RCamp: Introductory Applied Statistics

Tribal-State Relations Acknowledgment Statement

The State of Minnesota is home to 11 federally recognized Indian Tribes with elected Tribal government officials. The State of Minnesota acknowledges and supports the unique political status of Tribal Nations across Minnesota and their absolute right to existence, self-governance, and self-determination. This unique relationship with federally recognized Indian Tribes is cemented by the Constitution of the United States, treaties, statutes, case law, and agreements. The State of Minnesota and Tribal governments across Minnesota significantly benefit from working together, learning from one another, and partnering where possible.

Minnesota Department of Health recognizes, values, and celebrates the vibrant and unique relationships between the 11 Tribal Nations and the State of Minnesota. Partnerships formed through government-to-government relationships with these Tribes will effectively address health disparities and lead to better health outcomes for all of Minnesota.

In our work at the Office of Data Strategy and Interoperability, we demonstrate our commitment to Tribal-State relations by providing free assistance upon request and promoting health equity in data collection and use.

Purpose of DSI

To provide vision, direction, and leadership in advancing data strategies and data exchange across MDH through:

- Coordinating and streamlining the exchange of data with MDH
- Overseeing and supporting state solutions and common tools
- Facilitating efforts to maximize MDH data by creating data and process standards and tools with the whole Minnesota Public Health System in mind

Vision of DTA

To support **data needs** for ALL staff in:

- MDH
- Local Public Health
- Tribal Health

Data needs we support:

- Project planning and design
- Data wrangling and analysis
- Data visualization and report preparation
- Data literacy

Acknowledgments

Thank you to the State of Minnesota R user group!

★Special thanks to our founders Barbara Monaco, Dorian Kvale, Derek Nagel, and Kristi Ellickson.

Introductory Applied Statistics Overview

- Today we will cover:
  - Types of data, summary statistics, and distributions
  - Hypothesis testing and P-value
  - T-tests, Mann-Whitney U Test, Wilcoxon Signed Rank Test
  - ANOVA
  - Chi-Squared Test
  - Correlation
  - Linear Regression

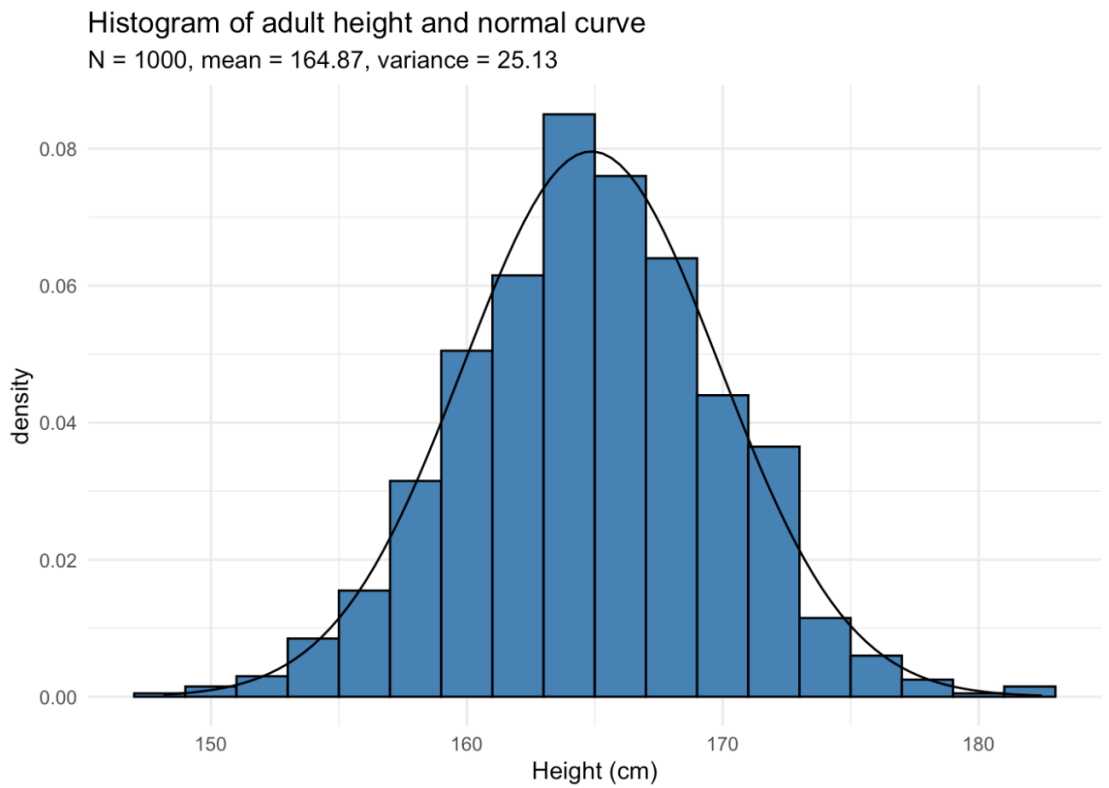
Types of Quantitative Data

- Continuous data
  - Data that can take on any value within a given range, including decimals and fractions (height, weight, temperature)
  - Might or might not be normally distributed
  - We will mostly focus on continuous data today
- Discrete data
  - Data that can only take on specific, separate values, typically whole numbers or categories
  - Binary data: discrete data with only two possible outcomes (e.g. dear or alive, sick or healthy)
  - Counts: whole numbers representing the number of events, patients, hospitals, or anything else that can be counted
  - Nominal data: data categories with no order (blood type, treatment group)
  - Ordinal data: data categories with a particular order (pain scale, survey response categories)

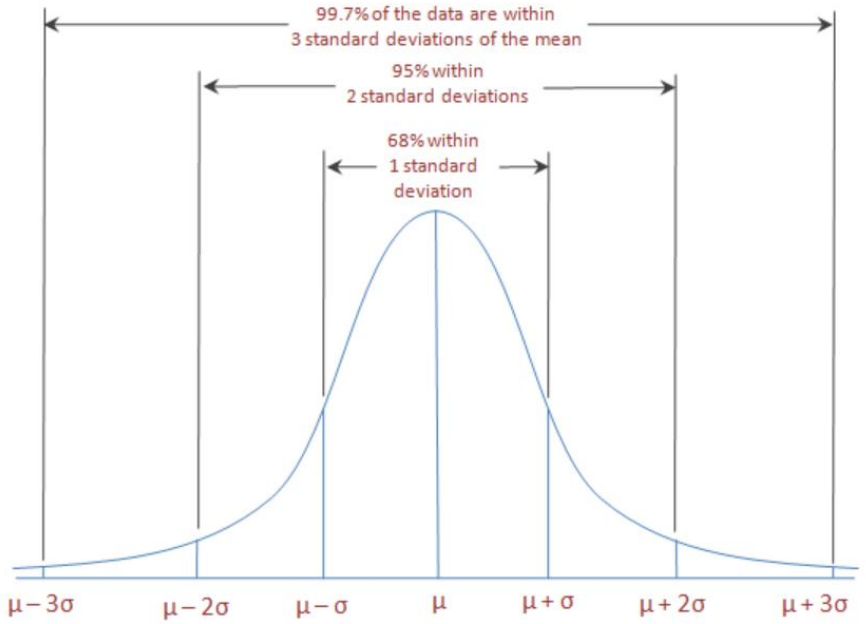
Summary Statistics

- Summary statistics summarize and provide information about your sample data.
- Summary statistics fall into three main categories:
  - Measures of **location**: where your data is centered at, or where a trend lies
    - Mean, median, mode
  - Measures of **spread** or distribution shape: how spread out or varied your data set is
    - range, standard deviation, skew and kurtosis
  - Graphs/charts: ways to display summary data
    - histogram, frequency distribution table, box plot, bar chart, scatter plot and pie chart

Normal Distribution

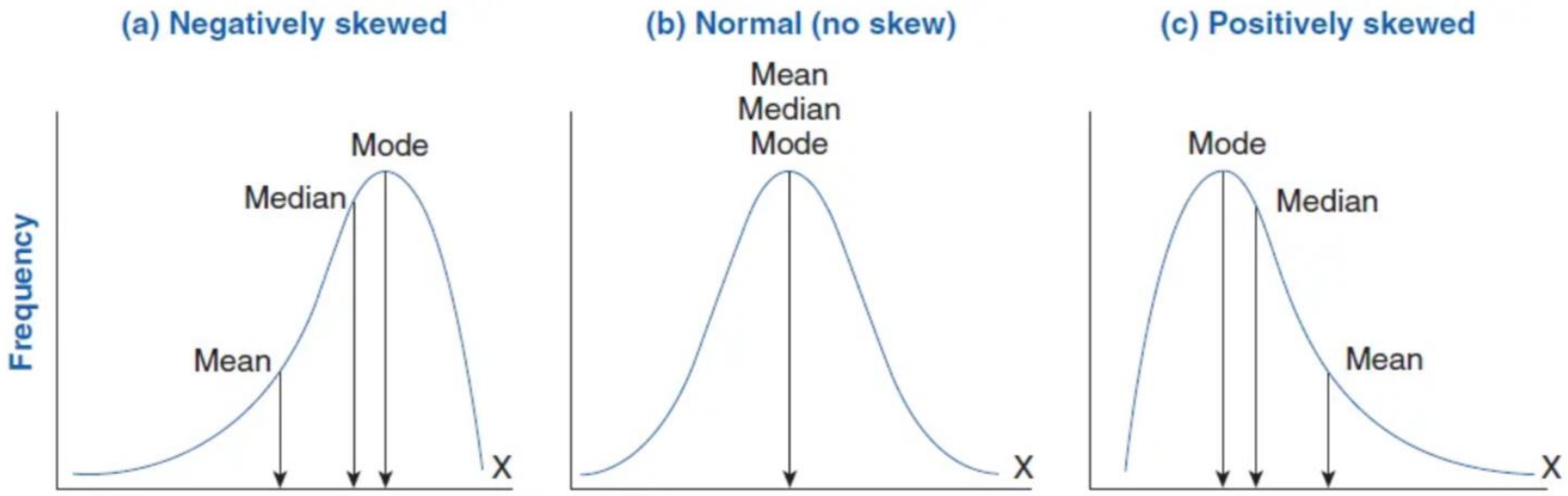


- $\mu \pm \sigma$ includes approximately 68% of the observations
- $\mu \pm 2 \cdot \sigma$ includes approximately 95% of the observations
- $\mu \pm 3 \cdot \sigma$ includes almost all of the observations (99.7% to be more precise)

