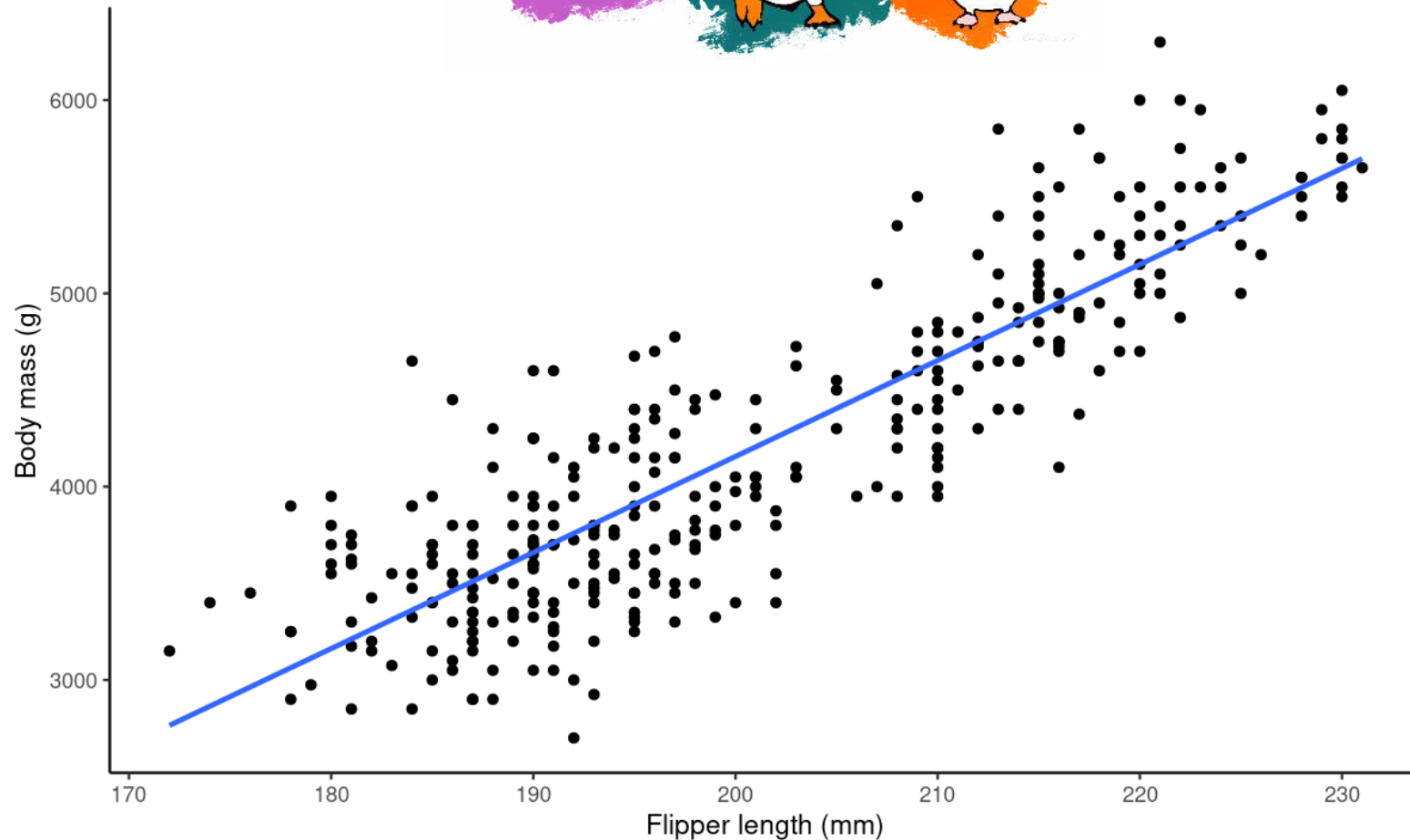
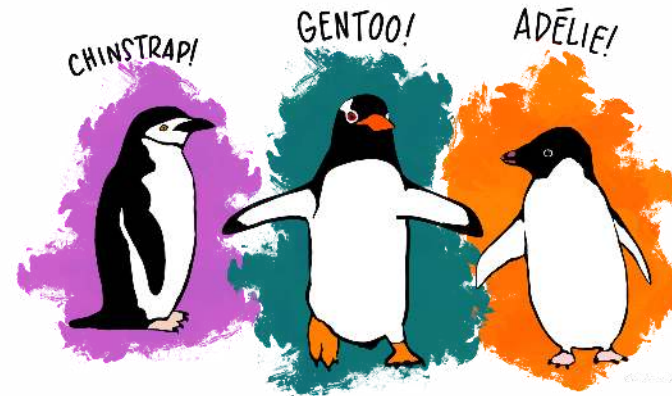


Linear Models

Regressions,
ANOVAs, and
Model assumptions



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)
```

How Are we Doing?

debugging



1.
I got this.



2.
Huh. Really
thought that
was it.



3.
(...)



4.
Fine. Restarting.



5.
OH WTF.



6.
Zombie
meltdown



7.



8.
A NEW HOPE!



9.
[insert awesome
theme song]



10.
I ♥ CODING!

Linear Models

Linear Models

Running models in R

```
lm(y ~ x1 + x2, data = data)
```

- **y** is the **response** variable (**dependent**)
- **x** are the **explanatory** variables (**independent, predictor**)

Here we're assuming a **continuous y**

Linear Models

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Different types of models

- If we only have one **x** which is continuous, this is a **simple linear regression**
- If both **x** are continuous, this is a **multiple linear regression**
- If both **x** are categorical, this is an **ANOVA**
- If **x1** is continuous and **x2** is categorical, this is an **ANCOVA**

Linear Models

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Different types of models

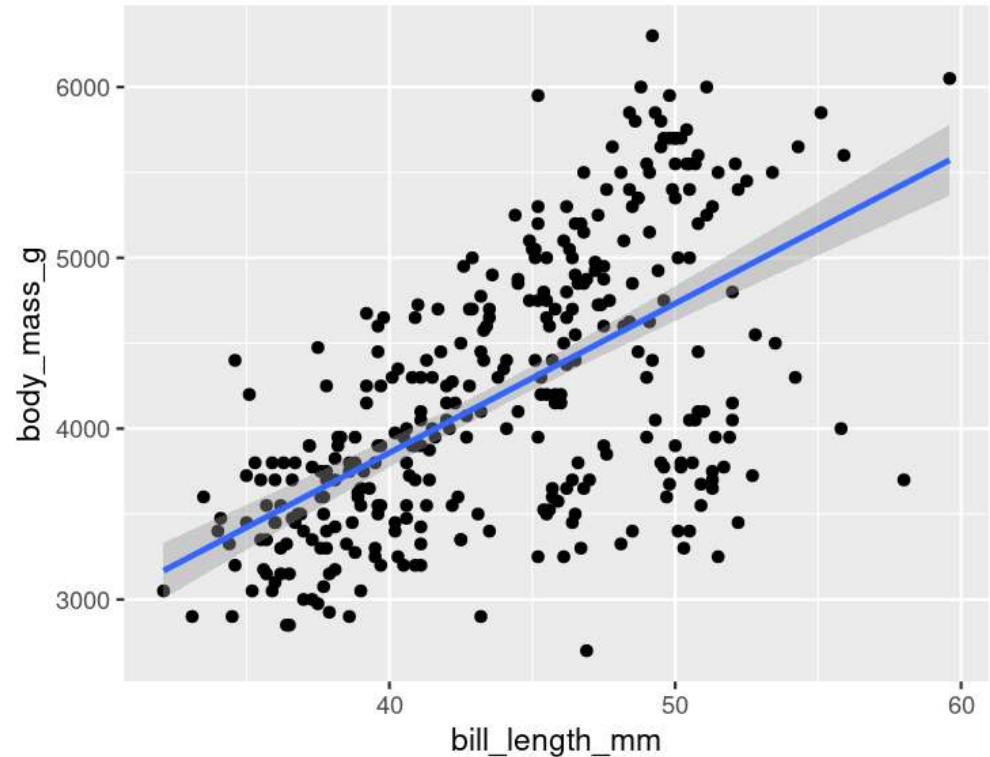
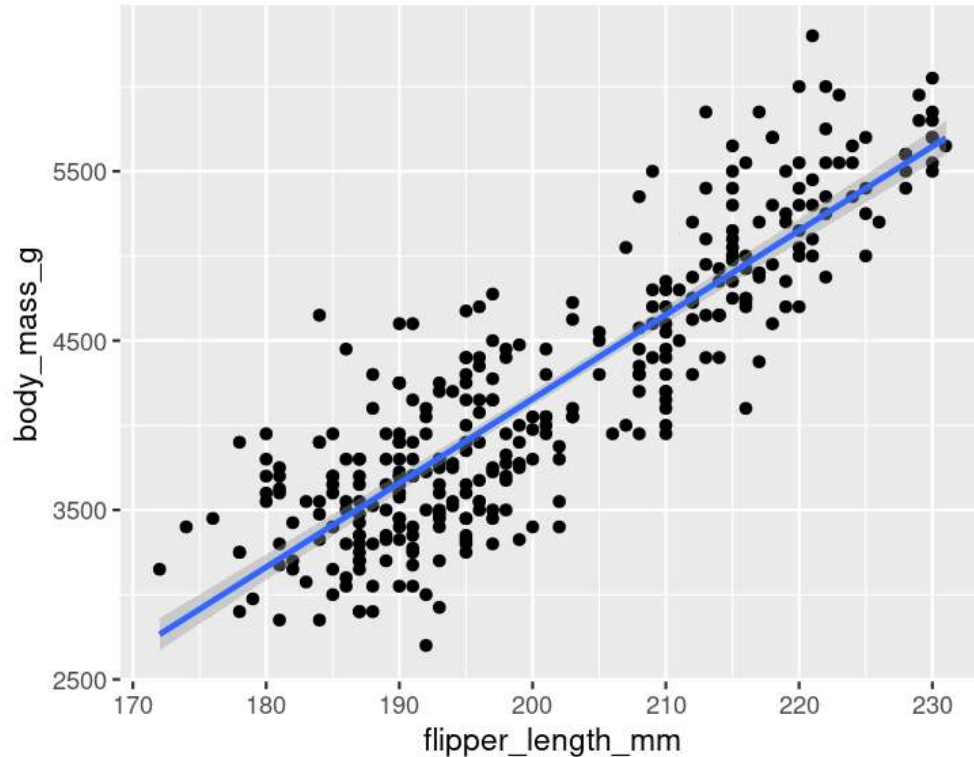
- If we only have one **x** which is continuous, this is a **simple linear regression**
- If both **x** are continuous, this is a **multiple linear regression**
- If both **x** are categorical, this is an **ANOVA**
- If **x1** is continuous and **x2** is categorical, this is an **ANCOVA**

R will figure it out for you

Regressions

Real example

- Is penguin body mass a function of skeletal size?
- Can it be predicted by flipper length and bill length?



Regressions

Real example

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

```
##  
## Call:  
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,  
##     data = penguins)  
##  
## Coefficients:  
##      (Intercept)  flipper_length_mm  bill_length_mm  
##      -5736.897         48.145           6.047
```

Regressions

Real example

```
lm(body_mass_g ~ flipper_length_mm + bill_length_mm, data = penguins)
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##  
## Coefficients:  
##      (Intercept)  flipper_length_mm  bill_length_mm  
##      -5736.897         48.145         6.047
```

Hmm, not a lot of detail...
Only **Intercept** and Slopes
(**flipper_length_mm** and **bill_length_mm**)

Regressions

Assign model to `m` (or any other name you want to give it)

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

`m` is a model object

```
class(m)
```

```
## [1] "lm"
```

This contains all the information about the model

Regressions

Use `summary()` to show summary table:

```
summary(m)
```

```
##  
## Call:  
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,  
##      data = penguins)  
##
```

Your turn!

Create a model with your response variable by two of your *continuous* predictors.

Look at the output of `summary()`

```
## flipper_length_mm 187.10 210.11 215.95 178.15 ***  
## bill_length_mm 6.047 5.180 1.168 0.244 ***  
## ---  
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 394.1 on 339 degrees of freedom  
## (2 observations deleted due to missingness)  
## Multiple R-squared: 0.76, Adjusted R-squared: 0.7585  
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Regressions

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Create a model with your response variable by two of your *continuous* predictors.

Look at the output of `summary()`

```
## flipper_length_mm 187.10 210.11 239.35 420.10 ***  
## bill_length_mm 6.047 5.180 1.168 0.244 ***  
## ---  
## 1. ' 0.1 ' ' 1  
##  
## Freedom  
##  
## 0.7585  
## F-statistic: 536.6 on 2 and 339 DF, p-value: < 2.2e-16
```

Wait!

