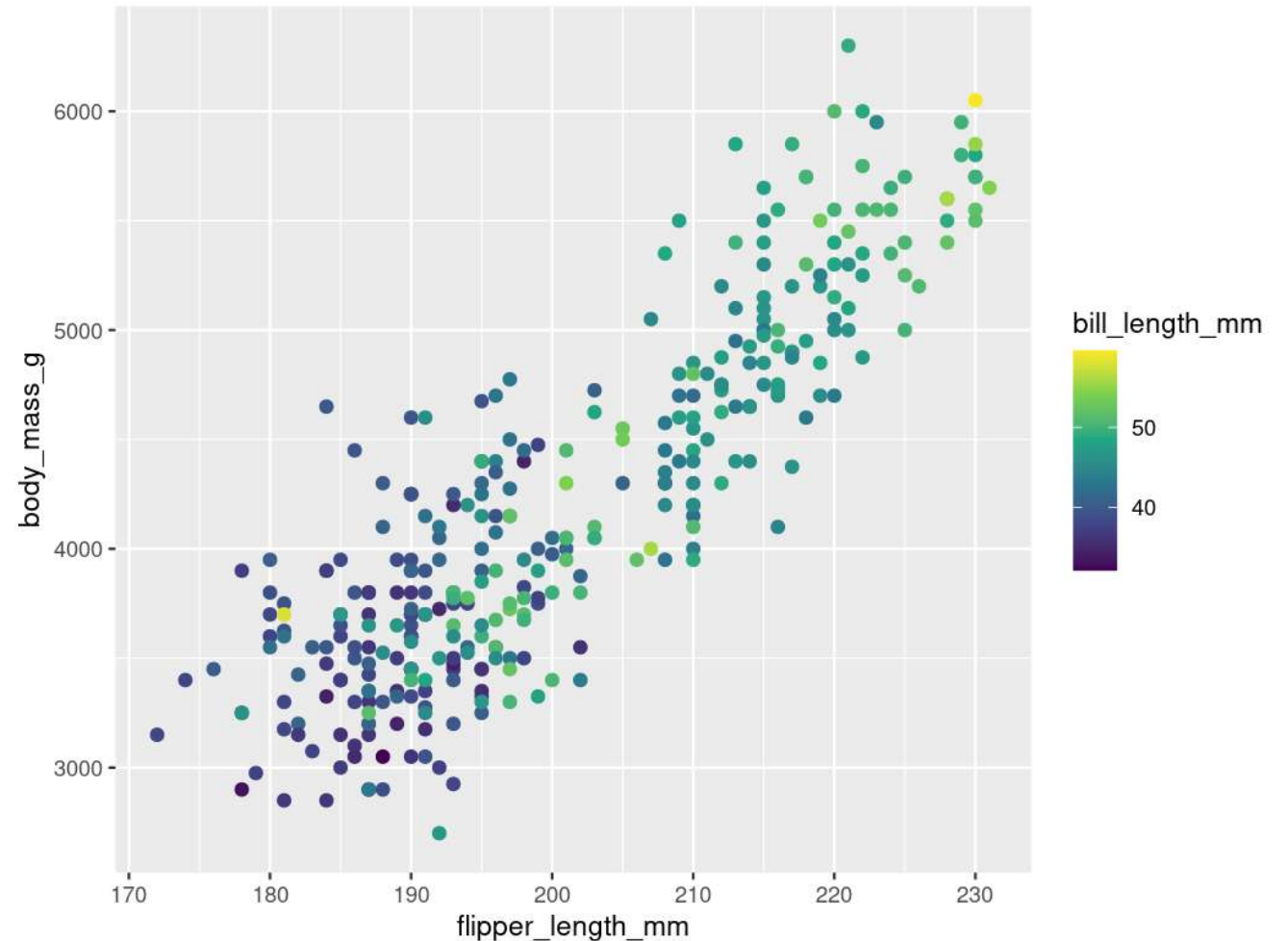
```
penguins_new
```

```
## # 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)
```