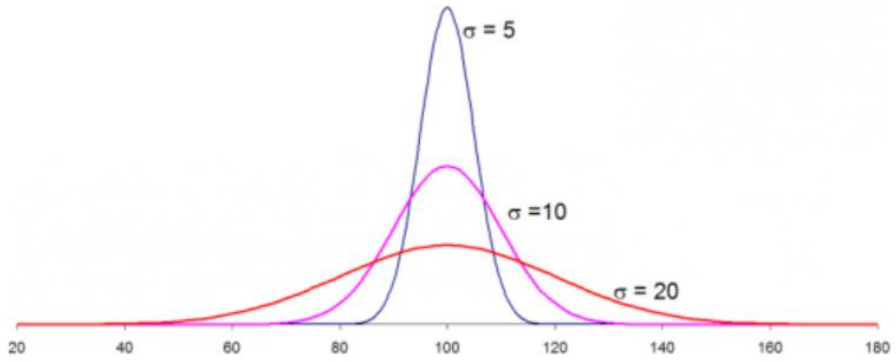


https://statsandr.com/blog/do-my-data-follow-a-normal-distribution-a-note-on-the-most-widely-used-distribution-and-how-to-test-for-normality-in-r/

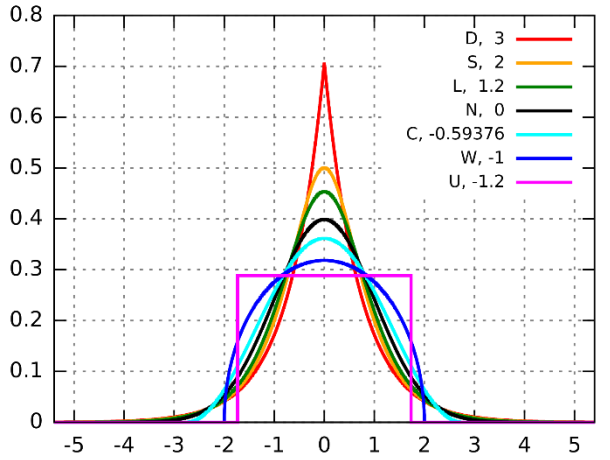
Skew, Standard Deviation, and Kurtosis



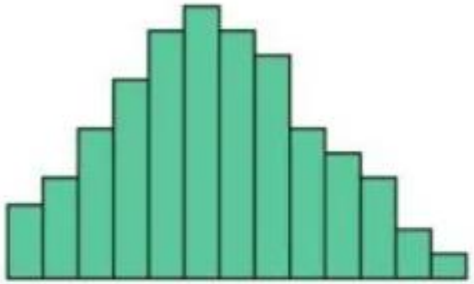
Various standard deviations



Various levels of kurtosis with the same sd

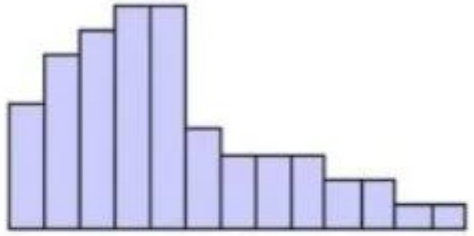


Non-Normal Distribution

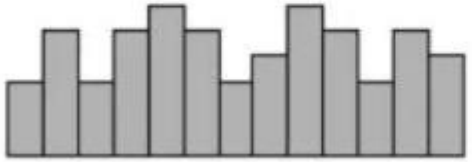


The shape has a bell shape.
It is symmetric.

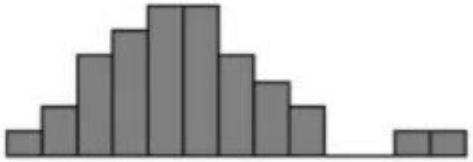
The shape has two humps.
It is bimodal.



The shape has a long tail.
It is not symmetric.



The shape is flat.

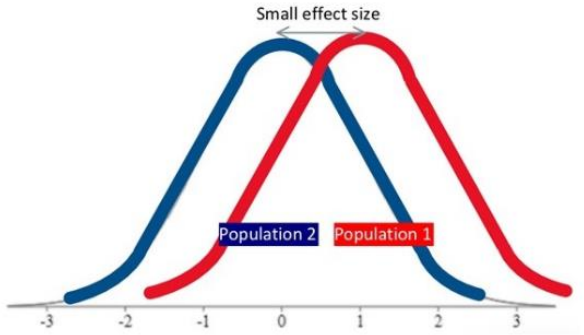


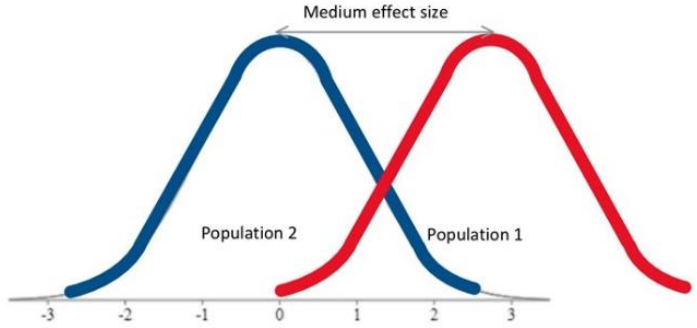
There are one or more outliers.

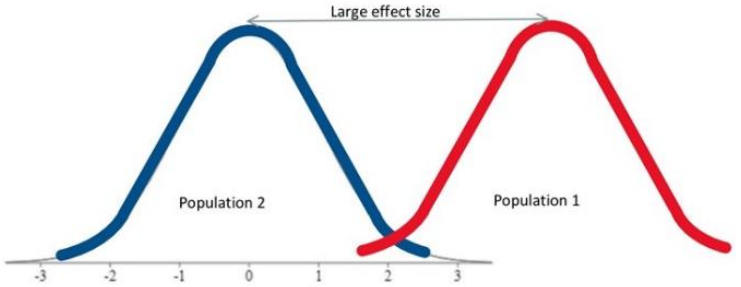
https://leanscape.io/data-distributions-explained-what-are-the-different-types-of-distribution/

Hypothesis Testing and P-value

- For example, we want to know if the average height between two groups of people is different or not
  - Null Hypothesis (H_0): There is no difference in average height between the two groups
  - Alternative Hypothesis (H_A or H_1): There is a difference in average height between the two groups
- P-value (probability value) tells us how likely is the difference in height that we see if the null hypothesis is true (there is actually no difference)
  - A commonly accepted P-value for statistical significance is equal to or below $\alpha = 0.05$
  - That means that 5% of the time the height difference that you see would be there by random chance even if the null hypothesis was true (error rate you are willing to accept)
  - You are 95% confident that there is a statistical difference in height between the groups

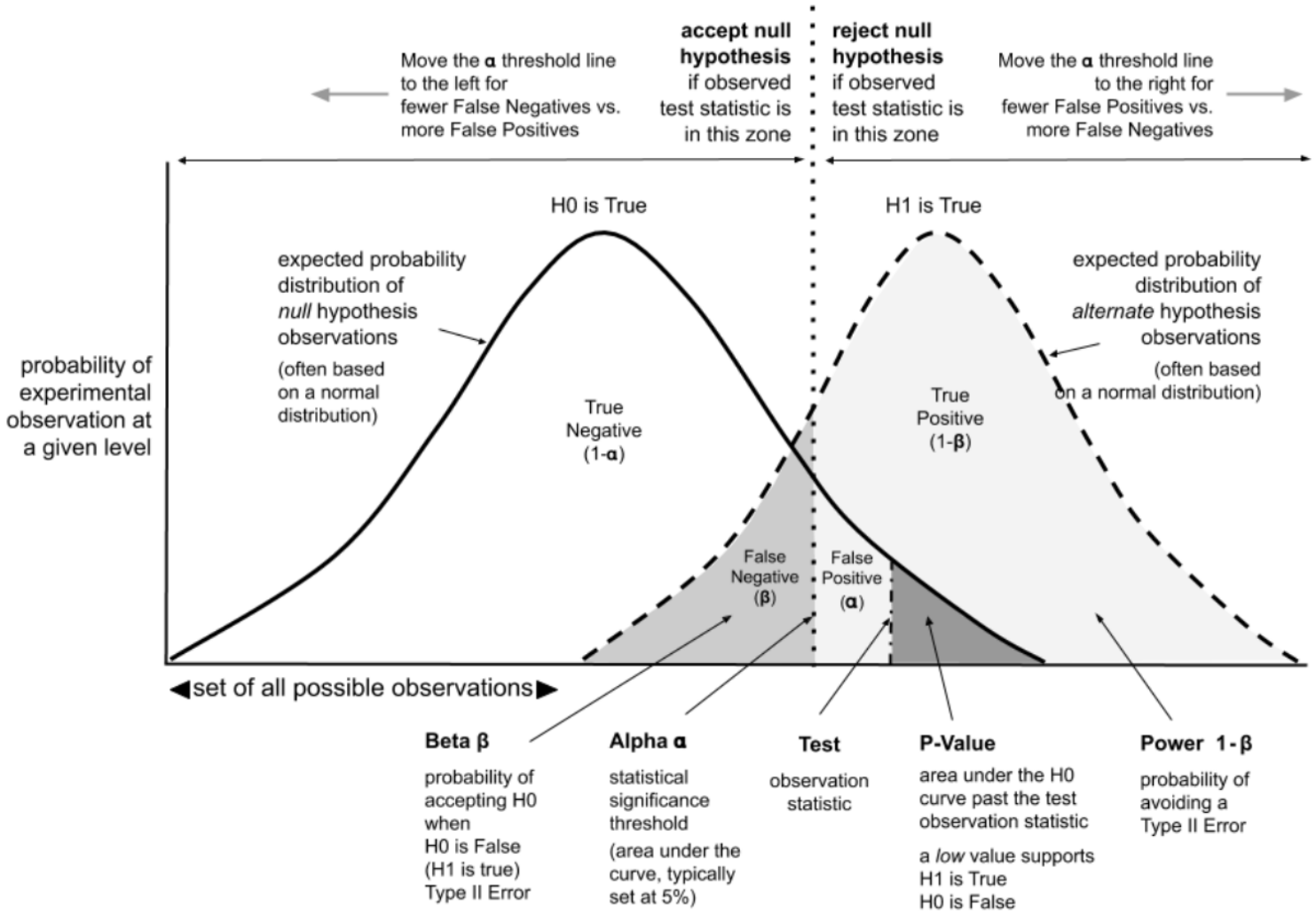






Error Types and Statistical Power

- Type I error: incorrectly reject H_0 when it is true (false positive)
  - α is the probability of Type I error
- Type II error: fail to reject H_0 when it is false (false negative)
  - β is the probability of Type II error
- Power = 1 – β
  - Probability that a test will correctly reject the H_0
- Visualization to explore:
  - https://rpsychologist.com/d3/nhst/