Shouldn't interpret until we know the model is solid

Model Diagnostics

Model Assumptions

- Normality (of residuals)
- Constant Variance (no heteroscedasticity)

Other cautions

- Influential observations (Cook's D)
- Multiple collinearity (with more than one **x** or explanatory variables)

Model Diagnostics

First let's get our relevant variables into a diagnostic data frame:

- **residuals** (regular and standardized)
- **fitted values**
- **cooks distance**
- **obs number**

```
d <- data.frame(residuals = residuals(m),  
                std_residuals = rstudent(m),  
                fitted = fitted(m),  
                cooks = cooks.distance(m))  
  
d <- mutate(d, obs = 1:n())
```

Model Diagnostics

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                fitted = fitted(m),  
                cooks = cooks.distance(m))  
  
d <- mutate(d, obs = 1:n())
```

```
head(d)
```

##	residuals	std_residuals	fitted	cooks	obs
## 1	536.220898	1.368529806	3213.779	5.539153e-03	1
## 2	343.077607	0.873050231	3456.922	1.609402e-03	2
## 3	-645.064115	-1.644516798	3895.064	3.797384e-03	3
## 5	-327.003441	-0.833002736	3777.003	1.992863e-03	4
## 6	1.707668	0.004338503	3648.292	3.338060e-08	5
## 7	412.430396	1.051400111	3212.570	3.272886e-03	6

Side Note: **tidyverse** functions

- From **dplyr** package (part of **tidyverse**)

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

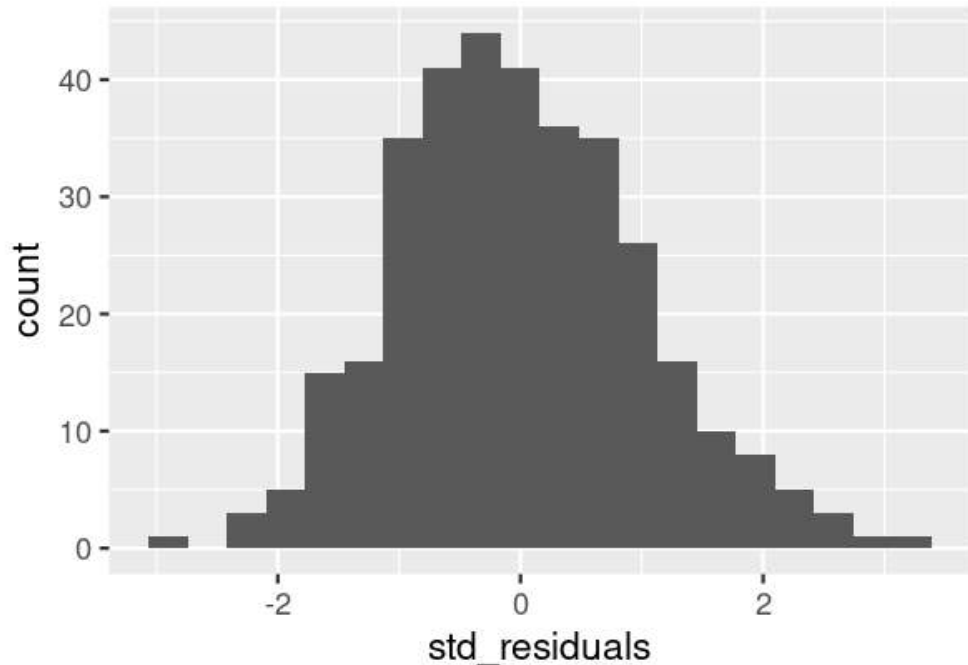
mutate()

- **tidyverse** functions always start with the **data**, followed by **other arguments**
- **mutate()** adds **new columns** to your data
- Also note: **1:5** is the same as **c(1,2,3,4,5)**

Normality

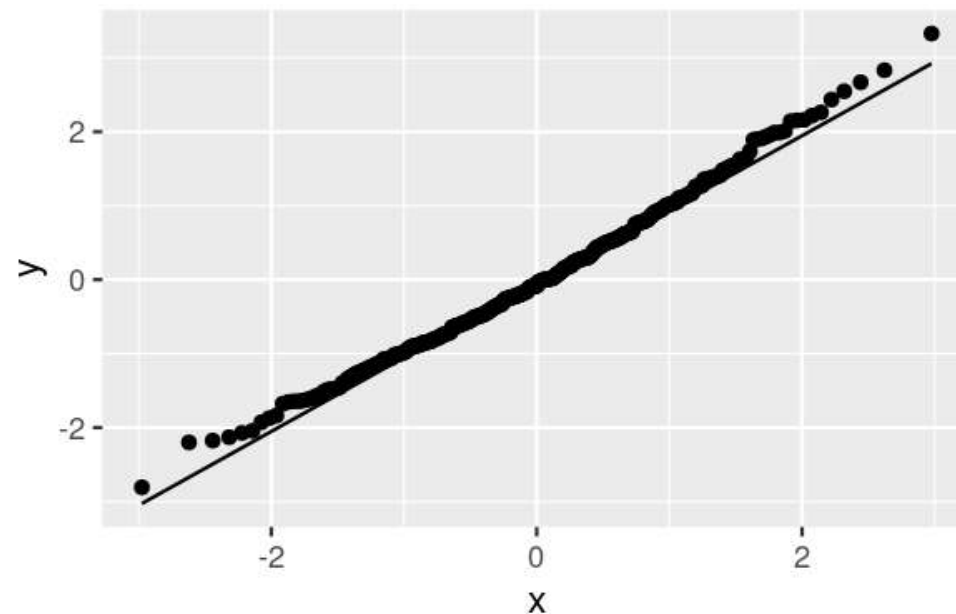
Histogram of residuals

```
ggplot(data = d, aes(x = std_residuals)) +  
  geom_histogram(bins = 20)
```



QQ Normality plot of residuals

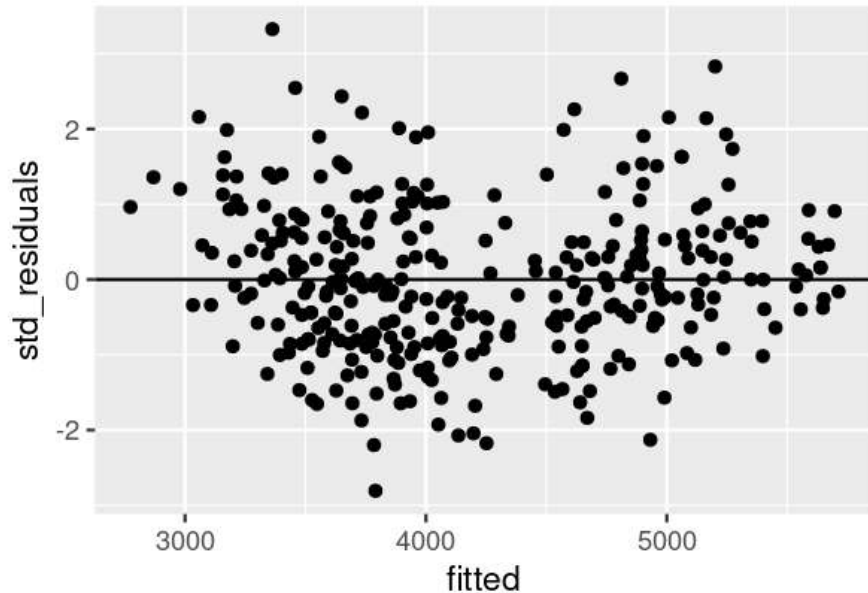
```
ggplot(data = d, aes(sample = std_residuals)) +  
  stat_qq() +  
  stat_qq_line()
```



Variance and Influence

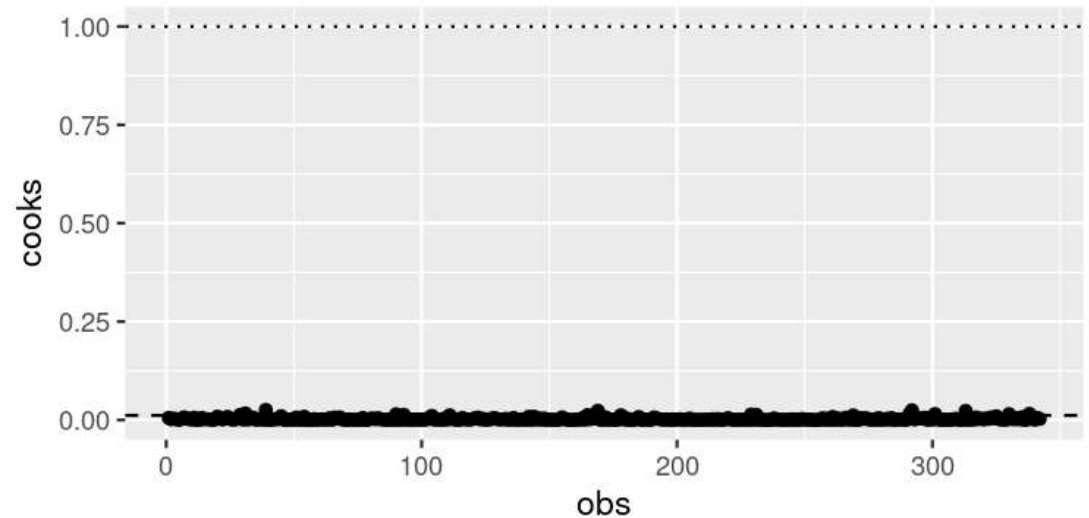
Check heteroscedasticity

```
ggplot(d, aes(x = fitted, y = std_residuals)) +  
  geom_point() +  
  geom_hline(yintercept = 0)
```



Cook's D

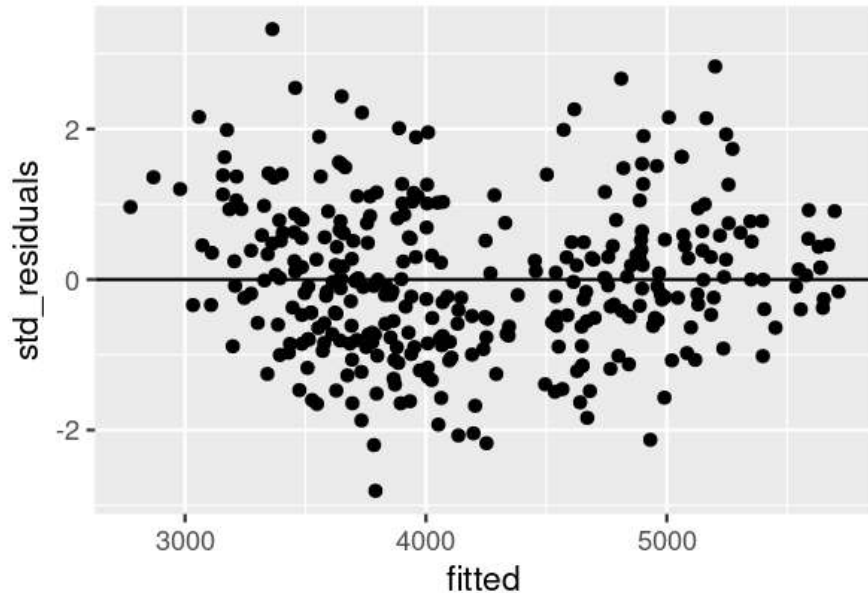
```
ggplot(d, aes(x = obs, y = cooks)) +  
  geom_point() +  
  geom_hline(yintercept = 1, linetype = "dotted") +  
  geom_hline(yintercept = 4/nrow(penguins),  
             linetype = "dashed")
```



Variance and Influence

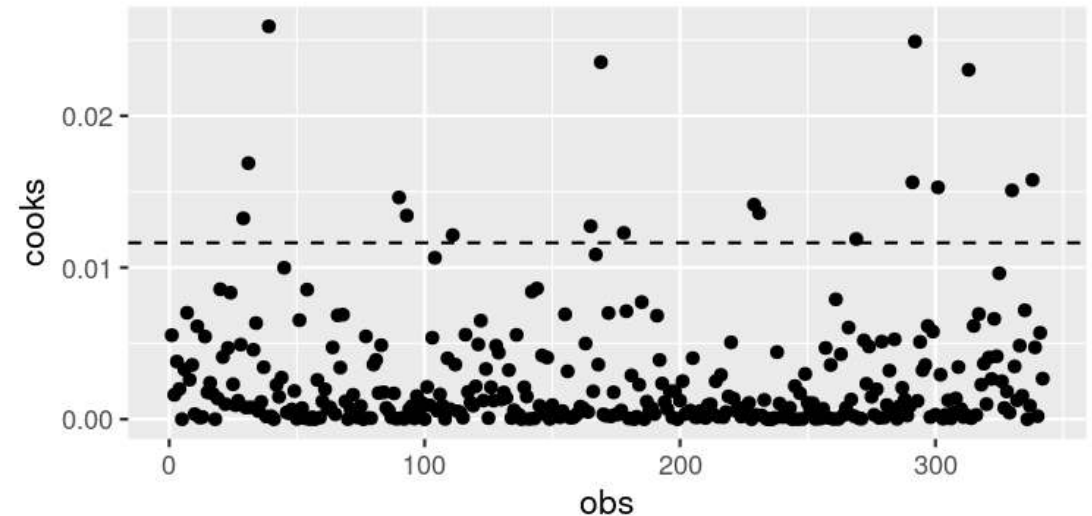
Check heteroscedasticity