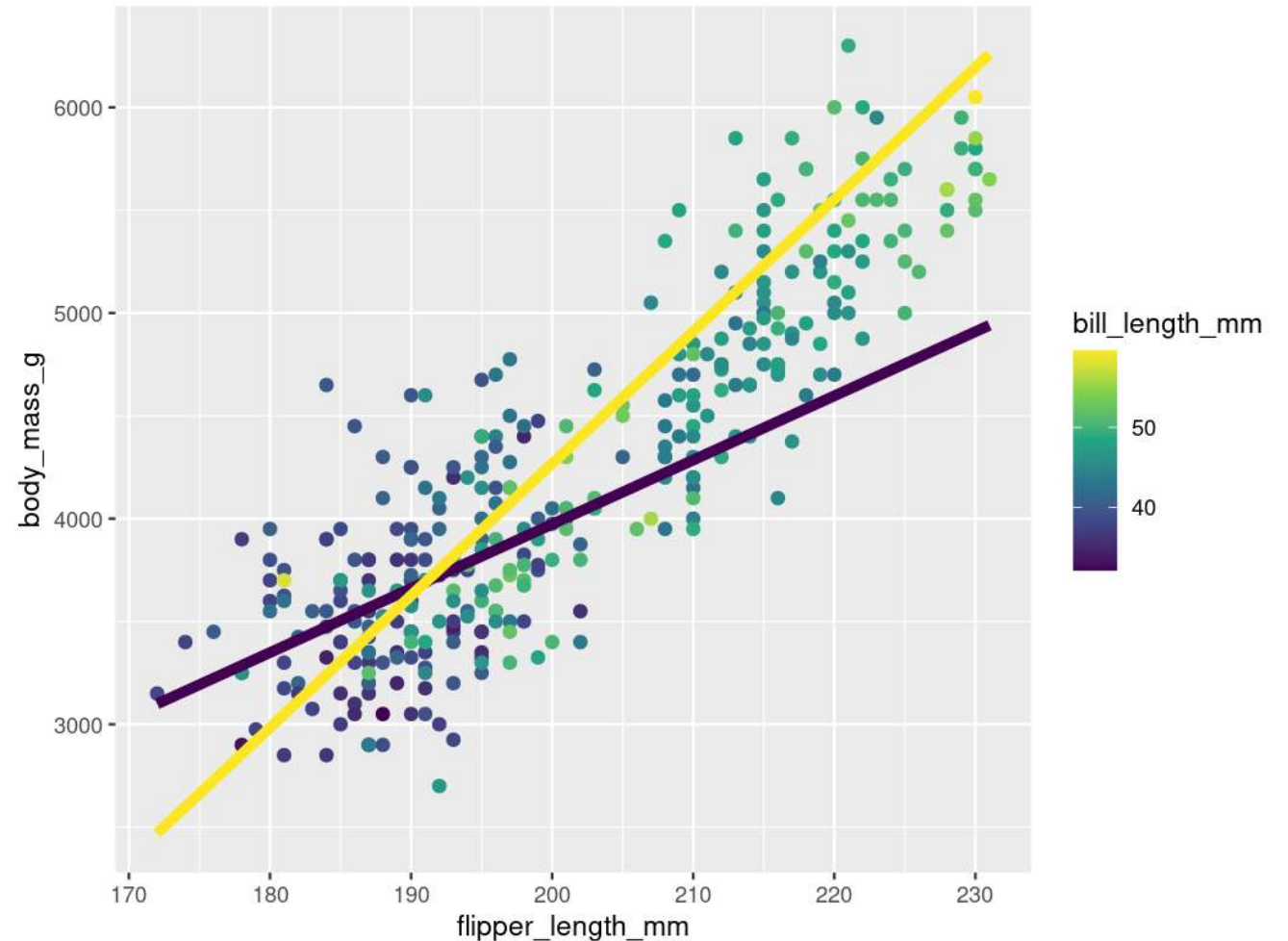




# Plotting Interactions

## Raw data + Model interaction

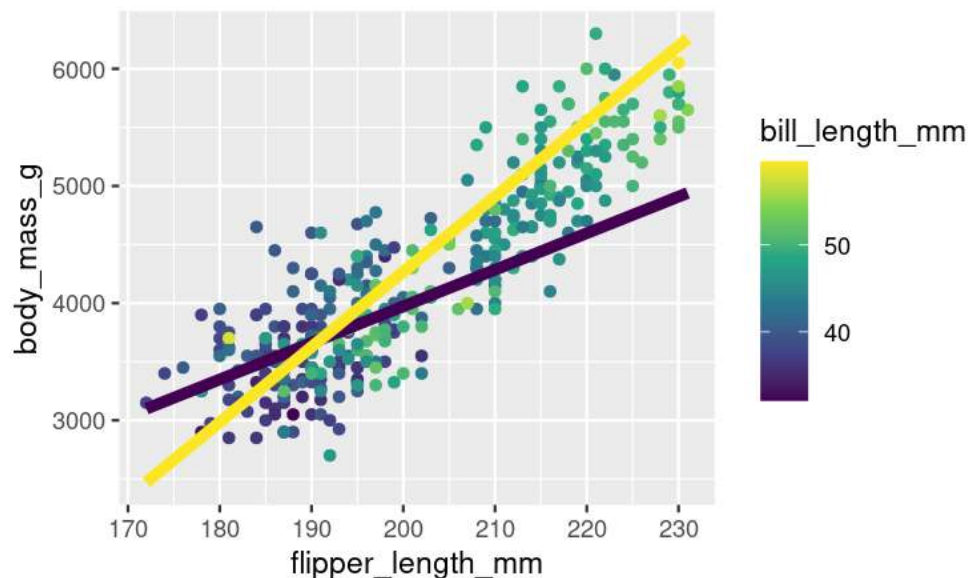
```
ggplot(data = penguins,  
       aes(x = flipper_length_mm,  
           y = body_mass_g,  
           colour = bill_length_mm)) +  