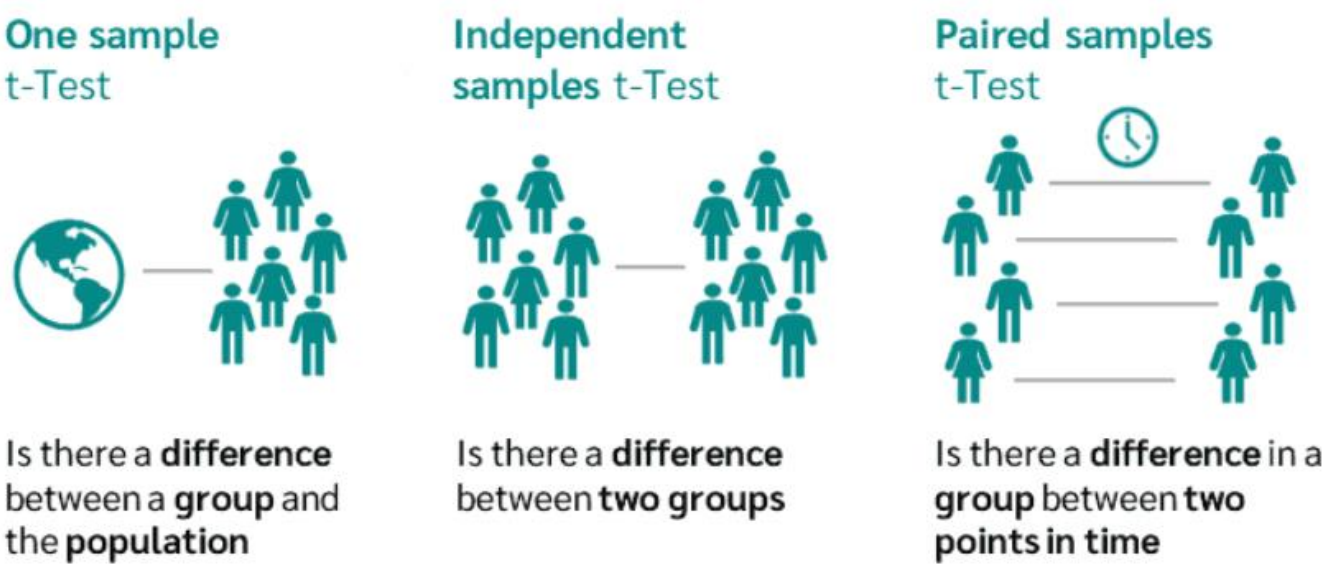


https://www.ml-science.com/statistical-power-of-a-test

T-Test

- Compares the means of two groups and tells whether the difference is significant
- Lets you know the likelihood those differences could have happened by random chance (P-value)
- Different kinds of t-tests:

- A two tailed t-test checks whether there is a general difference between two groups.
- A one tailed t-test checks whether one group is specifically larger or smaller (has a direction)



T-tests were first developed to test the consistency Guiness beer!

https://datatab.net/tutorial/one-sample-t-test

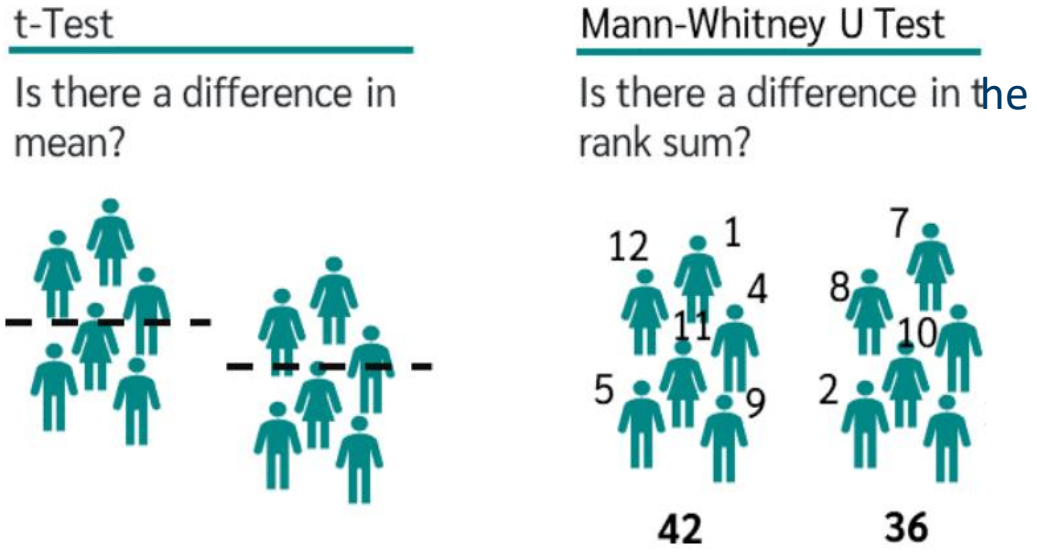
T-Test Assumptions

- Assumptions are extremely important in statistics! Tests are only valid when **all** the assumptions are met.
  - The data is numeric and continuous
  - The data comes from a random, representative sample
  - The data is normally distributed
    - To formally test for normality, you can use the Shapiro-Wilks test. A p-value <0.05 suggests that the data is not normally distributed
  - The variance of data in both groups is approximately equal
  - The data in two groups is independent from each other (only relevant for the non-paired tests)
- What if we can't meet some of those assumptions?

https://datatab.net/tutorial/one-sample-t-test

Mann-Whitney U-Test

- If the data isn't normally distributed, you can use the Mann-Whitney U-Test
- The independent t-test counterpart for data that is not normally distributed.
- Tests that require assumptions about data distributions are called **parametric**. Tests that do not are called **nonparametric**.
- Instead of comparing groups directly, the test ranks everyone in both groups from shortest to tallest, sums the ranks in both groups, and compares this rank sum between the groups.



https://datatab.net/tutorial/mann-whitney-u-test

Wilcoxon Signed Rank Test

- What if the data is not normally distributed but is paired?
  - Use the Wilcoxon Signed Rank Test, the nonparametric counterpart to the paired t-test
  - Works just like the Mann-Whitney u-Test by comparing rank sums
- There are more types of tests for different situations, but these are some of the most common when comparing **two** groups or **one** sample group and the general population.
- What if you want to compare more than two groups at a time?

ANOVA

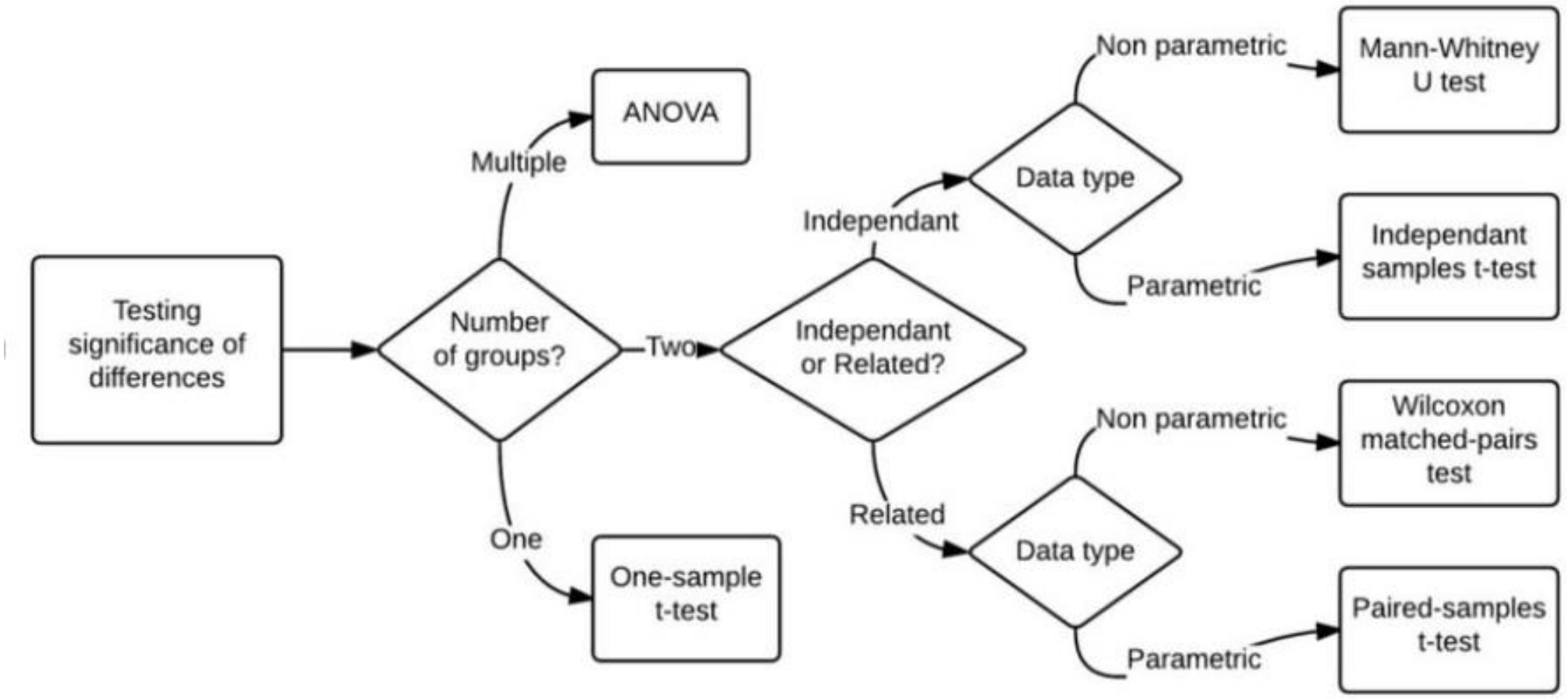
- Analysis of Variance (ANOVA) can be used to compare the means of more than two groups at a time
- One-way ANOVA compares **one** variable across multiple categories