```
ggplot(d, aes(x = fitted, y = std_residuals)) +  
  geom_point() +  
  geom_hline(yintercept = 0)
```



Cook's D

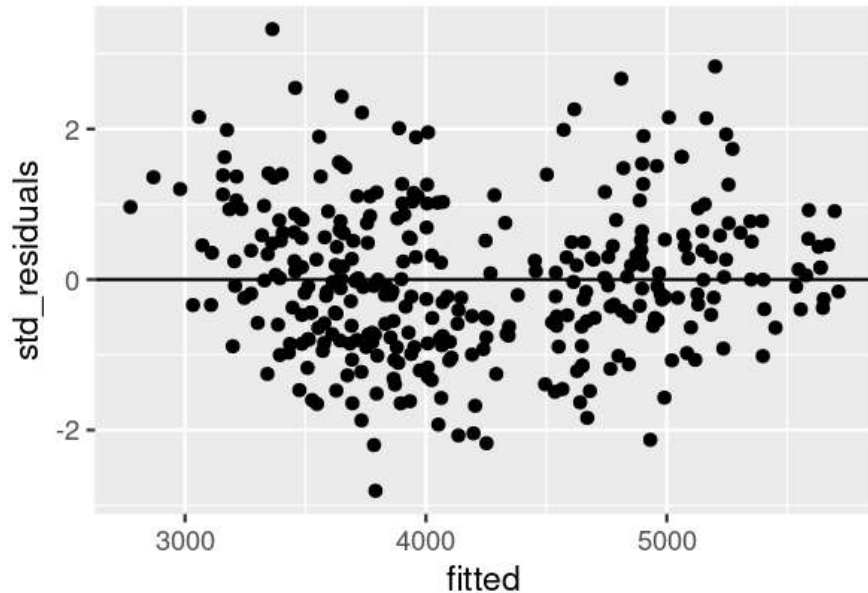
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```



Variance and Influence

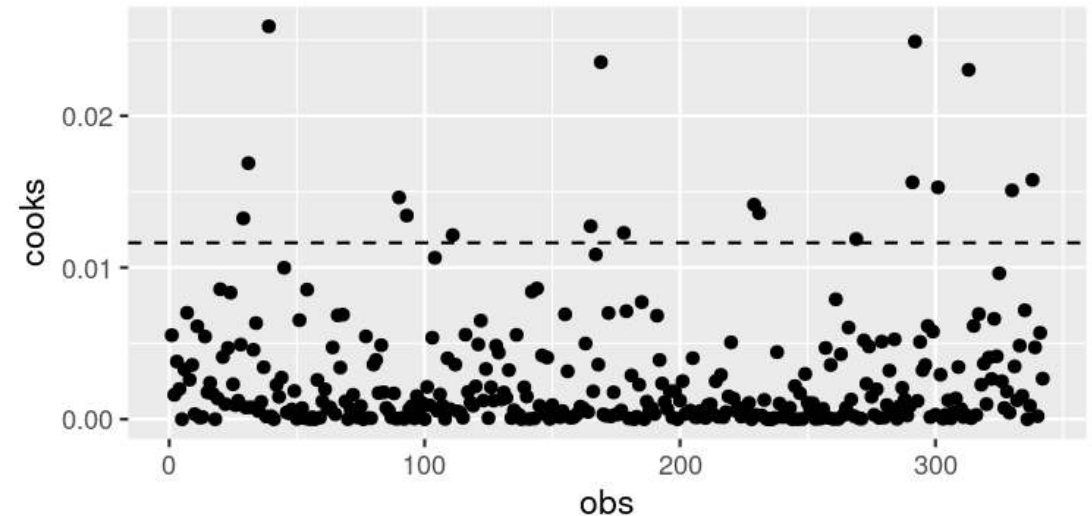
Check heteroscedasticity

```
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```



Cook's D

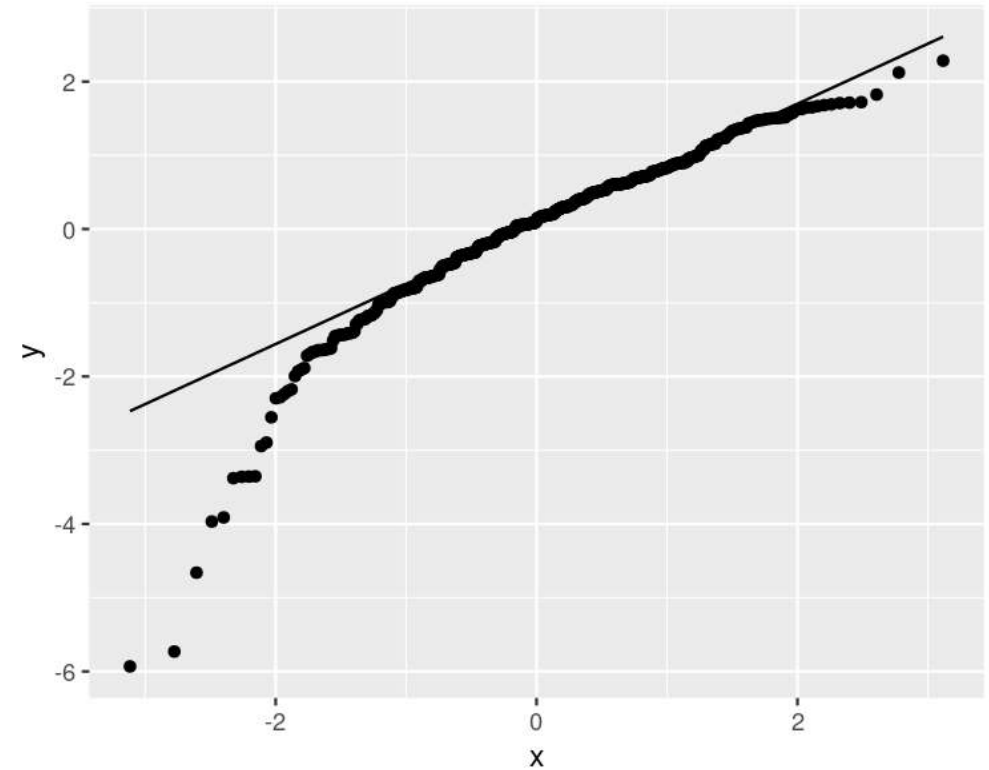
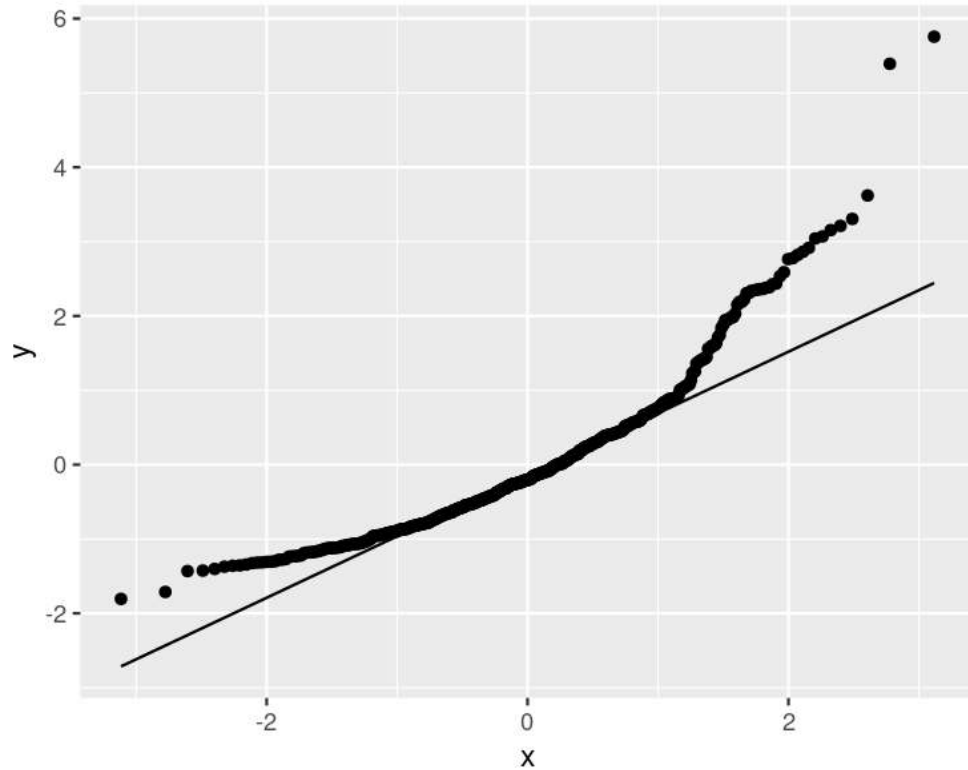
```
ggplot(d, aes(x = obs, y = cooks)) +  
  geom_point() +  
  geom_hline(yintercept = 4/nrow(penguins),  
             linetype = "dashed")
```



Pretty good!

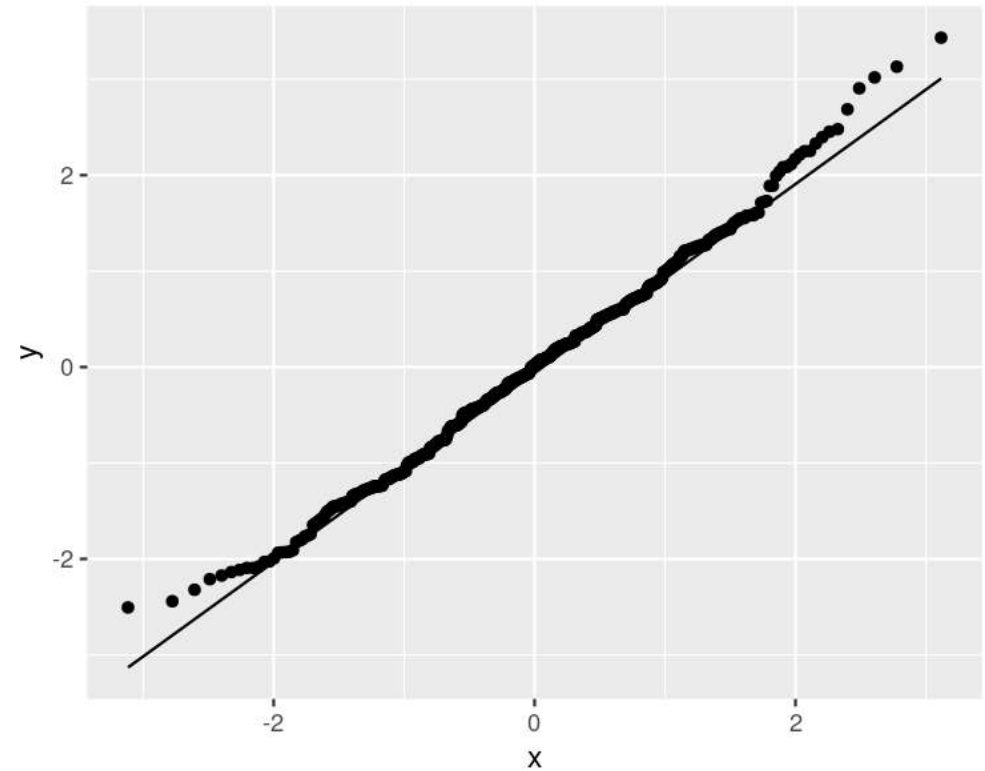
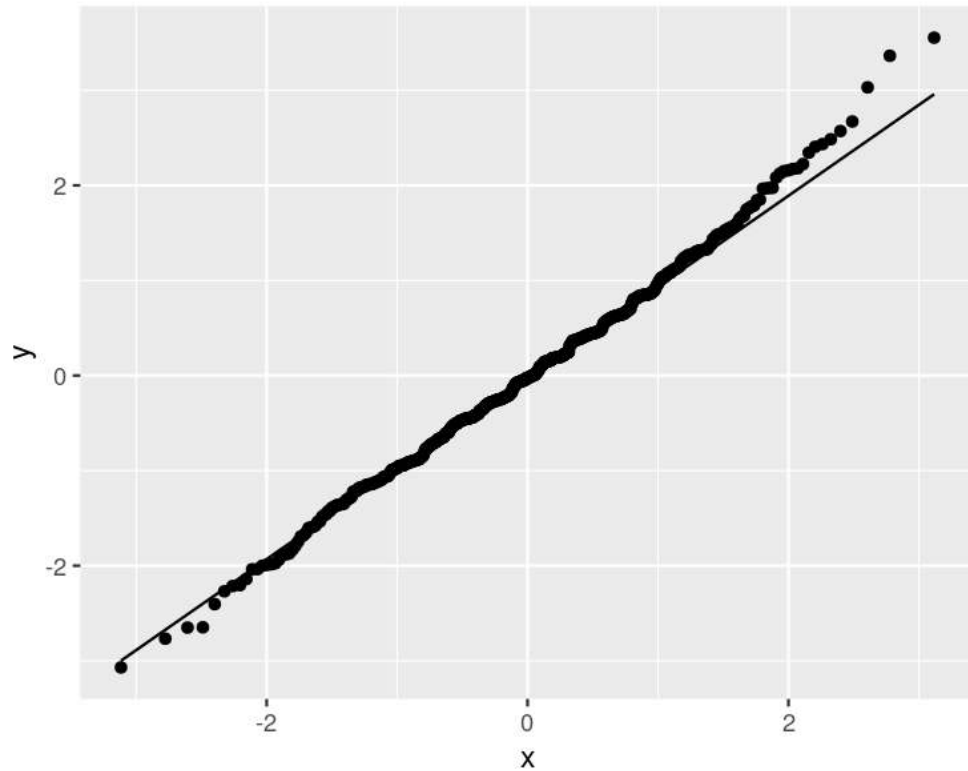
What is a 'Good' Normality Plot?

Problematic



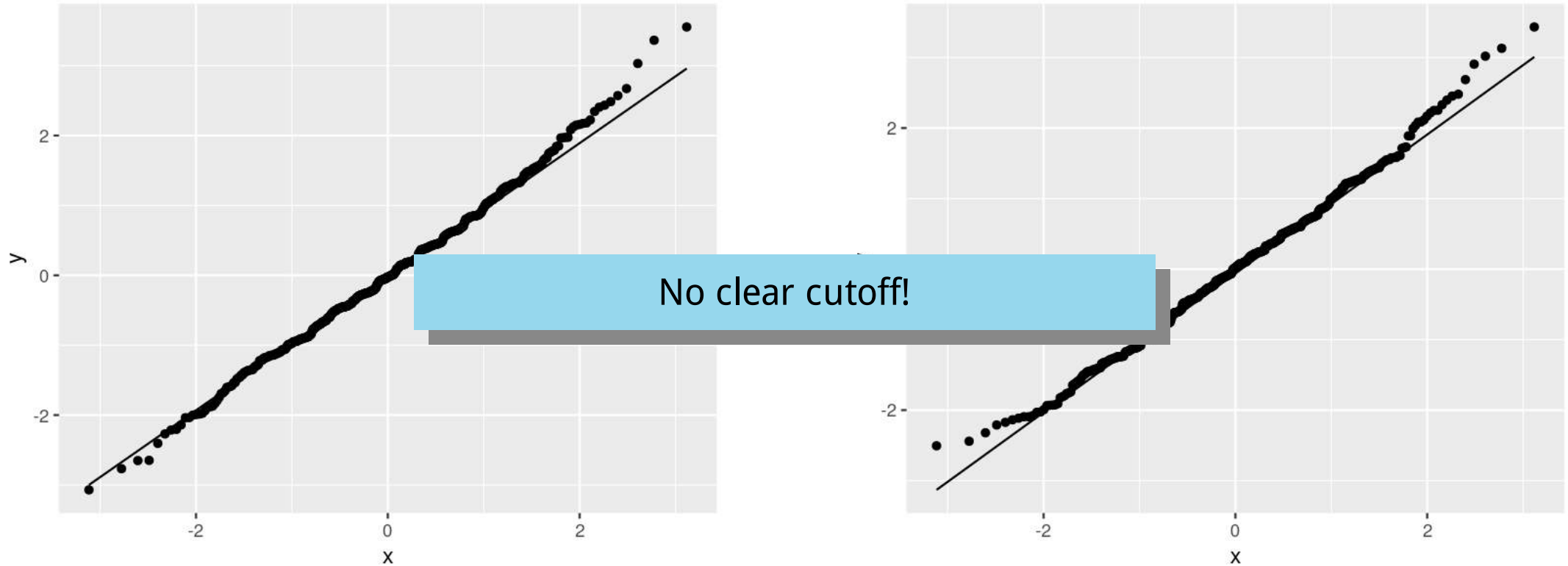
What is a 'Good' Normality Plot?