  geom_point(size = 2) +  
  geom_line(data = penguins_new,  
            aes(group = bill_length_mm),  
            size = 2)
```



# Plotting Interactions

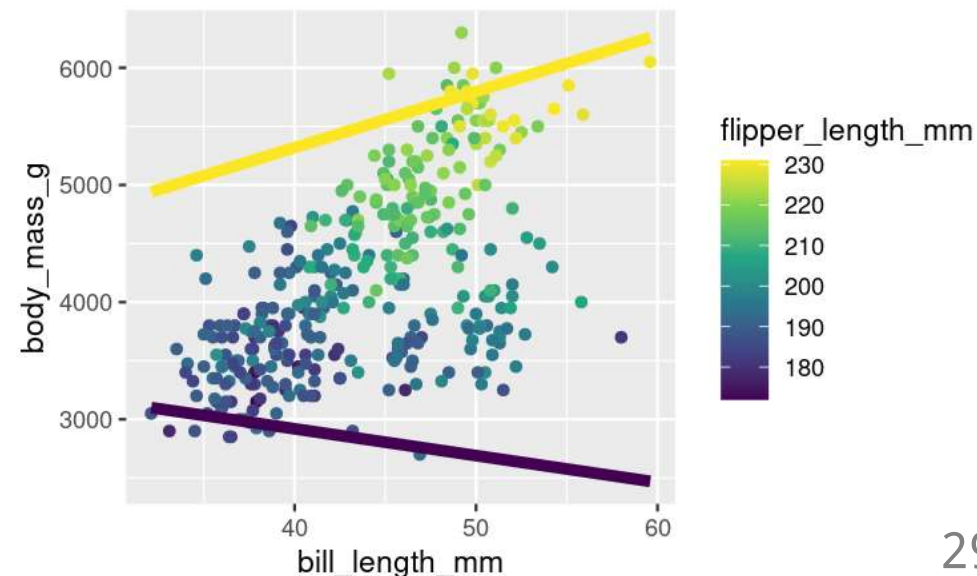
## From a Flipper Length perspective

```
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)
```