  Example: Average disease duration in three cohorts receiving different treatment
- Two-way ANOVA compares **two** variables across multiple categories, as well as their interaction

  Example: Average disease duration in three cohorts receiving different treatment and accounting for patient sex

	Men	Women
Cohort 1	9 days	10.2 days
Cohort 2	7.2 days	7.0 days
Cohort 3	5.6 days	4.8 days

Statistical Test Decision Tree



Chaudy, Yaelle. (2015). An Assessment and Learning Analytics Engine for Games-based Learning. 10.13140/RG.2.1.4932.5040.

Chi-Square Test

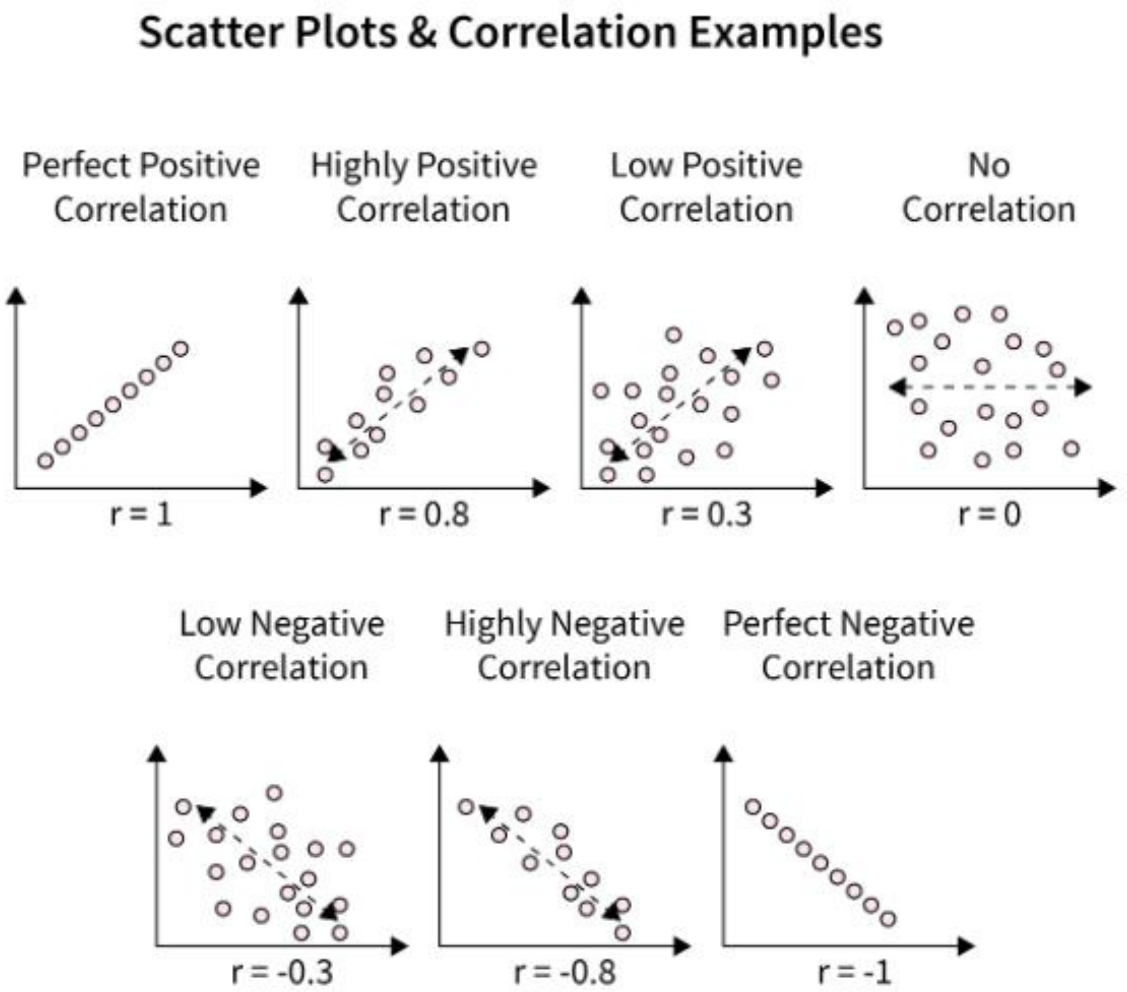
- If your data isn't continuous but is instead categorical, you can use the Chi-Square test
  - Example: we want to tell whether out of a sample of 300 people, diabetes rates are different between men and women
  - H_0: Diabetes rate are the same
  - H_A: Diabetes rate are different
- Assumptions:
  - Both datasets are categorial
  - Observations are independent
  - Each category (cell in the table) is mutually exclusive
  - Each value in the cell should be 5 or greater

	Diabetes	No Diabetes	Total
Men	43	114	157
Women	34	109	143
Total	77	223	300

Correlation

- Correlation describes the linear relationships between quantitative variables.
- **Pearson** correlation coefficient formulas (often shown as "r") are used to find the strength of a relationship between two normally distributed continuous variables. The formula returns a value between -1 and 1, where:
  - 1 indicates a strong positive relationship.
  - -1 indicates a strong negative relationship.
  - A result of zero indicates no relationship at all.
- **Spearman** correlation is used for data that is not normally distributed, is non-linear, or has significant outliers. Like other non-parametric alternative tests, it is based on rank rather than raw values