Good



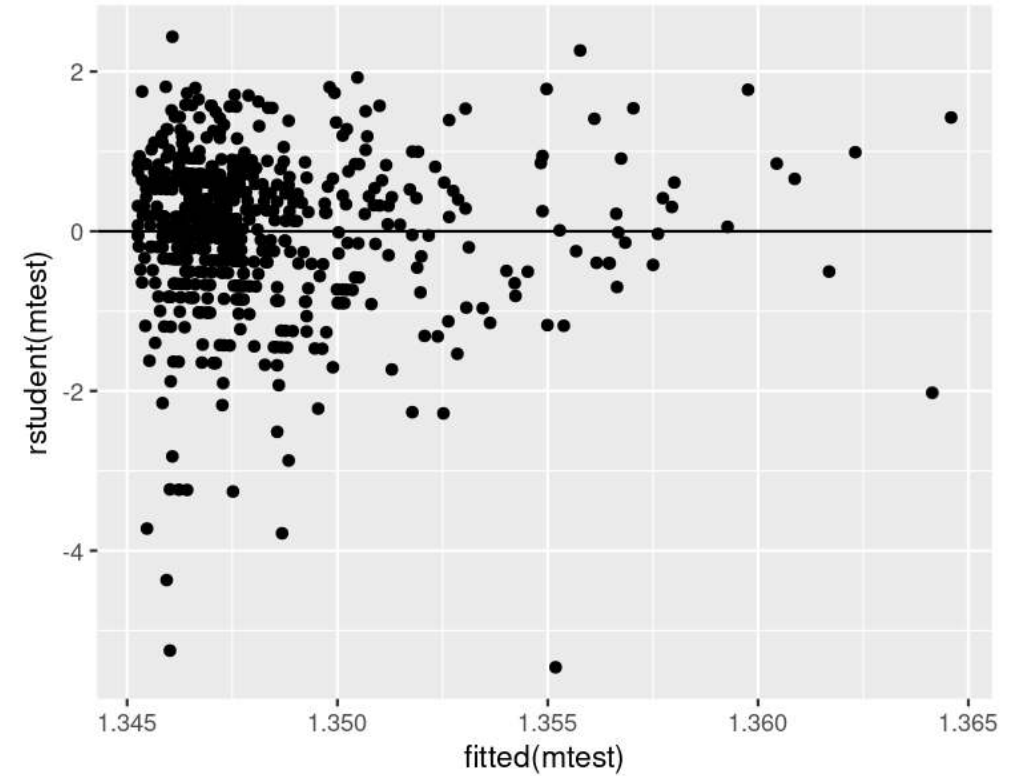
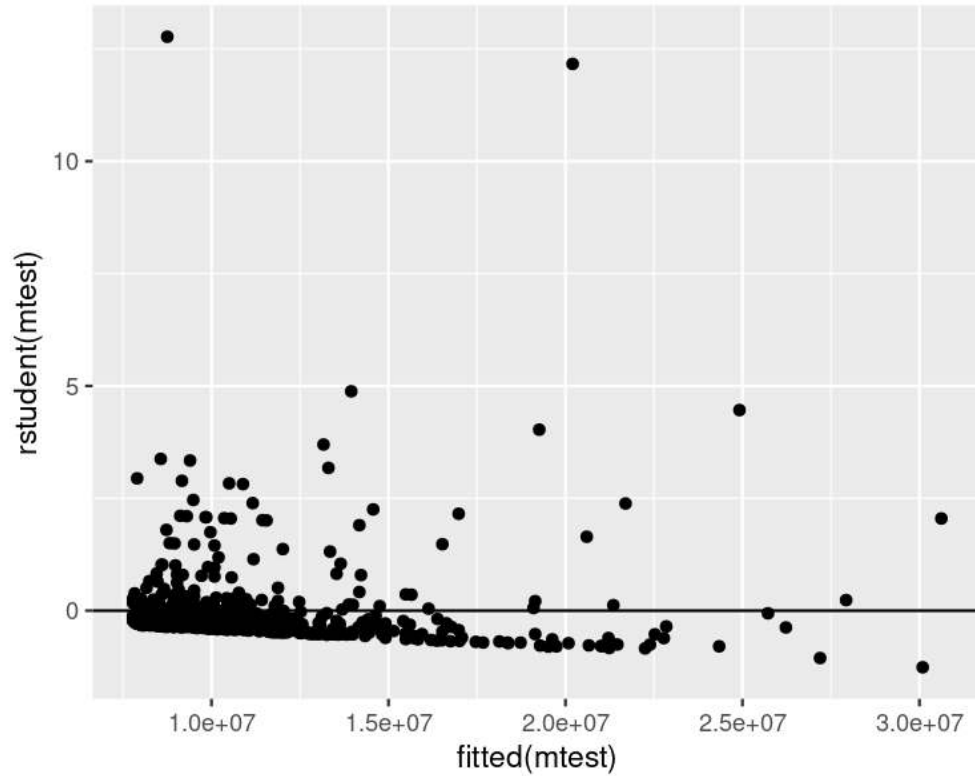
What is a 'Good' Normality Plot?

Good



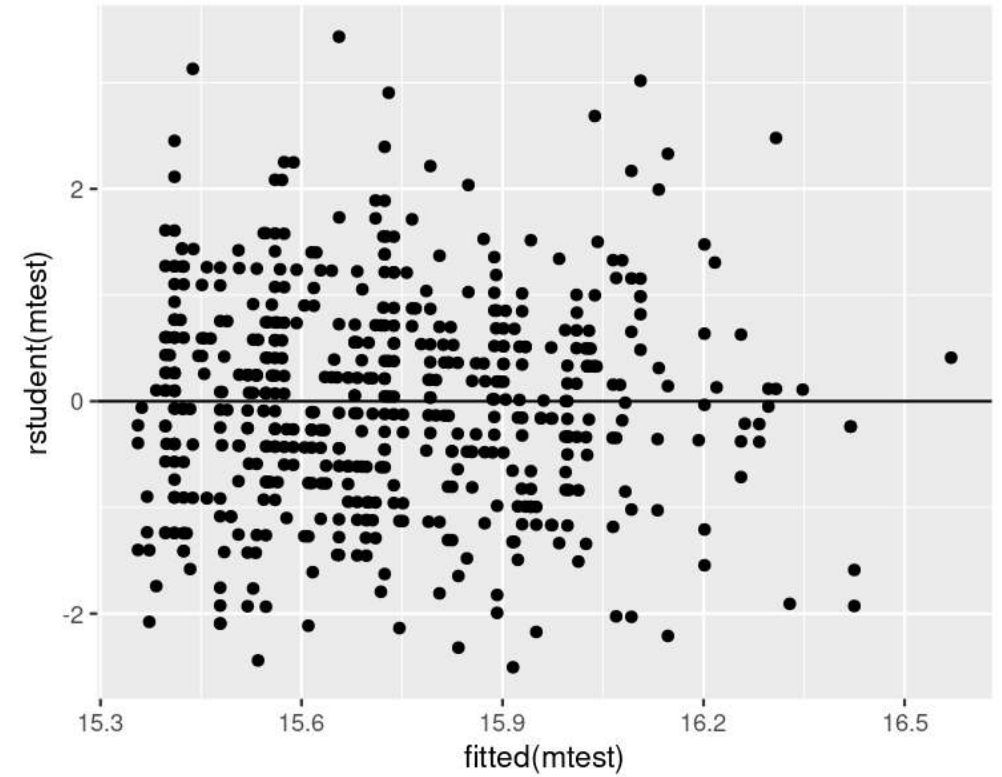
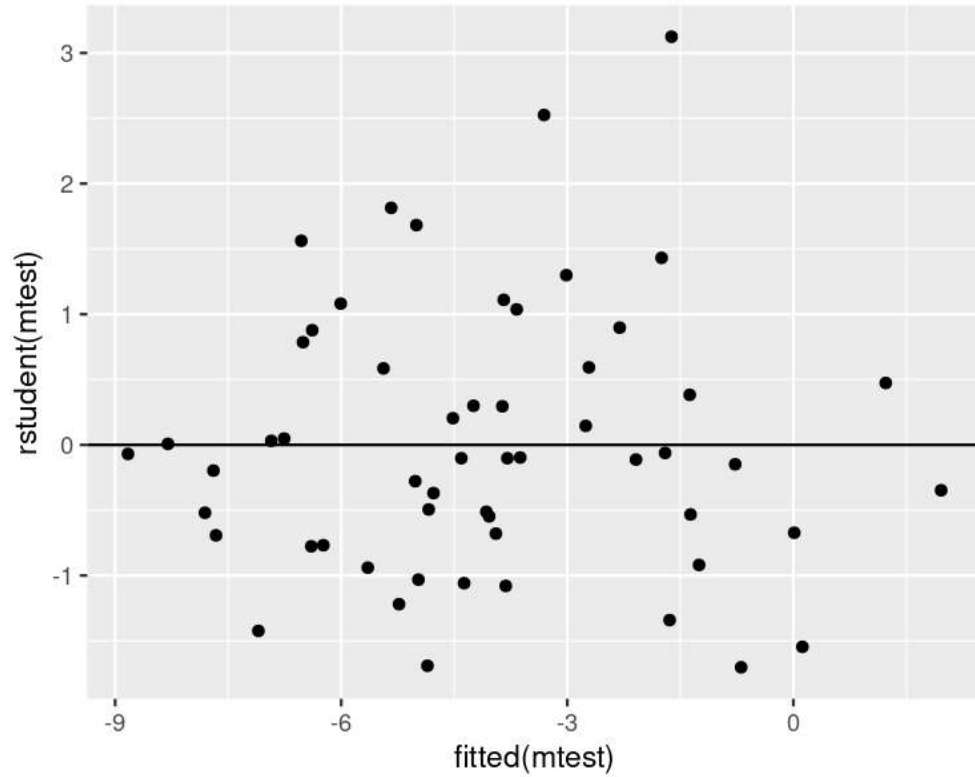
What is a 'Good' Heteroscedasticity Plot?

Problematic



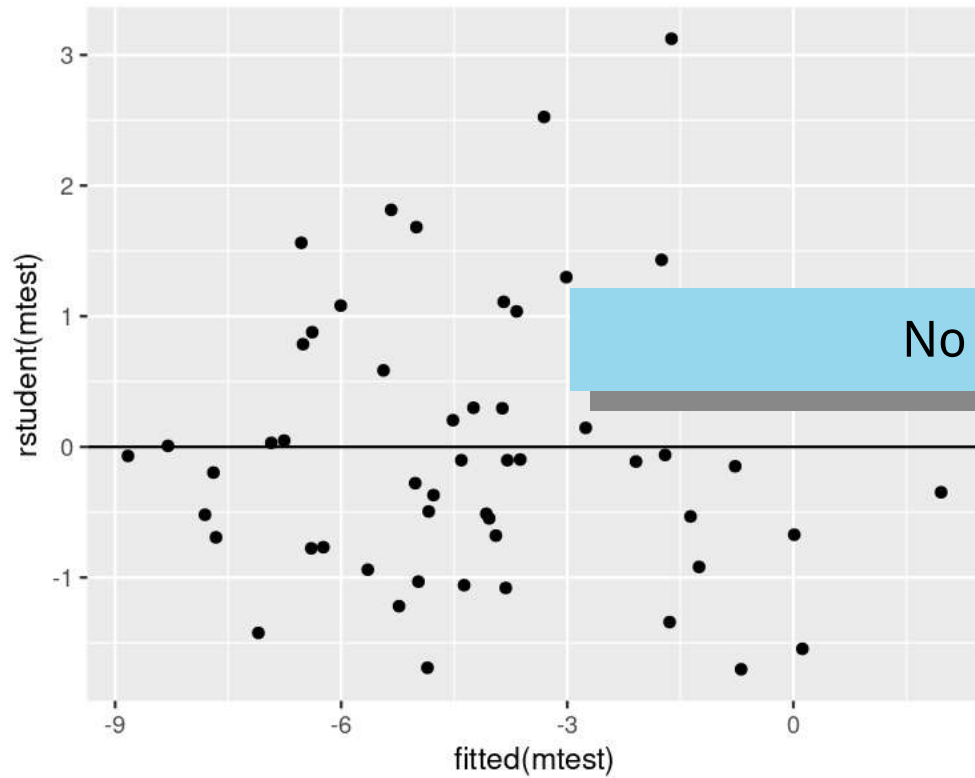
What is a 'Good' Heteroscedasticity Plot?