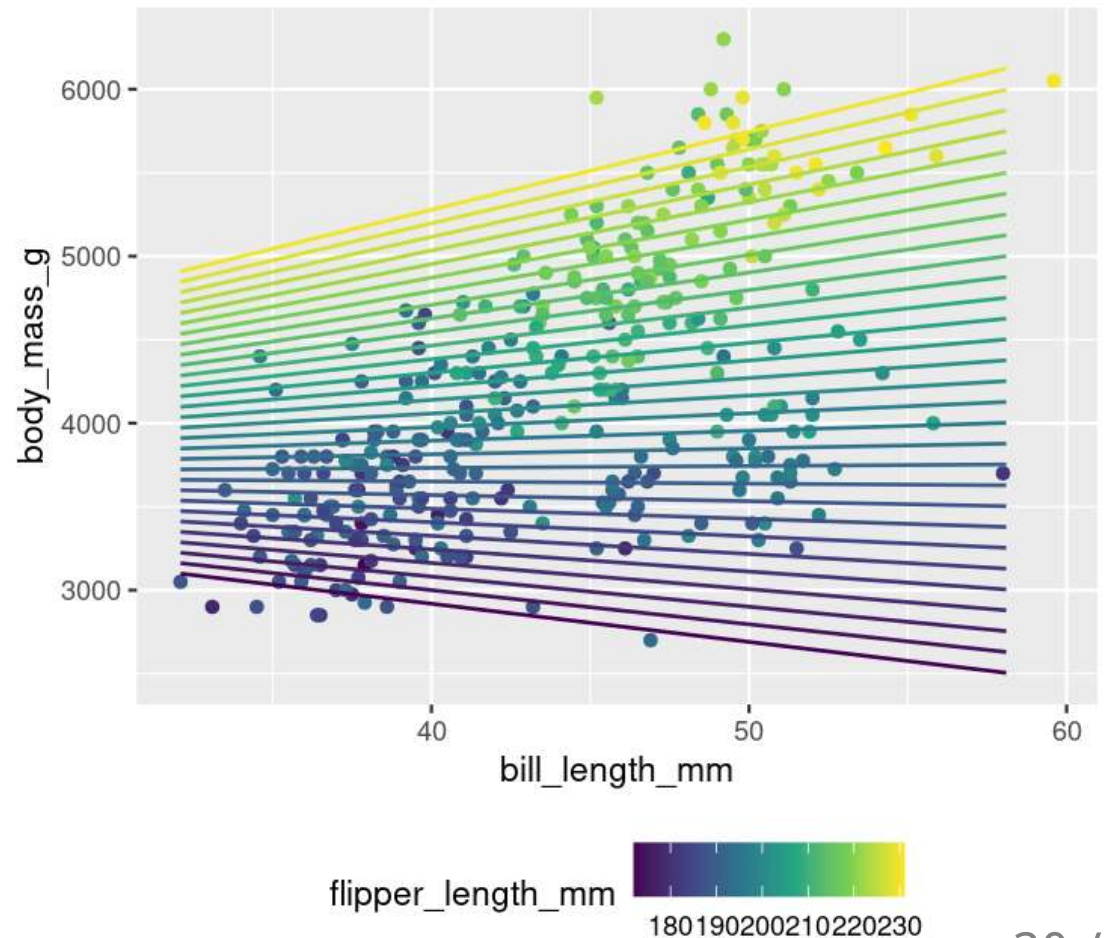
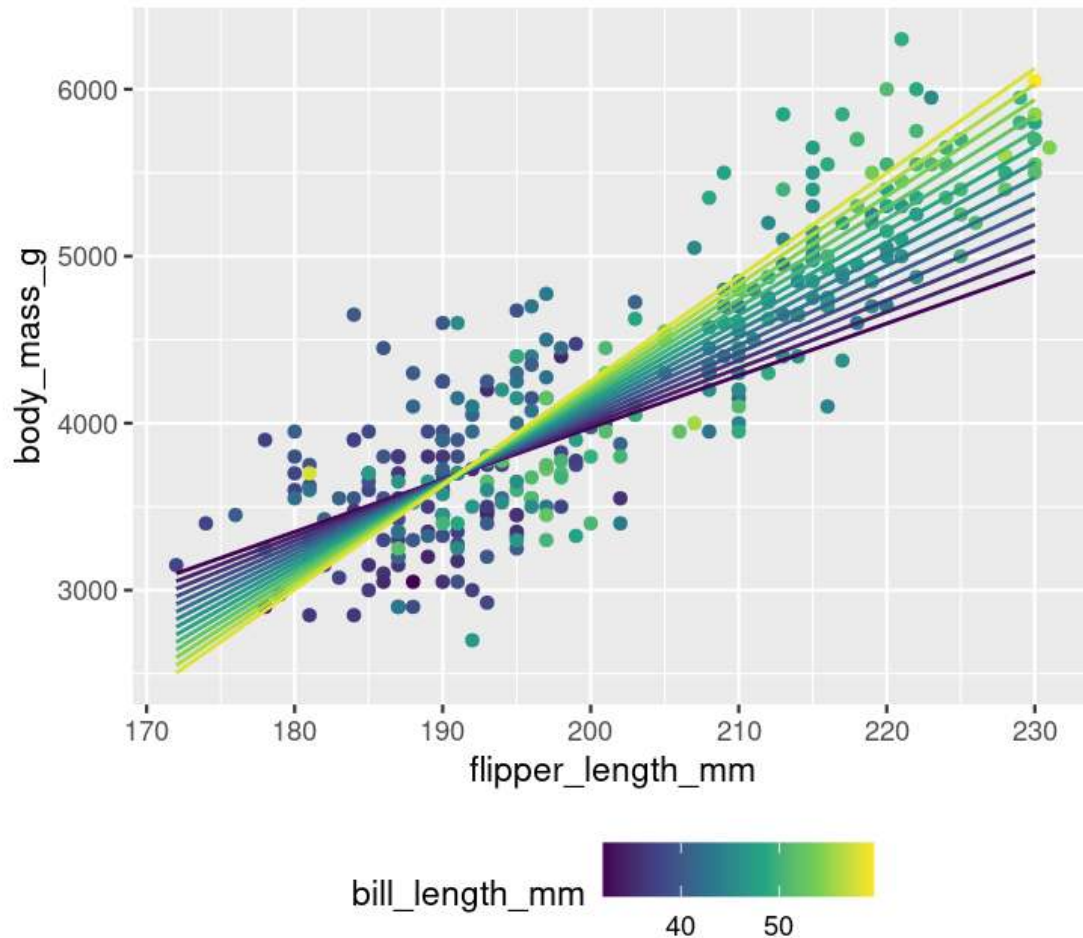
## From a Bill Length perspective

```
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		