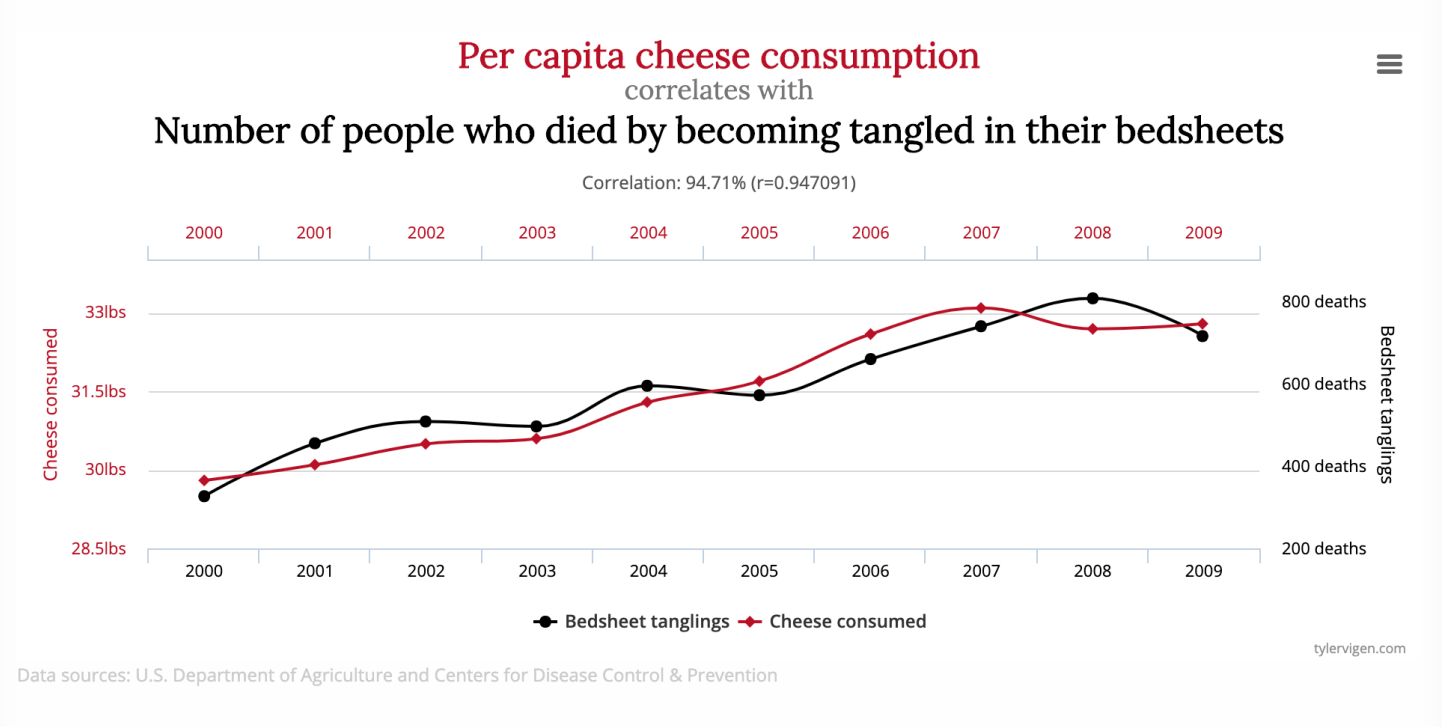
Correlation Visual Examples

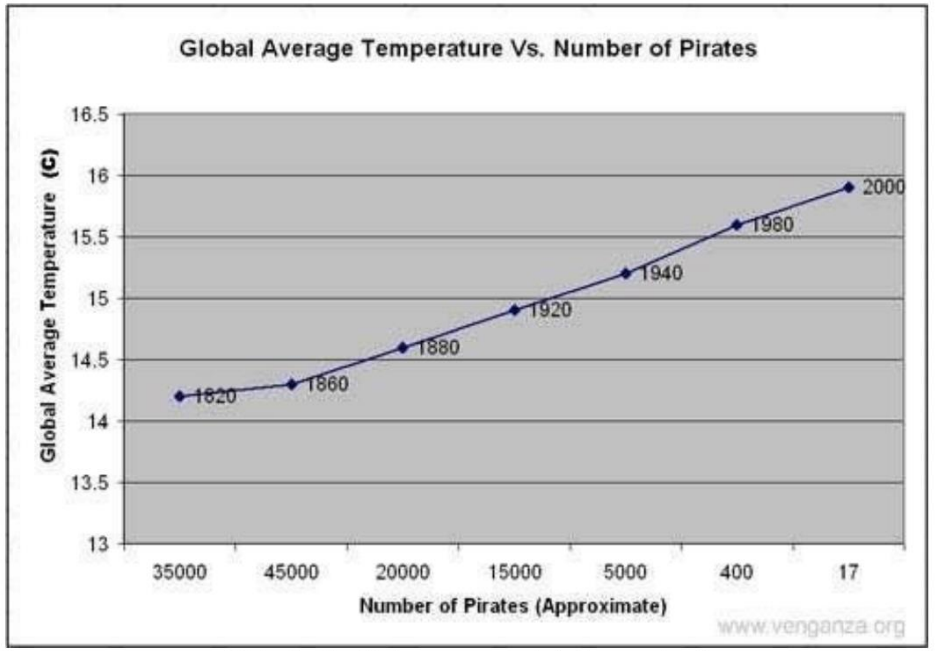


https://www.scaler.com/topics/data-science/covariance-and-correlation/

Correlation is not Causation

- Correlation is not causation! just because two things correlate does not necessarily mean that one causes the other.





Did a lack of piracy cause global warming?

Palmer Penguin Dataset

- Now let's look how these kinds of tests can be run in R
- This data was collected between 2007 and 2009 on the Palmer archipelago in the Antarctic
- https://journal.r-project.org/articles/RJ-2022-020/

species	island	bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g	sex	diet	life_stage	health_metrics	year
Adelie	Biscoe	53.4	17.8	219	5687	female	fish	adult	overweight	2021
Adelie	Biscoe	49.3	18.1	245	6811	female	fish	adult	overweight	2021
Adelie	Biscoe	55.7	16.6	226	5388	female	fish	adult	overweight	2021
Adelie	Biscoe	38	15.6	221	6262	female	fish	adult	overweight	2021
Adelie	Biscoe	60.7	17.9	177	4811	female	fish	juvenile	overweight	2021
Adelie	Biscoe	35.7	16.8	194	5266	female	fish	juvenile	overweight	2021
Adelie	Biscoe	61	20.8	211	5961	female	fish	adult	overweight	2021
Adelie	Biscoe	66.1	20.8	246	6653	male	fish	adult	overweight	2021
Adelie	Biscoe	61.4	19.9	270	6722	male	fish	adult	overweight	2021

Regression Analysis

- Regression analysis provides you with an equation for a graph so that you can make predictions or draw insight about your data.
- Simple regression analysis uses a single x variable for each dependent “y” variable.
- Multiple regression analysis is used to see if there is a statistically significant relationship between sets of variables. It’s used to find trends in those sets of data.
- Regression is often more powerful and flexible than many other statistical tests and is a staple of statistical analysis

Linear Regression

- Linear regression equation:

$$y = b_0 + b_1 * x + \epsilon, \epsilon \sim \text{Norm}(0, \sigma^2)$$

  - y – dependent variable
  - x – independent variable
  - b1 – slope
  - b0 – intercept
  - ε – the error term that represents all the variation in y that the model cannot explain

- Linear regression error term is normally distributed

$$\epsilon \sim \text{Norm}(0, \sigma^2)$$

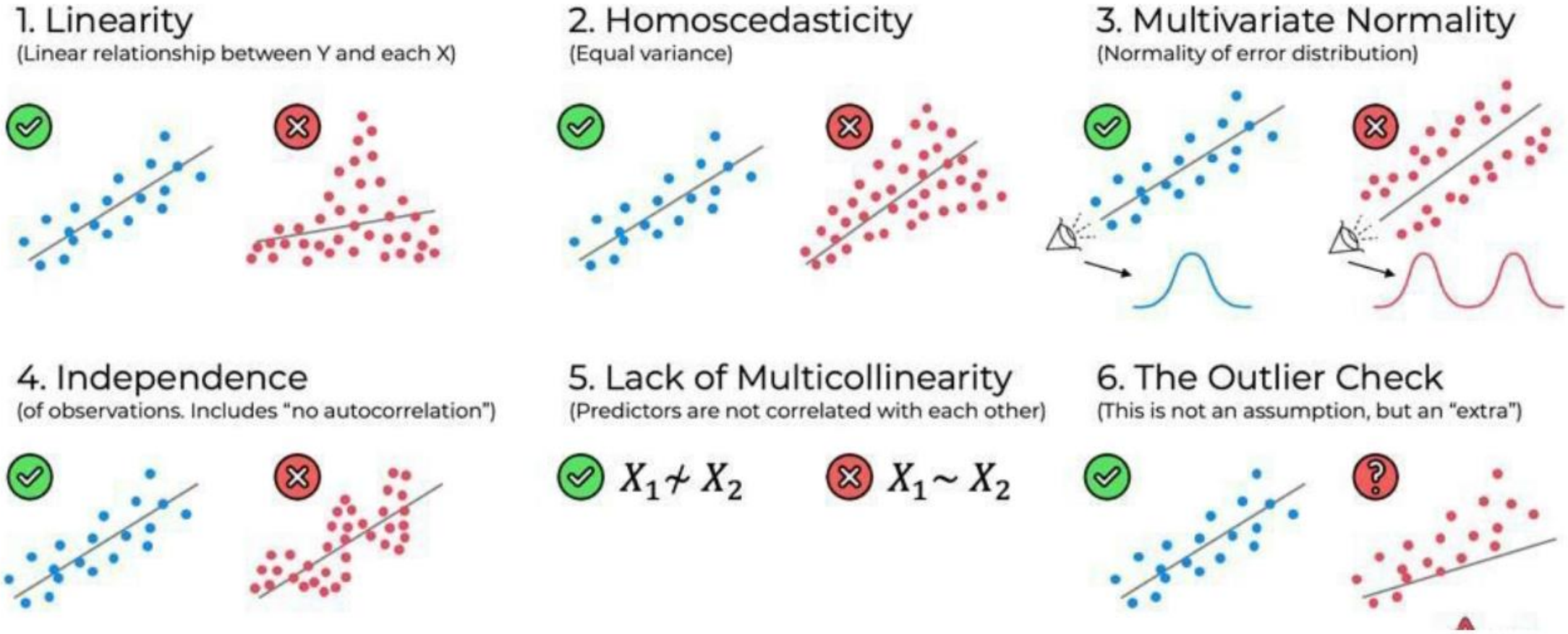
  - 0 – the mean of the normal distribution
  - σ_2 – standard deviation squared, also known as variance

- Linear regression visualization: https://ryansafner.shinyapps.io/ols_estimation_by_min_sse/

Linear Regression Assumptions

- The dependent variable (outcome) is continuous
- The relationship between predictors (x) and outcome (y) is linear
- The residuals of the regression (differences between observed and estimated values) are normally distributed
  - Note that the data itself does not have to be normally distributed
- No multicollinearity: independent variables should not correlate with each other more than ~0.8
- Homoscedasticity: the variance of the errors is constant across all levels of the independent variable
- Error terms are independent of each other

Linear Regression Assumptions



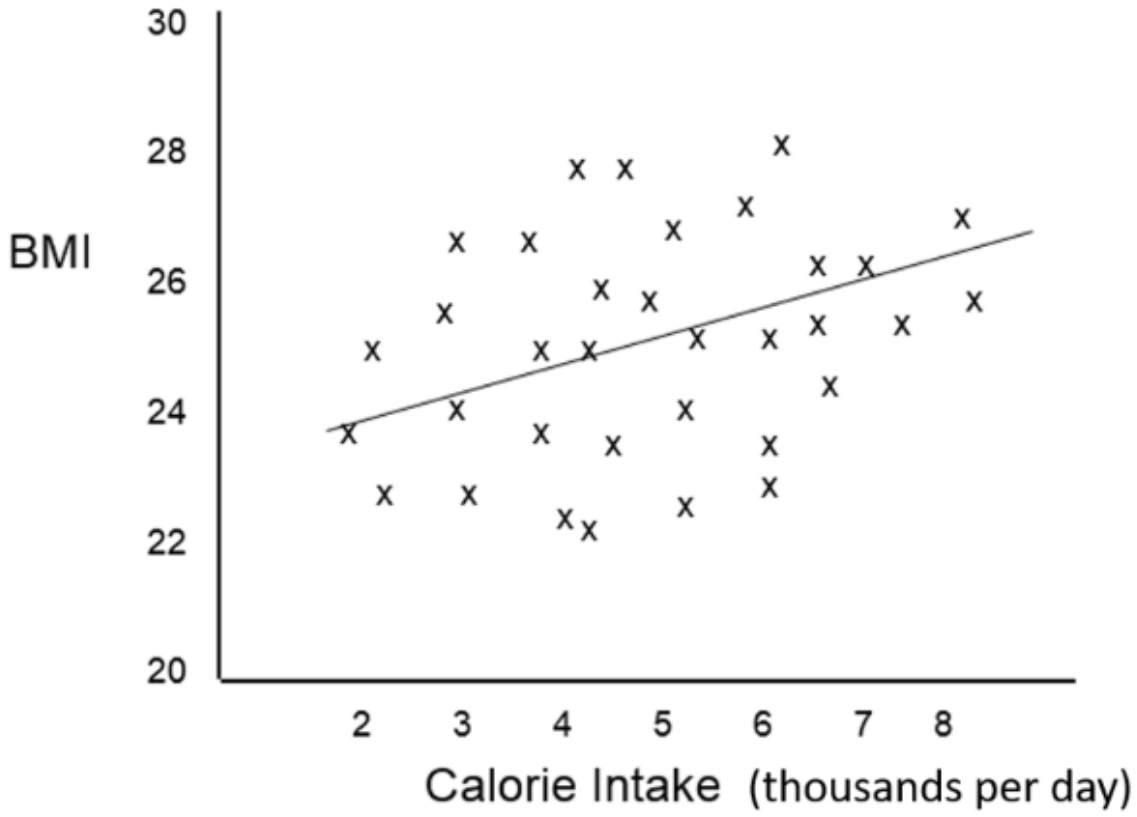
https://www.geeksforgeeks.org/machine-learning/assumptions-of-linear-regression/