Good

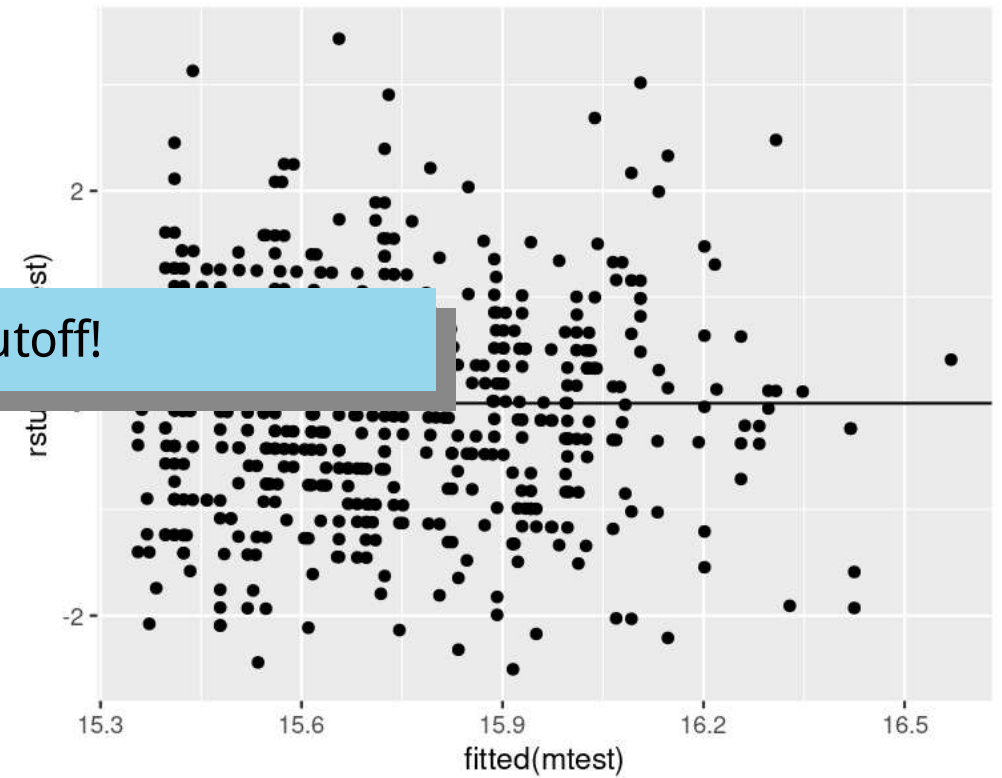


What is a 'Good' Heteroscedasticity Plot?

Good



No clear cutoff!



Multicollinearity (collinearity)

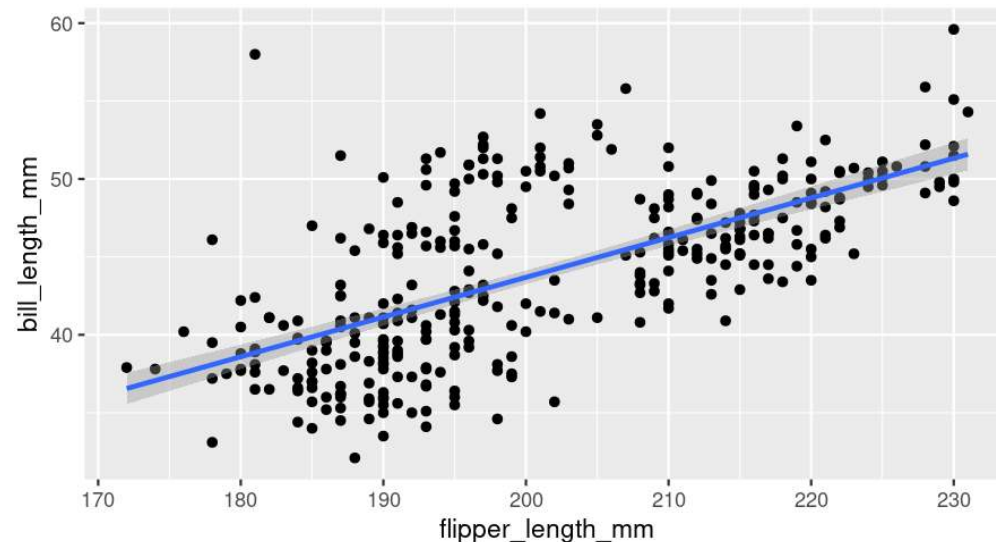
- Only relevant with **more than one explanatory variable**
- If explanatory variables too correlated, can interfere with model interpretation

Multicollinearity (collinearity)

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- If explanatory variables too correlated, can interfere with model interpretation

Look at our two explanatory variables

```
ggplot(data = penguins, aes(x = flipper_length_mm, y = bill_length_mm)) +  
  geom_point() +  
  stat_smooth(method = "lm")
```

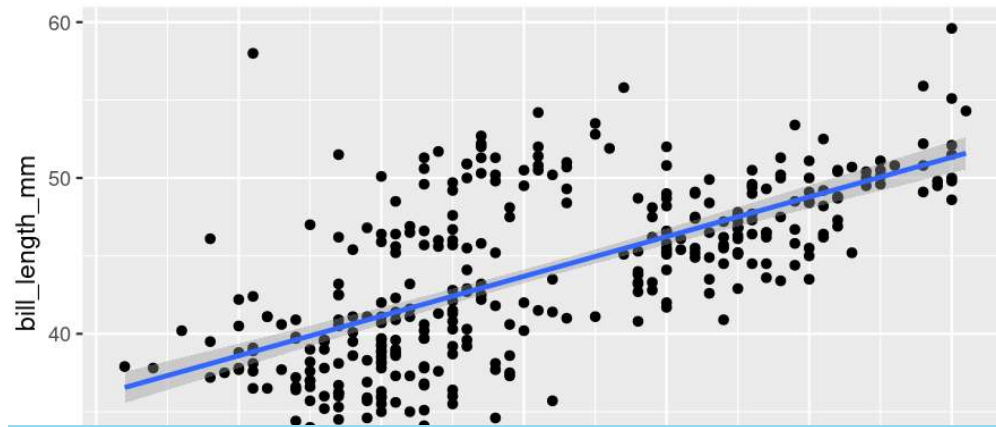


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```



Correlated, but not necessarily a problem

Multicollinearity (collinearity)

- Only relevant with **more than one explanatory variable**
- If explanatory variables too correlated, can interfere with model interpretation
- Correlations between variables *might* be problematic (but not necessarily)

Use **vif()** function from **car** package (vif = variance inflation factor*)

```
library(car)
vif(m)
```

```
## flipper_length_mm    bill_length_mm
##           1.756154           1.756154
```

Hmm, that's pretty good (looking for < 10)

* Can be interpreted as how much influence the variable has on the model

Interpreting Regressions

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

```
summary(m)
```

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,
##     data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1090.5   -285.7    -32.1    244.2   1287.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5736.897    307.959  -18.629  <2e-16 ***
## flipper_length_mm    48.145      2.011   23.939  <2e-16 ***
## bill_length_mm     6.047      5.180    1.168    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 394.1 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.76,    Adjusted R-squared:  0.7585
## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
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Interpreting Regressions

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Model

```
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Interpreting Regressions

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```

```
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```

Effects

```
##
## Call:
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Interpreting Regressions

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```

```
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```

Missing observations

```
##
## Call:
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Interpreting Regressions

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```

```
summary(m)
```

R^2 and adjusted R^2

- Adjusted for the number of parameters

```
##
## Call:
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## Residuals:
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Interpreting Regressions

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```

```
summary(m)
```

Specific Details

- **Estimate**
 - Slope of the effect
- **Std. Error**
 - Variability in the estimates
- **t value**
 - Test statistic
 - Think of it as a holistic combination of estimate and variability
- **Pr(>|t|)**
 - **P-value**, significance of the results
 - Probability of getting **t-value** by chance

```
##
## Call:
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##     data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1090.5   -285.7    -32.1    244.2   1287.5
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Interpreting Regressions

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```

```
summary(m)
```

Specific Details

Intercept

- Significant ($P < 2e^{-16}$ *)
- Penguins with a flipper length of 0 mm are predicted to have a body mass of -5736.9g
 - Not useful!

* $2e^{-16} = 0.0000000000000002$, R uses this as the smallest number

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,
##     data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1090.5   -285.7    -32.1    244.2   1287.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5736.897     307.959  -18.629  <2e-16 ***
## flipper_length_mm    48.145       2.011   23.939  <2e-16 ***
## bill_length_mm     6.047       5.180    1.168    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 394.1 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.76,    Adjusted R-squared:  0.7585
## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

Interpreting Regressions

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

```
summary(m)
```

Specific Details

Effect of Flipper Length

- Significant ($P < 2e^{-16}$ *)
- For each 1 mm increase in flipper length, body mass is predicted to increase by 48.14g

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,
##     data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1090.5   -285.7    -32.1    244.2   1287.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5736.897    307.959  -18.629  <2e-16 ***
## flipper_length_mm    48.145      2.011   23.939  <2e-16 ***
## bill_length_mm     6.047      5.180    1.168    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
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## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

* $2e^{-16} = 0.00000000000000002$, R uses this as the smallest number

Interpreting Regressions

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

```
summary(m)
```

Specific Details

Effect of Flipper Length

- Significant ($P < 2e^{-16}$ *)
- For each 1 mm increase in flipper length, body mass is predicted to increase by 48.14g

Effect of Bill Length

- Non-significant ($P = 0.244$, i.e. $P < 0.05$)
- Therefore no effect (in this model) (and no interpretation of estimate)

* $2e^{-16} = 0.0000000000000002$, R uses this as the smallest number

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,
##     data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1090.5   -285.7    -32.1    244.2   1287.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5736.897     307.959  -18.629  <2e-16 ***
## flipper_length_mm    48.145       2.011   23.939  <2e-16 ***
## bill_length_mm     6.047       5.180    1.168    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 394.1 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.76,    Adjusted R-squared:  0.7585
## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
```


Interpreting Regressions

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

```
summary(m)
```

Therefore

There is a significant relationship between flipper length and body mass
But not between bill length and body mass (when including flipper length)

Specific Details

Effect of Flipper Length

- Significant ($P < 2e^{-16}$ *)
- For each 1 mm increase in flipper length, body mass is predicted to increase by 48.14g

Effect of Bill Length

- Non-significant ($P = 0.244$, i.e. $P < 0.05$)
- Therefore no effect (in this model) (and no interpretation of estimate)

* $2e^{-16} = 0.00000000000000002$, R uses this as the smallest number

```
## data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1090.5   -285.7    -32.1    244.2   1287.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5736.897    307.959  -18.629  <2e-16 ***
## flipper_length_mm    48.145      2.011   23.939  <2e-16 ***
## bill_length_mm     6.047      5.180    1.168    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 394.1 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.76,    Adjusted R-squared:  0.7585
## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

Interpreting Regressions

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

```
summary(m)
```

Specific Details

Effect of Flipper Length

- Significant ($P < 2e^{-16}$ *)
- For each 1 mm increase in flipper length, body mass is predicted to increase by 48.14g

Effect of Bill Length

- Non-significant ($P = 0.244$, i.e. $P < 0.05$)
- Therefore no effect (and no interpretation of estimate)

* $2e^{-16} = 0.0000000000000002$, R uses this as the smallest number

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,
##     data = penguins)
##
## Residuals:
##      Min       1Q   median       3Q      Max
## -1090.5   -285.7    -32.1     244.2    1287.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5736.897     307.959  -18.629  <2e-16 ***
## flipper_length_mm    48.145       2.011   23.939  <2e-16 ***
## bill_length_mm     6.047       5.180    1.168    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 394.1 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.76,    Adjusted R-squared:  0.7585
## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

$$y = mx + b$$

Interpreting Regressions

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

```
summary(m)
```

Specific Details

Effect of Flipper Length

- Significant ($P < 2e^{-16}$ *)
- For each 1 mm increase in flipper length, body mass is predicted to increase by 48.14g

Effect of Bill Length

- Non-significant ($P = 0.244$, i.e. $P < 0.05$)
- Therefore no effect (and no interpretation of estimate)

* $2e^{-16} = 0.0000000000000002$, R uses this as the smallest number

```
##  
## Call:  
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,  
##     data = penguins)  
##  
## Residuals:  
##      Min       1st Qu       Med       3rd Qu      Max  
## -1090.5   -285.7    -32.1     244.2    1287.5  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)  
## (Intercept)   -5736.897    307.959  -18.629  <2e-16 ***  
## flipper_length_mm    48.145      2.011   23.939  <2e-16 ***  
## bill_length_mm      6.047      5.180    1.168    0.244  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 394.1 on 339 degrees of freedom  
## (2 observations deleted due to missingness)  
## Multiple R-squared:  0.76,    Adjusted R-squared:  0.7585  
## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

$$y = m_1x_1 + m_2x_2 + b$$

Interpreting Regressions

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

```
summary(m)
```

Specific Details

Effect of Flipper Length

- Significant ($P < 2e^{-16}$ *)
- For each 1 mm increase in flipper length, body mass is predicted to increase by 48.14g

Effect of Bill Length

- Non-significant ($P = 0.244$, i.e. $P < 0.05$)
- Therefore no effect (and no interpretation of estimate)