-----------	----------	-----	--	--

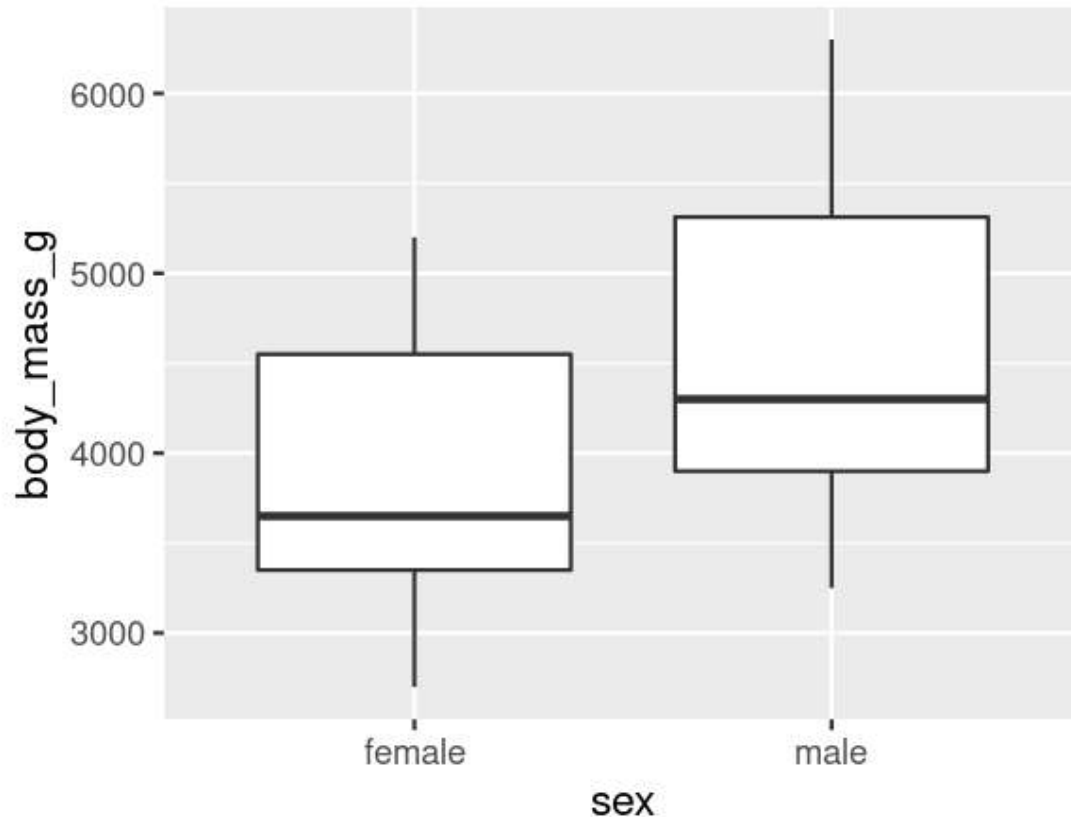
```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