Multiple Linear Regression

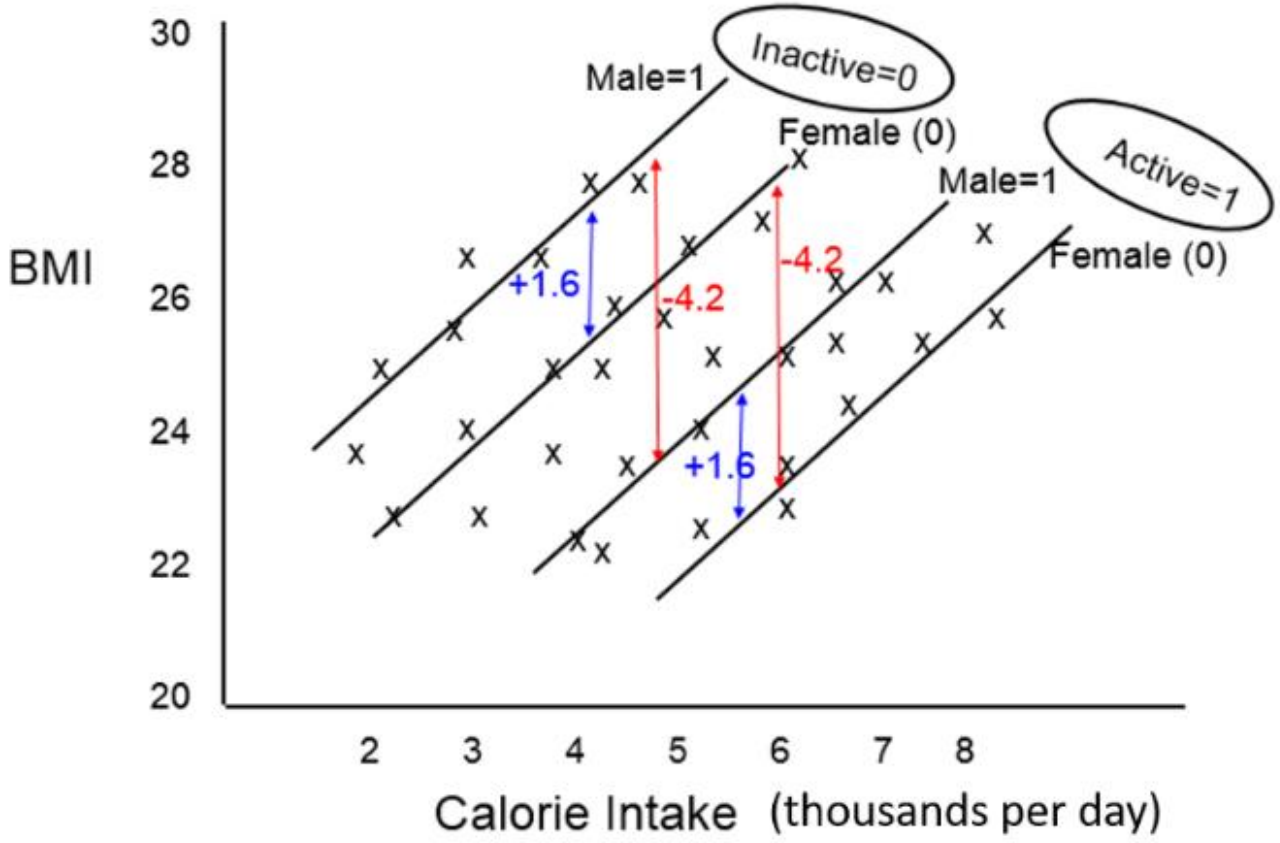
Consider a hypothetical situation evaluating BMI and Calorie Intake.

Multiple R squared value (a statistic to help assess the wellness of the regression fit) in this case was 0.12 , so caloric intake alone does not predict BMI well.

What other variables could influence BMI? Perhaps activity level and gender?



Multiple Linear Regression



The equation for this would be:

BMI = 15.0 + 1.5 (cal) + 1.6 (if male) - 4.2 (if active)

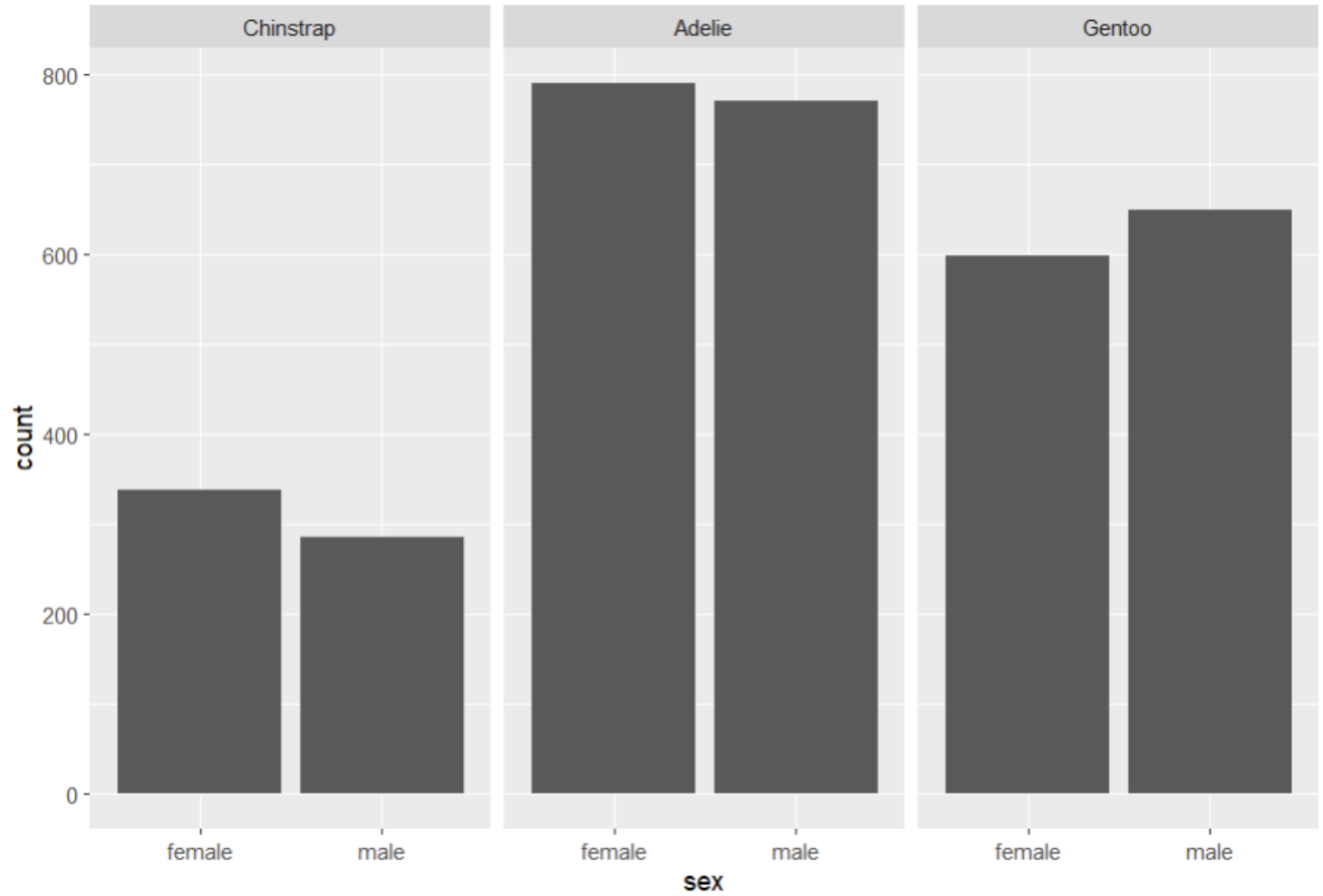
What can be said about active and inactive populations as it relates to gender, calorie intake, and BMI?