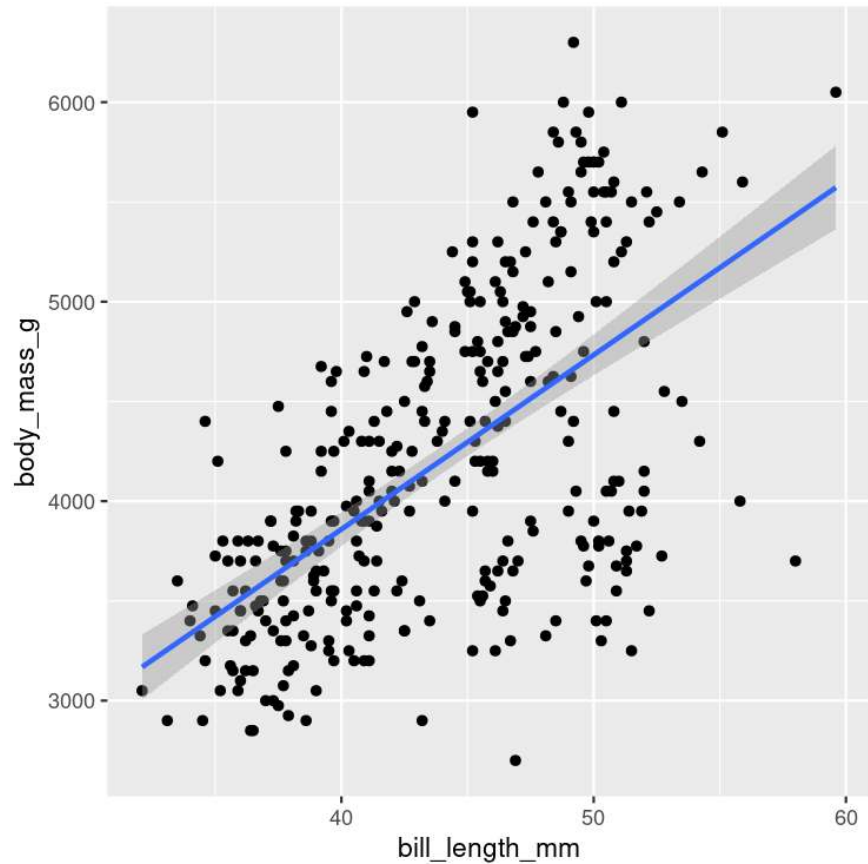
* $2e^{-16} = 0.0000000000000002$, R uses this as the smallest number

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm,
##     data = penguins)
##
## Residuals:
##      Min       1st Qu       Med       3rd Qu      Max
## -1090.5   -285.7    -32.1     244.2    1287.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5736.897    307.959  -18.629  <2e-16 ***
## flipper_length_mm    48.145      2.011   23.939  <2e-16 ***
## bill_length_mm     6.047      5.180    1.168    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 394.1 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.76,    Adjusted R-squared:  0.7585
## F-statistic: 536.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

$$y = 48.14x_1 + 6.05x_2 + (-5736.9)$$

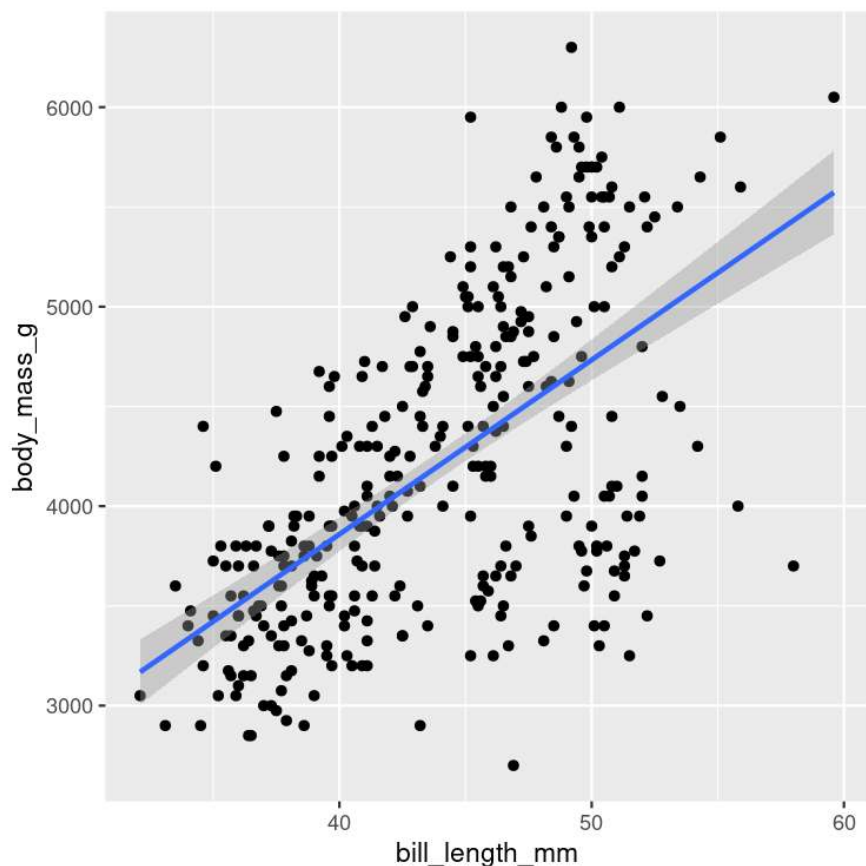
Extra

Why no effect of Bill Length?



Extra

Why no effect of Bill Length?



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

```
##
## Call:
## lm(formula = body_mass_g ~ bill_length_mm, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1762.08  -446.98    32.59   462.31  1636.86
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    362.307    283.345   1.279   0.202
## bill_length_mm    87.415     6.402  13.654 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 645.4 on 340 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.3542,    Adjusted R-squared:  0.3523
## F-statistic: 186.4 on 1 and 340 DF,  p-value: < 2.2e-16
```

Extra

Why no effect of Bill Length?

- Hypothesis of *causation* but really just correlation
- Flipper length is the 'better' predictor of body mass
- When flipper length in the model, no extra variation explained by bill length
- When flipper length *not* in the model, some variation left to be explained

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

```
##
## Call:
## lm(formula = body_mass_g ~ bill_length_mm, data = penguins)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
##	-1762.08	-446.98	32.59	462.31	1636.86

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
## (Intercept)	362.307	283.345	1.279	0.202
## bill_length_mm	87.415	6.402	13.654	<2e-16 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 645.4 on 340 degrees of freedom
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## Multiple R-squared:  0.3542,    Adjusted R-squared:  0.3523
## F-statistic: 186.4 on 1 and 340 DF,  p-value: < 2.2e-16
```

Homework (Practice)*

Consider **bill depth** your response and **bill length** your predictor

1. Plot the relationship
2. Create a linear regression model
3. Check your model diagnostics
 - Normality
 - Heteroscedasticity
 - Influential variables (i.e. Cook's distance)
4. Interpret the results of your model

ANOVAs

Linear Models

Running models in R

```
lm(y ~ x1 + x2, data = data)
```

- **y** is the **response** variable (**dependent**)
- **x** are the **explanatory** variables (**independent, predictor**)

Here we're assuming a **continuous y**

Linear Models

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lm(y ~ x1 + x2, data = data)
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- **y** is the **response** variable (**dependent**)
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Here we're assuming a **continuous y**

Different types of models

- If we only have one **x** which is continuous, this is a **simple linear regression**
- If both **x** are continuous, this is a **multiple linear regression**
- If both **x** are categorical, this is an **ANOVA**
- If **x1** is continuous and **x2** is categorical, this is an **ANCOVA**

Linear Models

Running models in R

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lm(y ~ x1 + x2, data = data)
```

- **y** is the **response** variable (**dependent**)
- **x** are the **explanatory** variables (**independent, predictor**)

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Different types of models

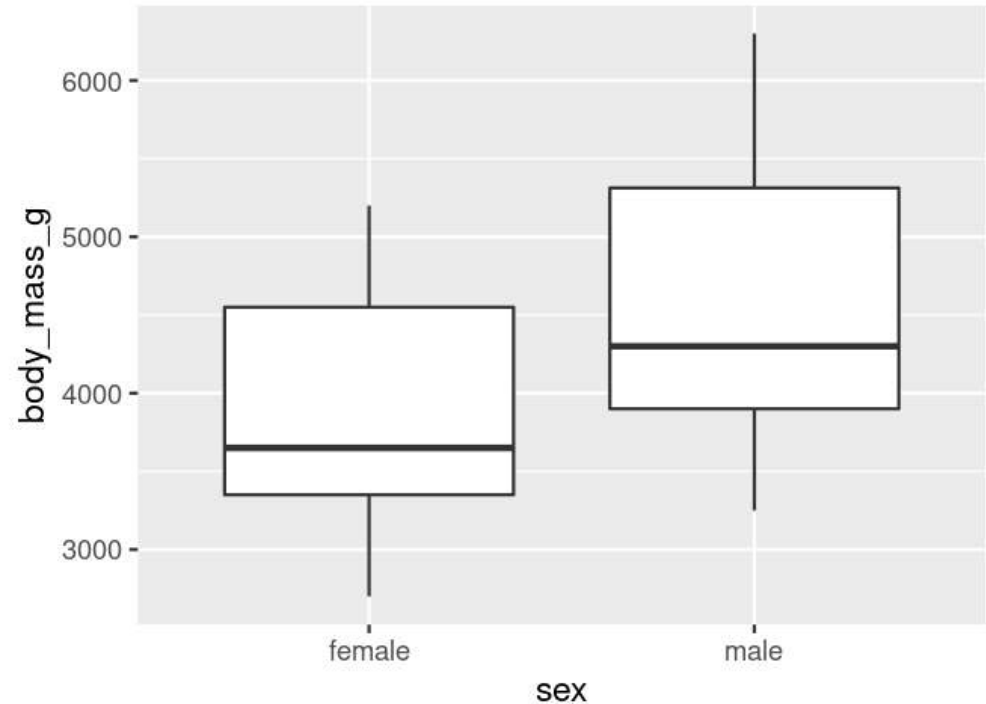
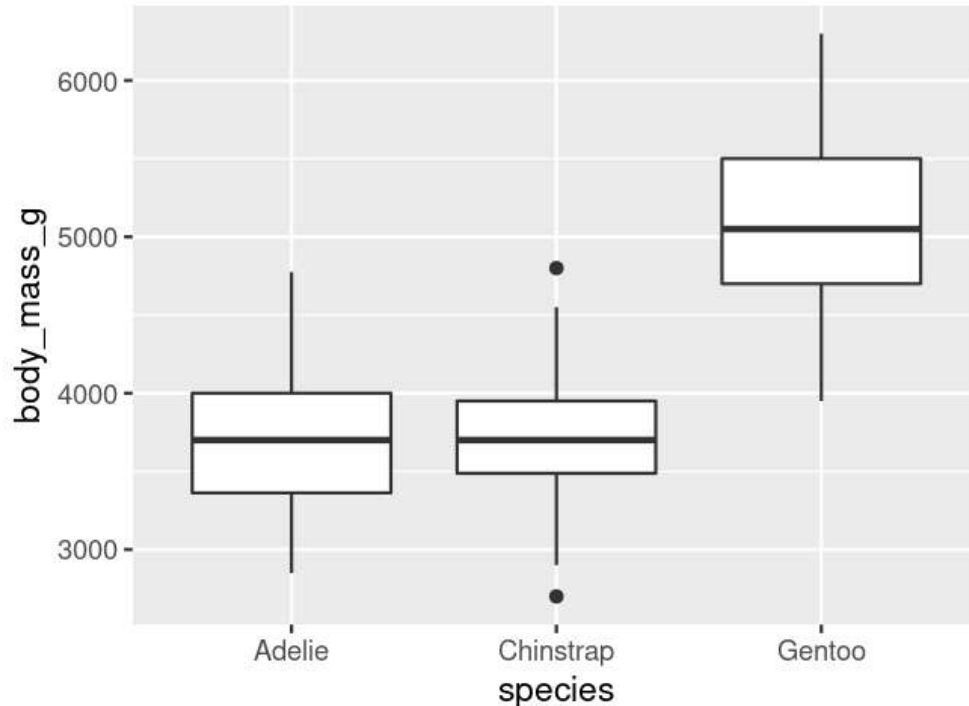
- If we only have one **x** which is continuous, this is a **simple linear regression**
- If both **x** are continuous, this is a **multiple linear regression**
- If both **x** are categorical, this is an **ANOVA**
- If **x1** is continuous and **x2** is categorical, this is an **ANCOVA**

R will figure it out for you

ANOVAs

Real example

- Are male penguins larger than female penguins?
- Are different species different sizes?
- Can body mass be predicted by species and sex?



ANOVAs

Real example

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

As we have two **categorical** predictors, this is an ANOVA

Your turn!

Create a model with your response variable by your *one categorical* predictor.

Look at the output of **summary()** and **anova()**

ANOVAs

Real example

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

As we have two **categorical** predictors, this is an ANOVA

Your turn!

Create a model with your response variable by your
one categorical predictor.

Look at the output of **summary()** and **anova()**

Wait!

Shouldn't interpret until we know the
model is solid

Model Diagnostics

Same as before! Let's get our relevant variables into a diagnostic data frame:

- **residuals** (regular and standardized)
- **fitted values**
- **cooks distance**
- **obs number**

```
d <- data.frame(residuals = residuals(m),  
                std_residuals = rstudent(m),  
                fitted = fitted(m),  
                cooks = cooks.distance(m))  
  
d <- mutate(d, obs = 1:n())
```


Model Diagnostics

Same as before! Let's get our relevant variables into a diagnostic data frame:

- **residuals** (regular and standardized)
- **fitted values**
- **cooks distance**
- **obs number**