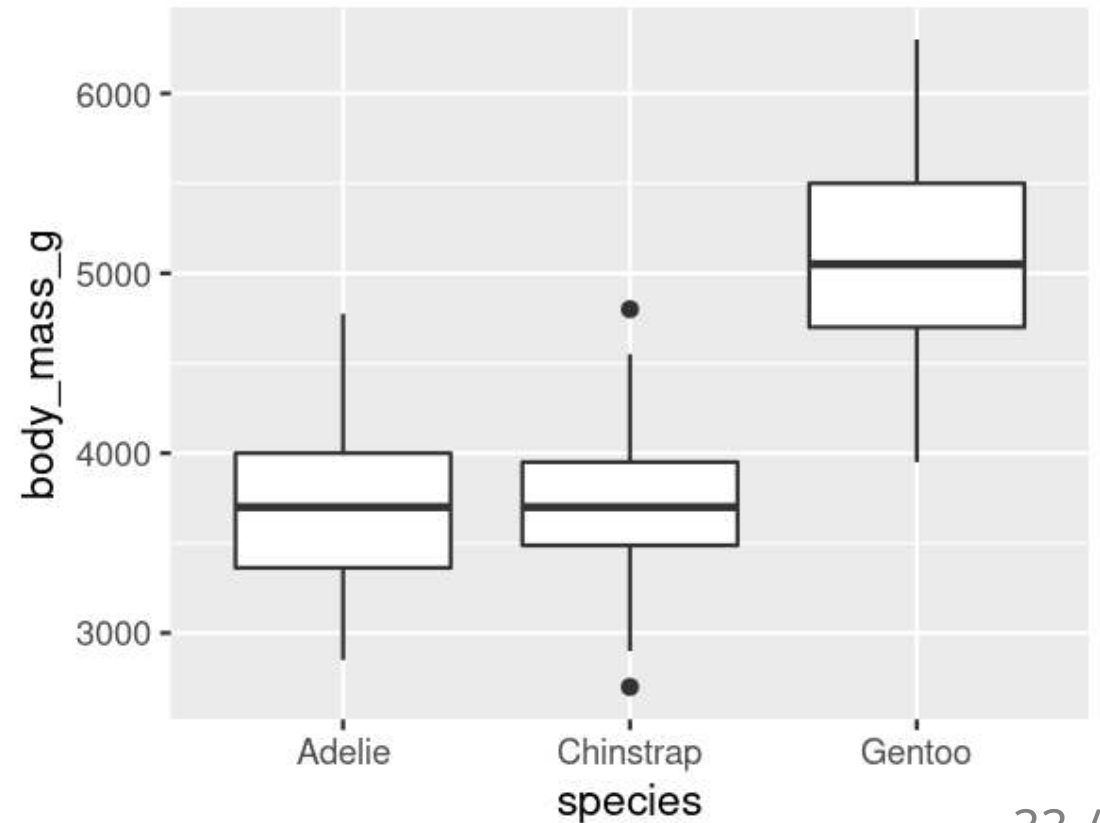
Differences within groups, but how are they different?