Solving this work by hand is very tedious, so we will use R

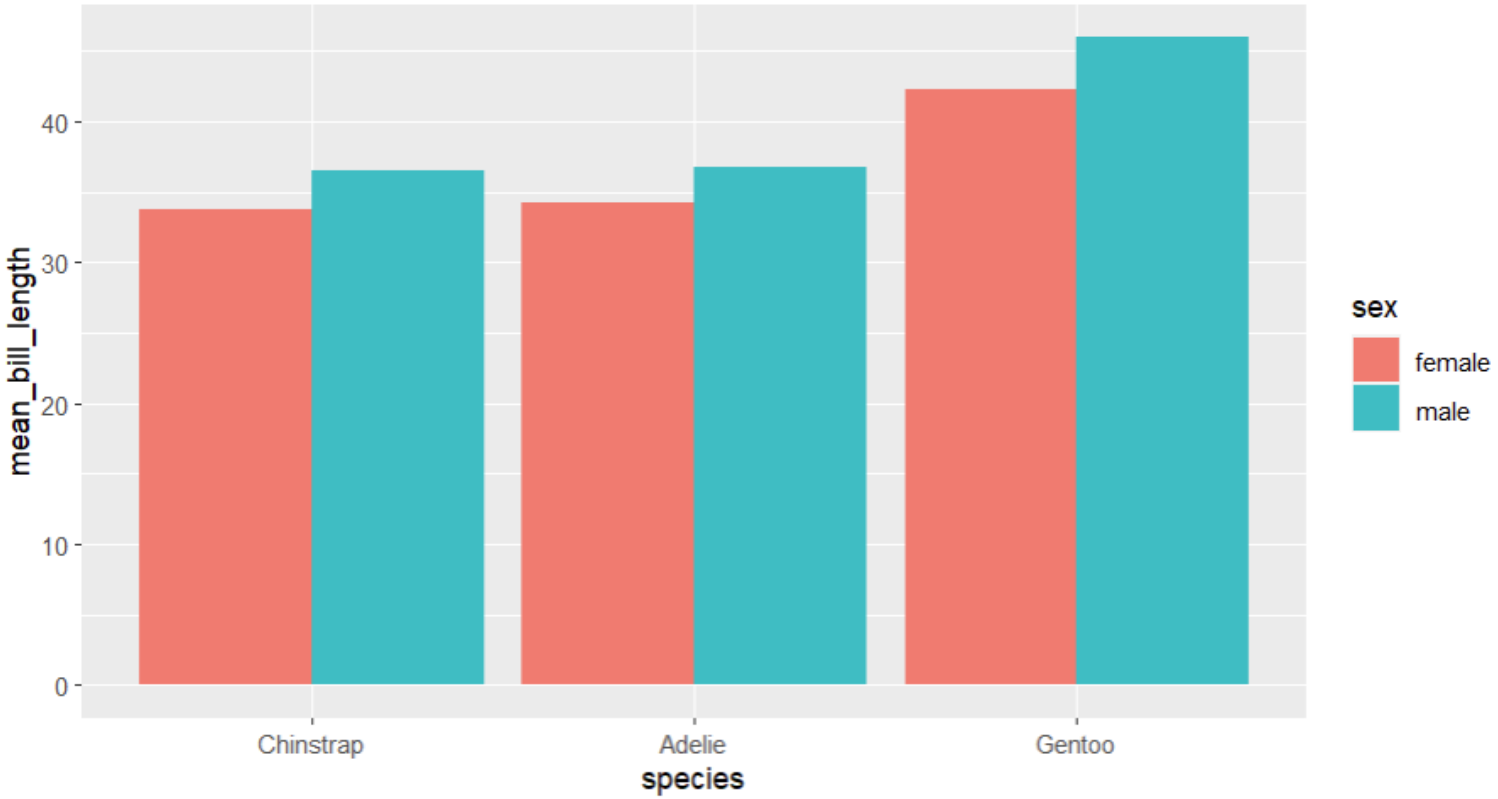
Many additional variables can be added into the equation to improve the model outcome

Exploring the Palmer Penguin Data

- Number of penguins by sex and species



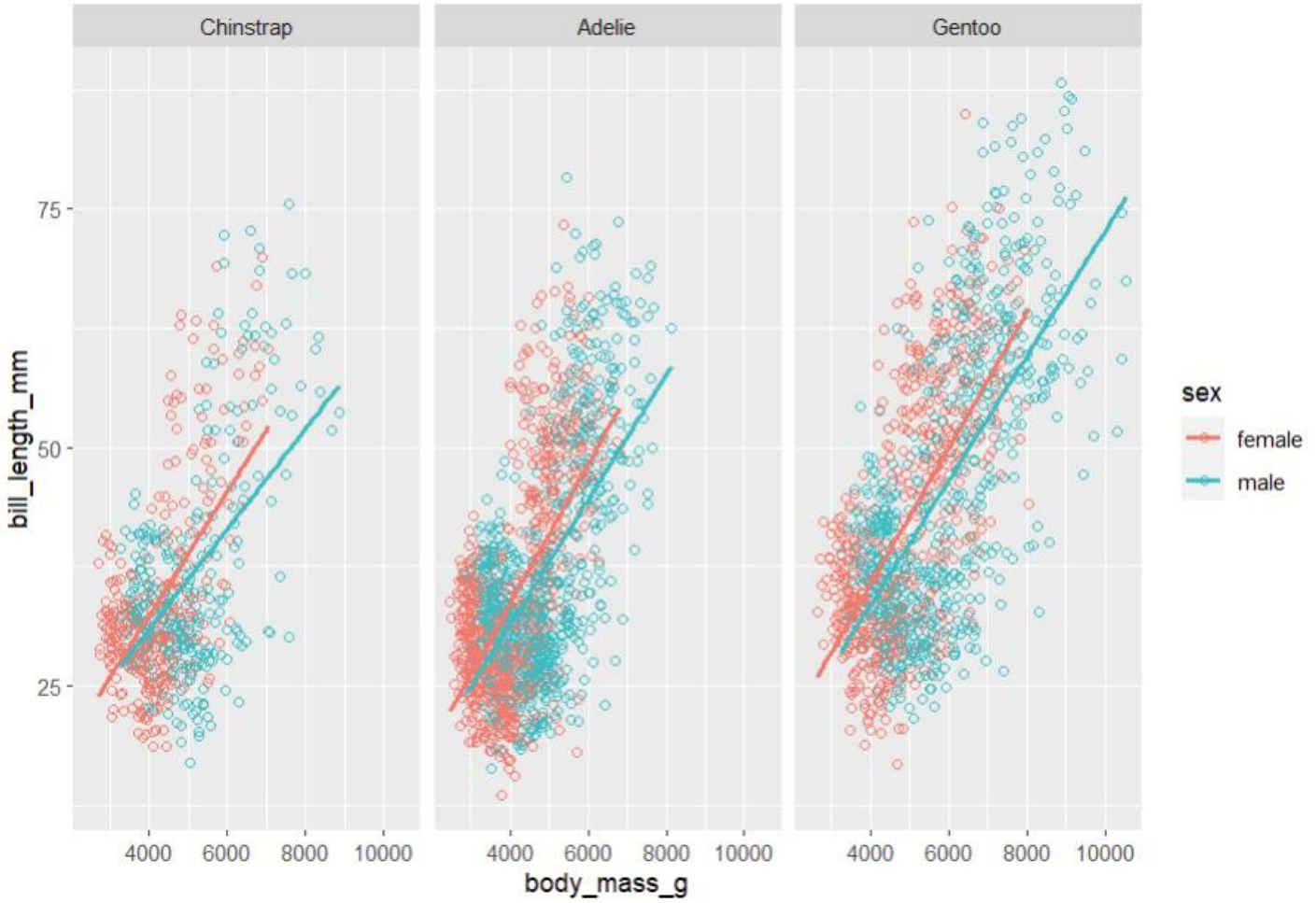
Exploring the Palmer Penguin Data



species	Chinstrap	Chinstrap	Adelie	Adelie	Gentoo	Gentoo
sex	female	male	female	male	female	male
mean_bill_length	33.8	36.5	34.2	36.7	42.2	46.0
mean_mass	4215.9	5061.0	4084.0	4816.4	4911.5	5922.5

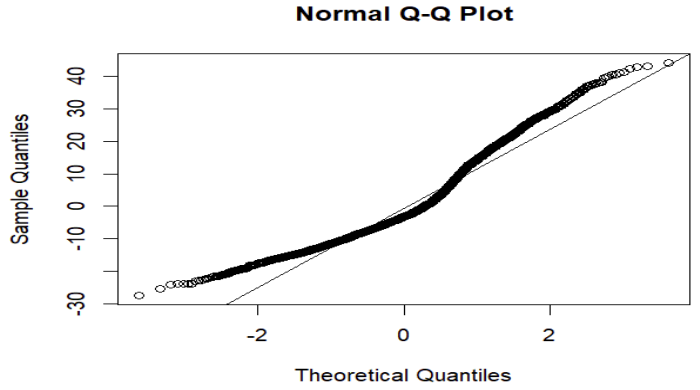
Exploring the Palmer Penguin Data

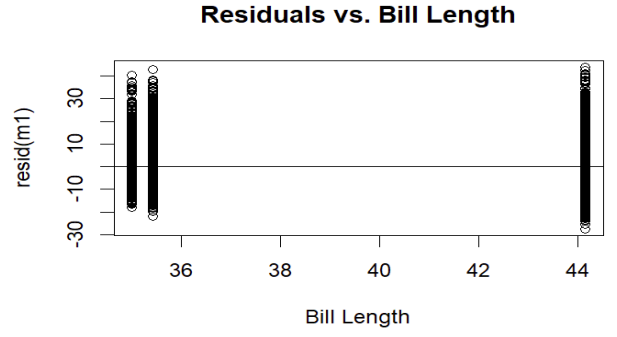
The relationship between penguin bill length, body mass, species, and sex



Linear Regression Interpretation 1

```
Call:
lm(formula = bill_length_mm ~ species, data = peng)

Residuals:
    Min      1Q  Median      3Q     Max
-27.362  -8.832  -3.215   7.538  44.038

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      35.4316     0.3157 112.214   <2e-16 ***
speciesChinstrap -0.4170     0.5911  -0.706    0.481
speciesGentoo     8.7303     0.4737  18.429   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 12.47 on 3427 degrees of freedom
Multiple R-squared:  0.1045,    Adjusted R-squared:  0.104
F-statistic: 200.1 on 2 and 3427 DF,  p-value: < 2.2e-16
```





Exploring the Palmer Penguin Data

Which species should serve as the reference category for the regressions?