```
d <- data.frame(residuals = residuals(m),  
                std_residuals = rstudent(m),  
                fitted = fitted(m),  
                cooks = cooks.distance(m))  
  
d <- mutate(d, obs = 1:n())
```

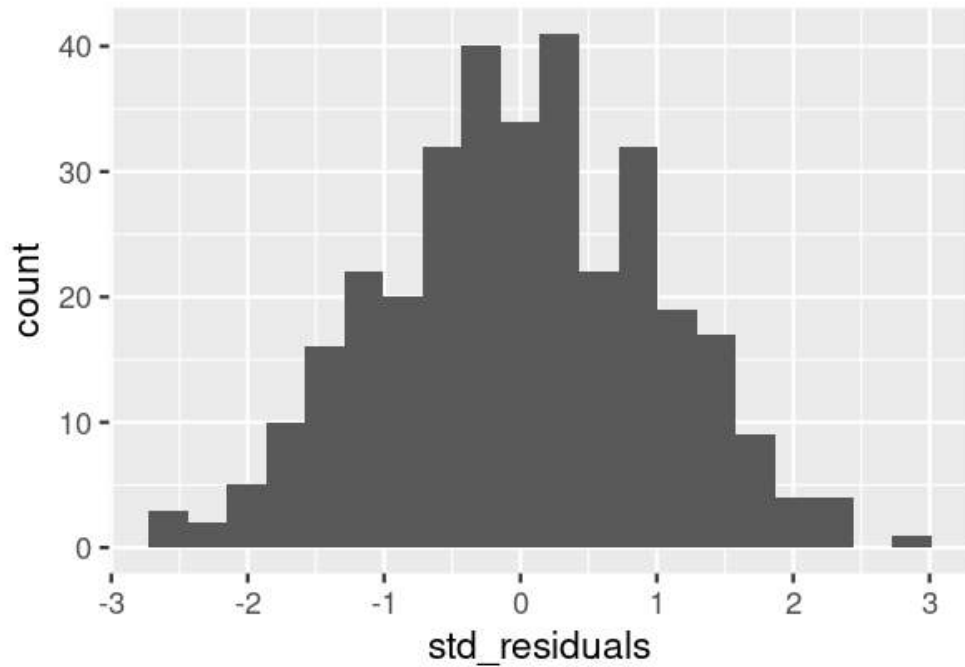
head(d)

##	residuals	std_residuals	fitted	cooks	obs
## 1	-289.94196	-0.9201062	4039.942	0.0021071103	1
## 2	427.61319	1.3590567	3372.387	0.0045831843	2
## 3	-122.38681	-0.3879729	3372.387	0.0003754346	3
## 5	77.61319	0.2460043	3372.387	0.0001509858	4
## 6	-389.94196	-1.2387413	4039.942	0.0038112292	5
## 7	252.61319	0.8013974	3372.387	0.0015994740	6

Normality

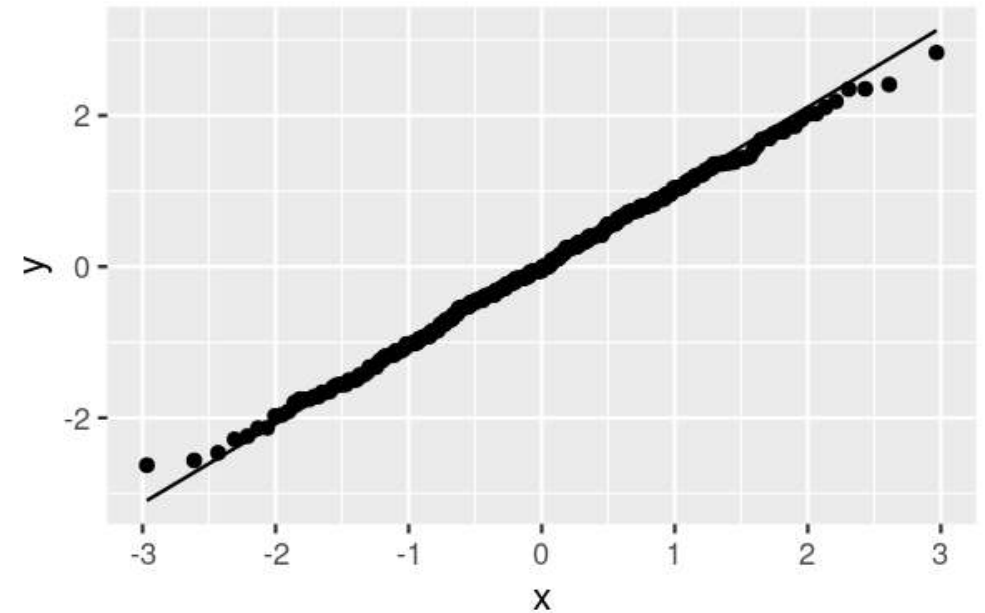
Histogram of residuals

```
ggplot(data = d, aes(x = std_residuals)) +  
  geom_histogram(bins = 20)
```



QQ Normality plot of residuals

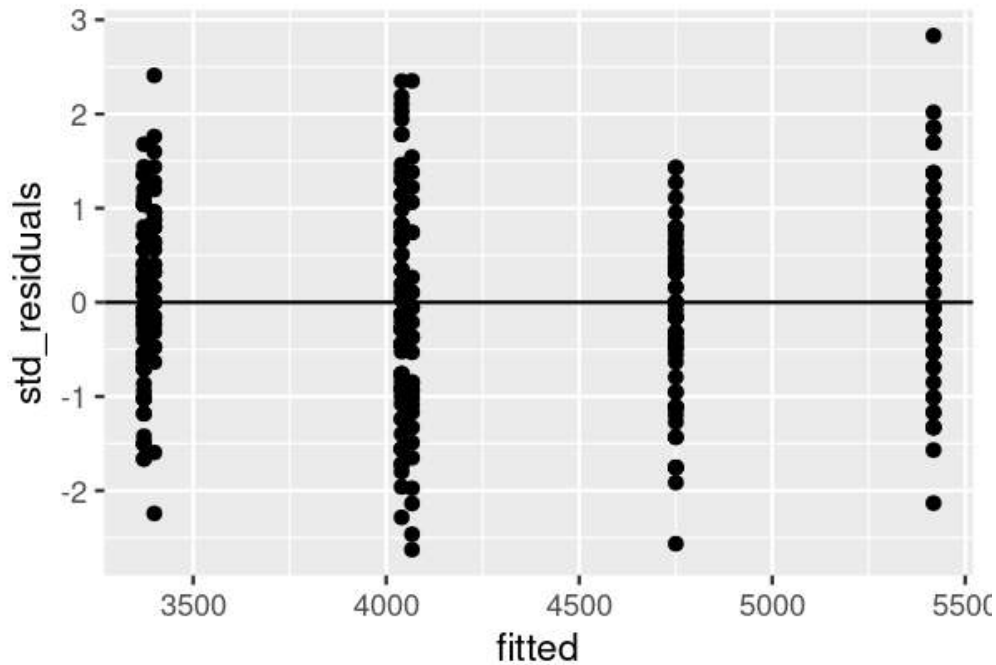
```
ggplot(data = d, aes(sample = std_residuals)) +  
  stat_qq() +  
  stat_qq_line()
```



Variance and Influence

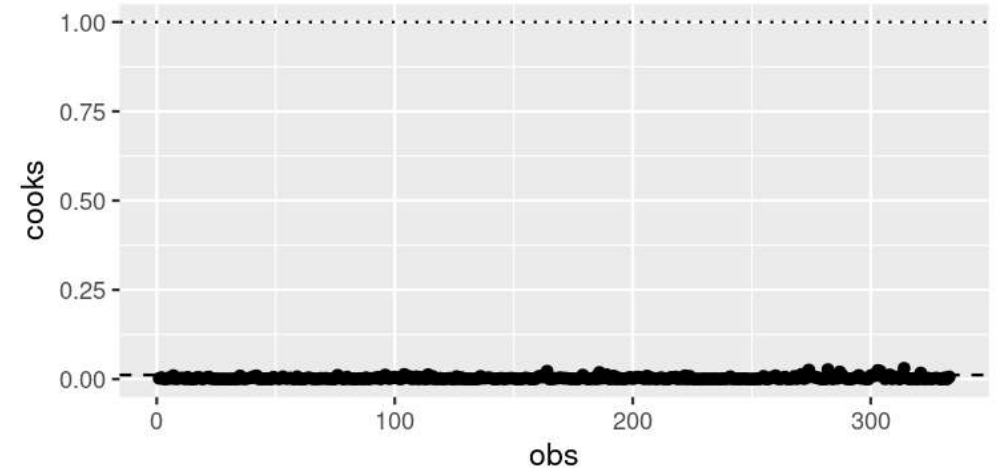
Check heteroscedasticity

```
ggplot(d, aes(x = fitted, y = std_residuals)) +  
  geom_point() +  
  geom_hline(yintercept = 0)
```



Cook's D

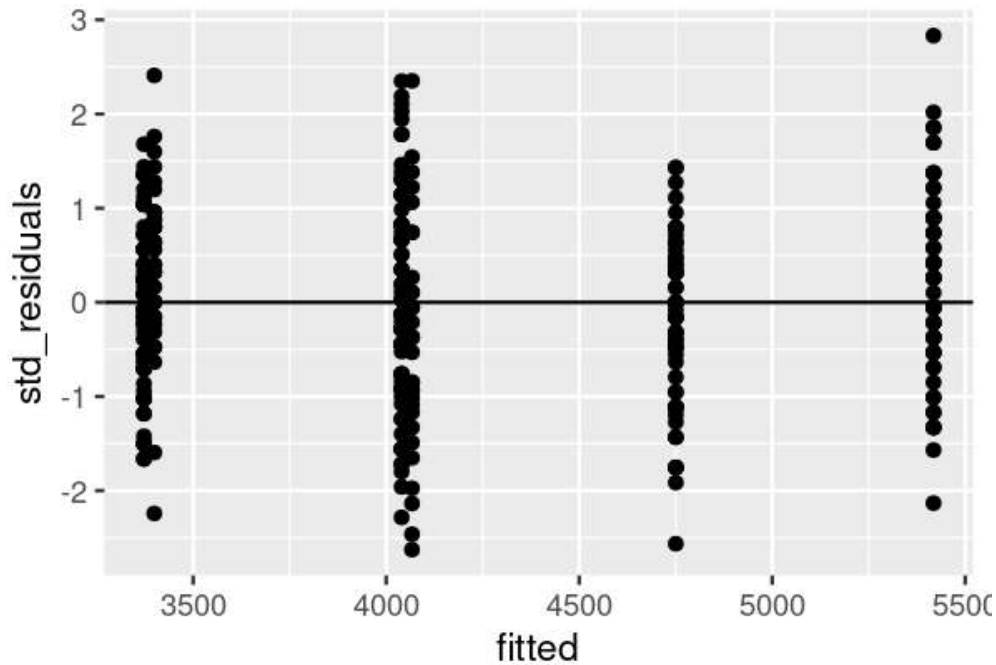
```
ggplot(d, aes(x = obs, y = cooks)) +  
  geom_point() +  
  geom_hline(yintercept = 1, linetype = "dotted") +  
  geom_hline(yintercept = 4/nrow(penguins),  
             linetype = "dashed")
```



Variance and Influence

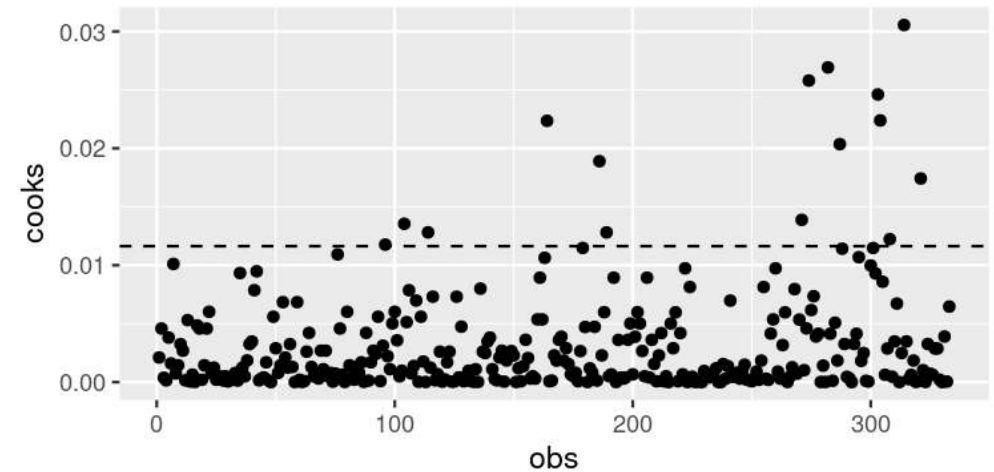
Check heteroscedasticity

```
ggplot(d, aes(x = fitted, y = std_residuals)) +  
  geom_point() +  
  geom_hline(yintercept = 0)
```



Cook's D

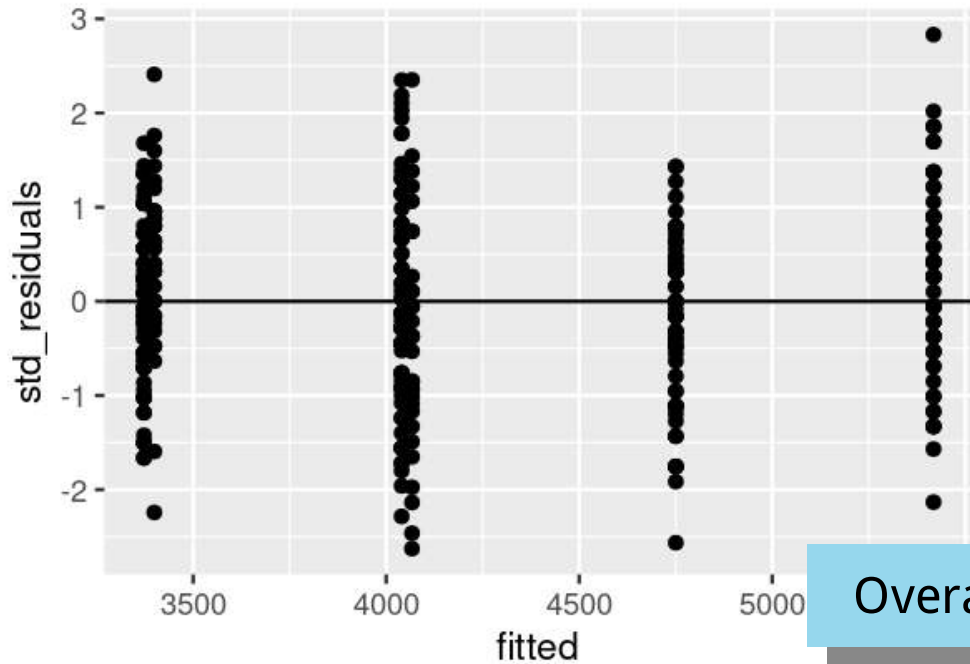
```
ggplot(d, aes(x = obs, y = cooks)) +  
  geom_point() +  
  geom_hline(yintercept = 4/nrow(penguins),  
             linetype = "dashed")
```



Variance and Influence

Check heteroscedasticity

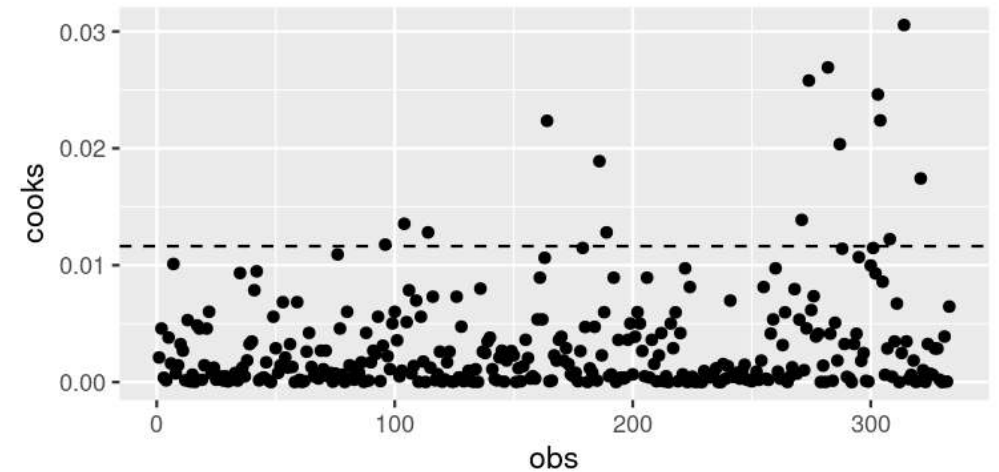
```
ggplot(d, aes(x = fitted, y = std_residuals)) +  
  geom_point() +  
  geom_hline(yintercept = 0)
```



Overall not too bad

Cook's D