# Post-Hoc Tests

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

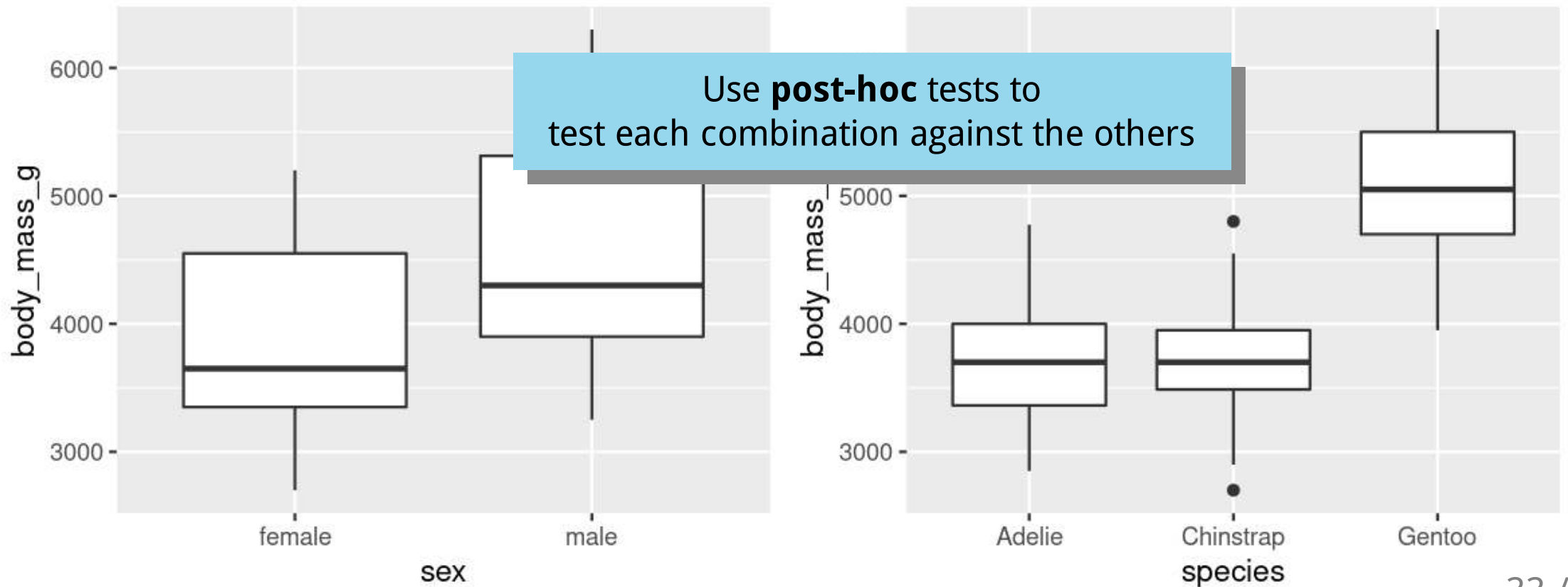


- Are Adelie and Chinstrap the same size?
- Looks like it, but no statistical support



# 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



# 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)
```

### Differences in Body Mass

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

##	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)
```

### 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)

##	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)
```

### 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)

```
## 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)
```

### 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)

```
## 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
```

**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

```
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`

```
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
##
```

```
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
```

# 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?

# 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	<a href="#">Benjamini-Hochberg Test or False Discovery Rate Test</a>
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	<a href="#">Holm Test</a>
hochberg	<a href="#">Hochberg Test</a>
hommel	<a href="#">Hommel Test</a>

# Post-Hoc Tests with Interactions

## Model: 2-way ANOVA

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

## Estimated Marginal Means

```
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")
```

## Differences in Body Mass

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

##	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)

##	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

```
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

```
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

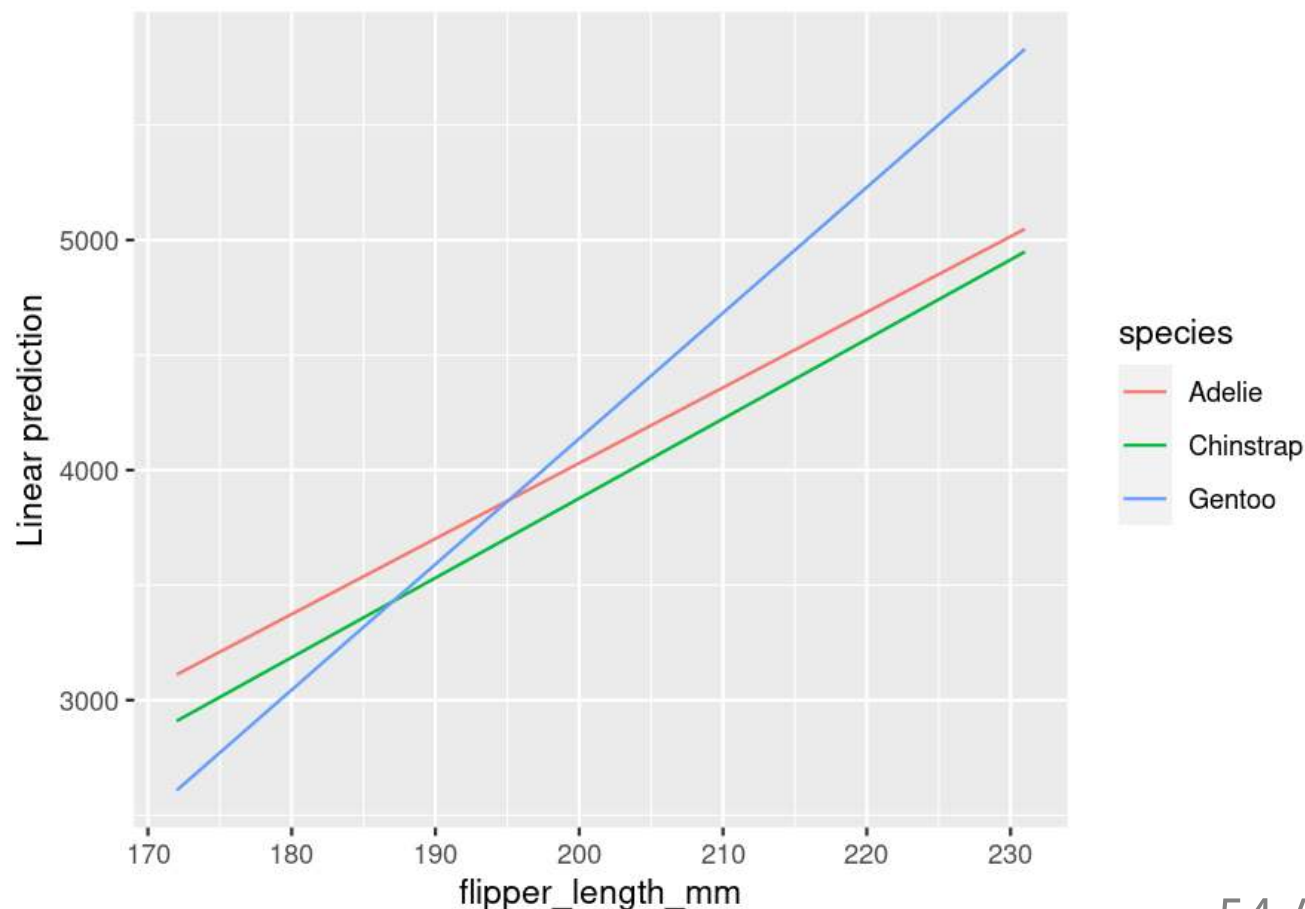
- The effect of Flipper Length on Body Mass is **not** different between Adelie and Chinstrap penguins (P value = 0.825)
- The effect of Flipper Length on Body Mass **is significantly less** in Adelie than in Gentoo penguins (Body Mass increases 21.8 g less per 1mm increase in Flipper Length; P value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