```
ggplot(d, aes(x = obs, y = cooks)) +  
  geom_point() +  
  geom_hline(yintercept = 4/nrow(penguins),  
             linetype = "dashed")
```



Multicollinearity (collinearity)

vif() function from **car** package

```
library(car)
vif(m)
```

```
##           GVIF Df GVIF^(1/(2*Df))
## species 1.000146  2      1.000036
## sex     1.000146  1      1.000073
```

Here we consider the **GVIF^(1/2*Df)** value*

Looks good!

* See **?vif** and the reference therein: Fox, J. and Monette, G. (1992) Generalized collinearity diagnostics. JASA, 87, 178–183.

Interpreting ANOVA Summaries

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

```
summary(m)
```

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-816.87	-217.80	-16.87	227.61	882.20

```
##
## 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 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 316.6 on 329 degrees of freedom
## (11 observations deleted due to missingness)
## Multiple R-squared:  0.8468,    Adjusted R-squared:  0.8454
## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries

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

```
summary(m)
```

Model

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
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## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```


Interpreting ANOVA Summaries

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

```
summary(m)
```

Effects

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 316.6 on 329 degrees of freedom
## (11 observations deleted due to missingness)
## Multiple R-squared:  0.8468,    Adjusted R-squared:  0.8454
## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries

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

```
summary(m)
```

Missing observations

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 316.6 on 329 degrees of freedom
## (11 observations deleted due to missingness)
## Multiple R-squared:  0.8468,    Adjusted R-squared:  0.8454
## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries

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

```
summary(m)
```

R^2 and adjusted R^2

- Adjusted for the number of parameters

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 316.6 on 329 degrees of freedom
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## Multiple R-squared:  0.8468,    Adjusted R-squared:  0.8454
## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries

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

```
summary(m)
```

Specific Details

- **Estimate**
 - Treatment contrasts
 - Average *differences* among categories compared to the base category
- **Std. Error**
 - Variability in the estimates
- **t value**
 - Test statistic
- **Pr(>|t|)**
 - **P-value**, significance of the *differences*
 - Probability of getting **t-value** by chance

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
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```

Interpreting ANOVA Summaries

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

```
summary(m)
```

Specific Details

- **Estimate**

- Treatment contrasts
- Average *difference* compared to the reference

Easier to interpret estimates if we consider a simpler model

- **Std. Error**

- Variability in the estimates

- **t value**

- Test statistic

- **Pr(>|t|)**

- **P-value**, significance of the *differences*
- Probability of getting **t-value** by chance

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
##              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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 316.6 on 329 degrees of freedom
## (11 observations deleted due to missingness)
## Multiple R-squared:  0.8468,    Adjusted R-squared:  0.8454
## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries

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

```
summary(m)
```

```
##
## Call:
## lm(formula = body_mass_g ~ species, data = penguins)
##
## Residuals:
```

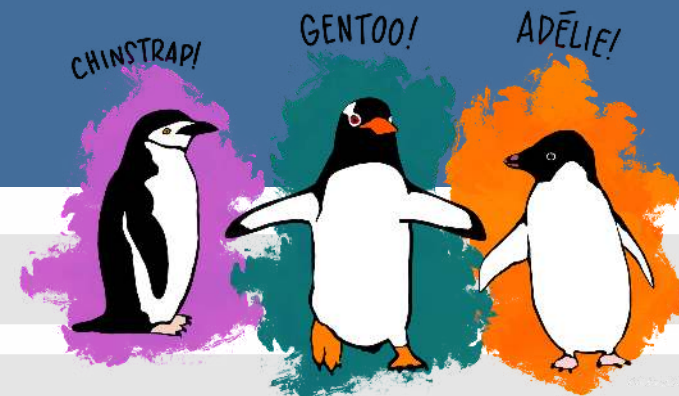
	Min	1Q	Median	3Q	Max
	-1126.02	-333.09	-33.09	316.91	1223.98

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3700.66	37.62	98.37	<2e-16 ***
speciesChinstrap	32.43	67.51	0.48	0.631
speciesGentoo	1375.35	56.15	24.50	<2e-16 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 462.3 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.6697,    Adjusted R-squared:  0.6677
## F-statistic: 343.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries



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

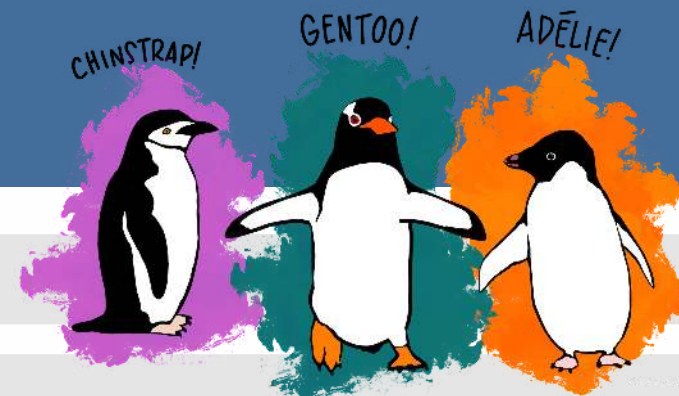
```
summary(m)
```

Effect of **Species**

- **(Intercept)** represents base category (i.e. Adelie penguins)
- Adelie have mean body mass of 3700.66 g
- On average, Chinstrap penguins are 32.43 g heavier than Adelie penguins
- On average, Gentoo penguins are 1375.35 g heavier than Adelie penguins

```
##
## Call:
## lm(formula = body_mass_g ~ species, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1126.02  -333.09   -33.09   316.91  1223.98
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3700.66      37.62   98.37  <2e-16 ***
## speciesChinstrap     32.43      67.51    0.48   0.631
## speciesGentoo    1375.35      56.15   24.50  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 462.3 on 339 degrees of freedom
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## Multiple R-squared:  0.6697,    Adjusted R-squared:  0.6677
## F-statistic: 343.6 on 2 and 339 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries



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

```
summary(m)
```

Effect of **Species**

- **(Intercept)** represents base category (i.e. Adélie penguins)
- Adélie have mean body mass of 3700.66 g
- On average, Chinstrap penguins are 32.43 g heavier than Adélie penguins
- On average, Gentoo penguins are 1375.35 g heavier than Adélie penguins

Back to original model

```
##
## Call:
## lm(formula = body_mass_g ~ species, data = penguins)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
##	-1126.02	-333.09	-33.09	316.91	1223.98

```
##
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3700.66      37.62   98.37  <2e-16 ***
## speciesChinstrap     32.43      67.51    0.48   0.631
## speciesGentoo    1375.35      56.15   24.50  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 462.3 on 339 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.6697,    Adjusted R-squared:  0.6677
## F-statistic: 343.6 on 2 and 339 DF,  p-value: < 2.2e-16
```


Interpreting ANOVA Summaries

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

```
summary(m)
```

Effect of **Species** and **Sex**

- **(Intercept)** represents base category but is a combination of factors
- Much more complicated to interpret
- Comparisons are often not of interest anyway (unless you've set up contrasts, which are advanced stats but awesome!)

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 316.6 on 329 degrees of freedom
## (11 observations deleted due to missingness)
## Multiple R-squared:  0.8468,    Adjusted R-squared:  0.8454
## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Summaries

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

```
summary(m)
```

Effect of **Species** and **Sex**

- **(Intercept)** represents base category but is a combination of factors
- Much more complicated to interpret
- Comparisons are often not of interest anyway (unless you've set up contrasts, which are advanced stats but awesome!)

So let's look at ANOVA tables instead

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -816.87 -217.80  -16.87   227.61   882.20
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 316.6 on 329 degrees of freedom
## (11 observations deleted due to missingness)
## Multiple R-squared:  0.8468,    Adjusted R-squared:  0.8454
## F-statistic: 606.1 on 3 and 329 DF,  p-value: < 2.2e-16
```

Interpreting ANOVA Tables

Type I

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

```
anova(m)
```

```
## Analysis of Variance Table
##
## Response: body_mass_g
##           Df      Sum Sq  Mean Sq F value    Pr(>F)
## species     2 145190219 72595110   724.21 < 2.2e-16
## ***
## sex          1  37090262 37090262   370.01 < 2.2e-16
## ***
## Residuals 329  32979185   100241
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
'.' 0.1 ' ' 1
```

Interpreting ANOVA Tables

Type I

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

```
anova(m)
```

Overall effects of **Species** and **Sex**

- Yes there are differences among **Species** ($P < 2.2e^{-16}$)
- Yes there are differences between **Sexes** ($P < 2.2e^{-16}$)

```
## Analysis of Variance Table
##
## Response: body_mass_g
##              Df      Sum Sq  Mean Sq  F value    Pr(>F)
## species        2 145190219  72595110    724.21 < 2.2e-16
## ***
## sex             1  37090262  37090262    370.01 < 2.2e-16
## ***
## Residuals 329  32979185    100241
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
                  '.' 0.1 ' ' 1
```

Interpreting ANOVA Tables

Type I

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

```
anova(m)
```

Overall effects of **Species** and **Sex**

- Yes there are differences among **Species** ($P < 2.2e^{-16}$)
- Yes there are differences between **Sexes** ($P < 2.2e^{-16}$)

```
## Analysis of Variance Table
##
## Response: body_mass_g
##              Df      Sum Sq  Mean Sq  F value    Pr(>F)
## species        2 145190219 72595110   724.21 < 2.2e-16
## ***
## sex            1  37090262 37090262   370.01 < 2.2e-16
## ***
## Residuals 329  32979185   100241
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
'.' 0.1 ' ' 1
```

Not a whole lot of information...
Stay tuned for **Post-Hoc** tests next week!

Interpreting ANOVA Tables

Type I

```
m1 <- lm(body_mass_g ~ species + sex, data =  
penguins)  
anova(m1)
```

```
## Analysis of Variance Table  
##  
## Response: body_mass_g  
##           Df      Sum Sq  Mean Sq F value    Pr(>F)  
## species     2 145190219 72595110   724.21 < 2.2e-16  
## ***  
## sex         1  37090262 37090262   370.01 < 2.2e-16  
## ***  
## Residuals 329  32979185   100241  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05  
'.' 0.1 ' ' 1
```

```
m2 <- lm(body_mass_g ~ sex + species, data =  
penguins)  
anova(m2)
```

```
## Analysis of Variance Table  
##  
## Response: body_mass_g  
##           Df      Sum Sq  Mean Sq F value    Pr(>F)  
## sex         1  38878897 38878897   387.86 < 2.2e-16  
## ***  
## species     2 143401584 71700792   715.29 < 2.2e-16  
## ***  
## Residuals 329  32979185   100241  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05  
'.' 0.1 ' ' 1
```

- For Type I ANOVAs, order matters with unbalanced samples
 - See that **Sum sq**, **Mean Sq** and **F value** all differ between the models
- Here, pretty minor, but important to remember with greater unbalances

Interpreting ANOVA Tables

Type III

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

```
library(car)  
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
```

Interpreting ANOVA Tables

Type III

```
m1 <- lm(body_mass_g ~ species + sex, data =  
penguins)  
Anova(m1, 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
```

```
m2 <- lm(body_mass_g ~ sex + species, data =  
penguins)  
Anova(m2, 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 ***  
## sex          37090262    1   370.01 < 2.2e-16 ***  
## species      143401584   2   715.29 < 2.2e-16 ***  
## Residuals    32979185 329  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05  
'.' 0.1 ' ' 1
```

- Type III and unbalanced samples: Not dependent on variable order

Homework (Practice)*

Consider flipper length your response variable and species and sex your predictor variables

1. Plot the relationship between flipper length and species and between flipper length and sex
2. Create an ANOVA model of flipper length and species
3. Check diagnostics
4. Interpret the **summary table**
5. Interpret the **ANOVA Table**
6. Create an ANOVA model of flipper length and species and sex
7. Check diagnostics
8. Interpret the **ANOVA Table**