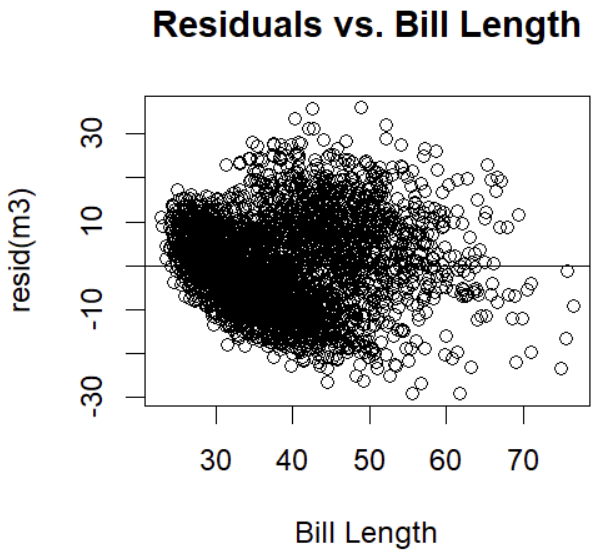
```
# A tibble: 3 × 2
  species   mean_bill_length
  <chr>                <dbl>
1 Adelie                35.4
2 Chinstrap             35.0
3 Gentoo                44.2
```

Linear Regression Interpretation 2

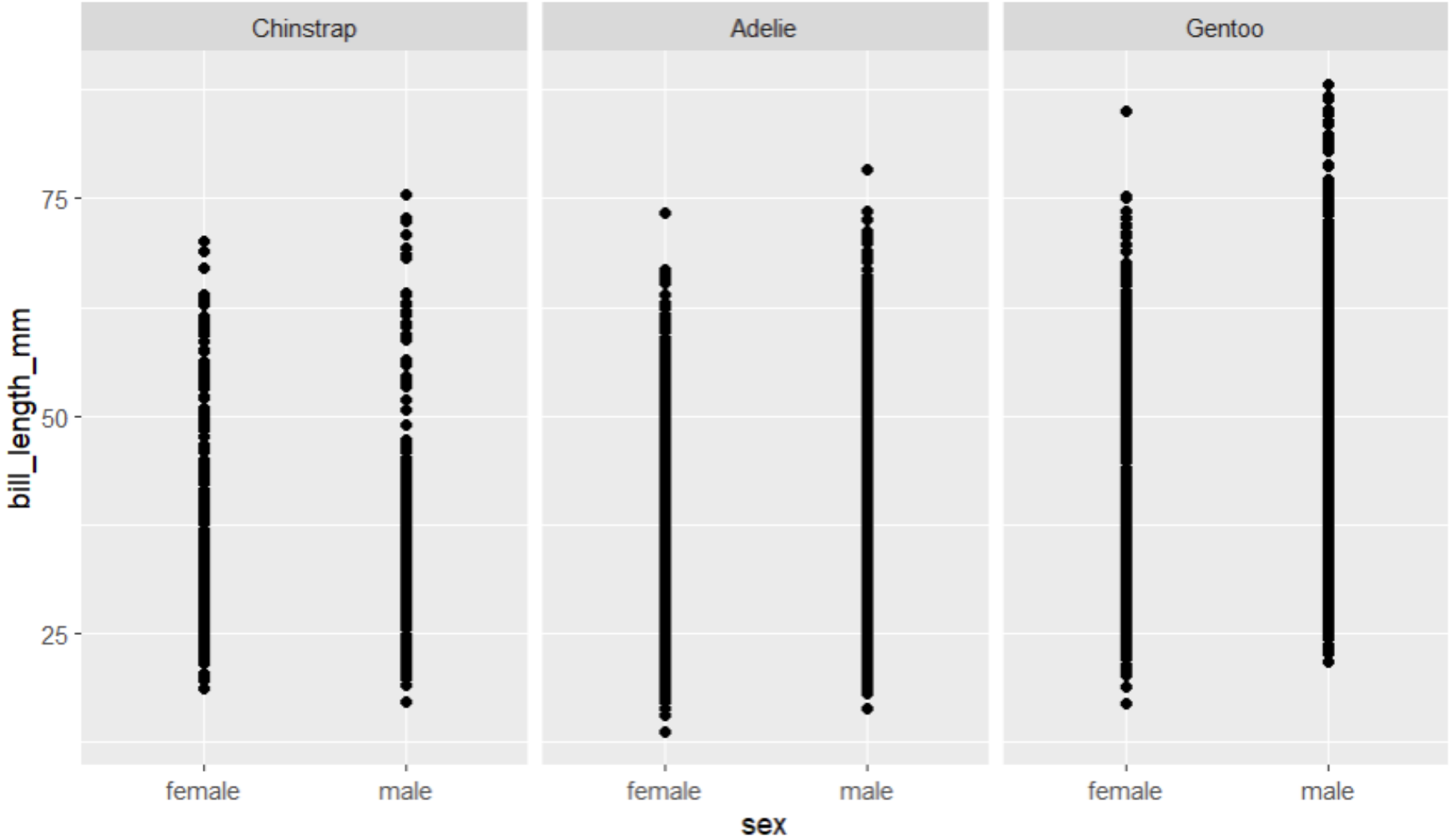
```
Call:
lm(formula = bill_length_mm ~ species, data = peng)

Residuals:
    Min      1Q  Median      3Q     Max
-27.362  -8.832  -3.215   7.538  44.038

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   35.0146     0.4996  70.079   <2e-16 ***
speciesAdelie  0.4170     0.5911   0.706    0.481
speciesGentoo  9.1473     0.6119  14.950   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 12.47 on 3427 degrees of freedom
Multiple R-squared:  0.1045,    Adjusted R-squared:  0.104
F-statistic: 200.1 on 2 and 3427 DF,  p-value: < 2.2e-16
```

Linear Regression Interpretation 3

```
Call:
lm(formula = bill_length_mm ~ body_mass_g, data = peng)

Residuals:
    Min      1Q  Median      3Q     Max
-29.134  -7.317  -0.517   6.759  36.037

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 6.4074805  0.6450241   9.934   <2e-16 ***
body_mass_g 0.0066441  0.0001288  51.598   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 9.886 on 3428 degrees of freedom
Multiple R-squared:  0.4371,    Adjusted R-squared:  0.437
F-statistic:  2662 on 1 and 3428 DF,  p-value: < 2.2e-16
```

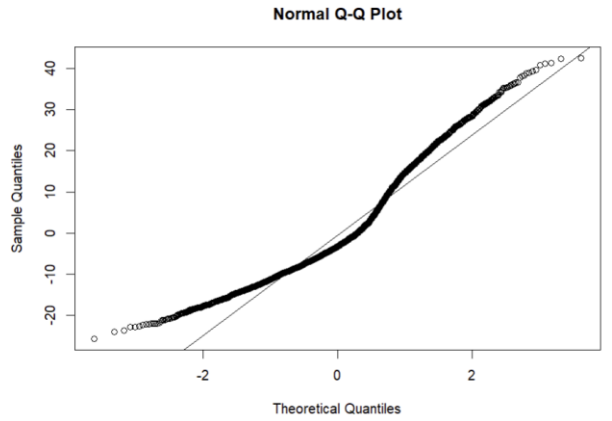


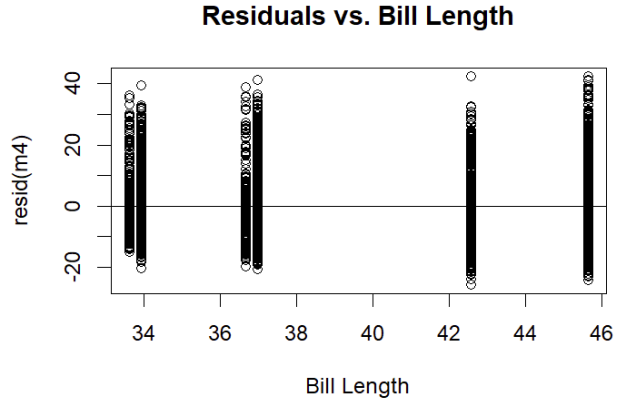
Bill Length by Species and Sex



Linear Regression Interpretation 4

```
Call:
lm(formula = bill_length_mm ~ sex + species, data = peng)

Residuals:
    Min      1Q  Median      3Q     Max
-25.770  -8.829  -3.281   7.609  42.571

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   33.6151     0.5324  63.140  < 2e-16 ***
sexmale        3.0593     0.4232   7.230 5.94e-13 ***
speciesAdelie  0.3065     0.5869   0.522    0.602
speciesGentoo  8.9546     0.6079  14.730  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 12.38 on 3426 degrees of freedom
Multiple R-squared:  0.118,     Adjusted R-squared:  0.1172
F-statistic: 152.8 on 3 and 3426 DF,  p-value: < 2.2e-16
```



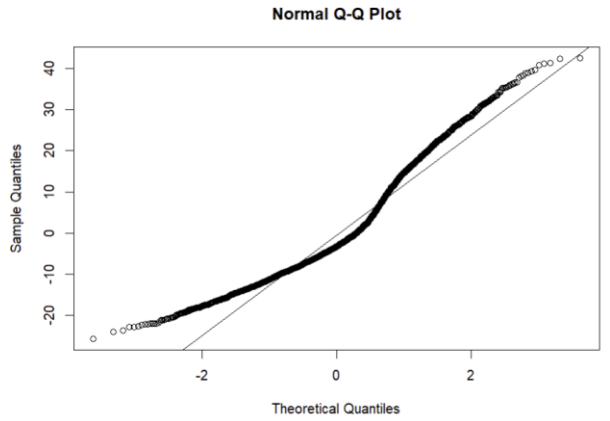


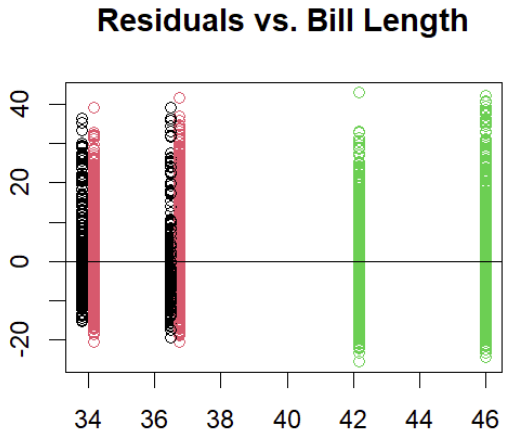
Exploring the Palmer Penguin Data

Is it possible that the difference in the bill length between females and males varies by species?

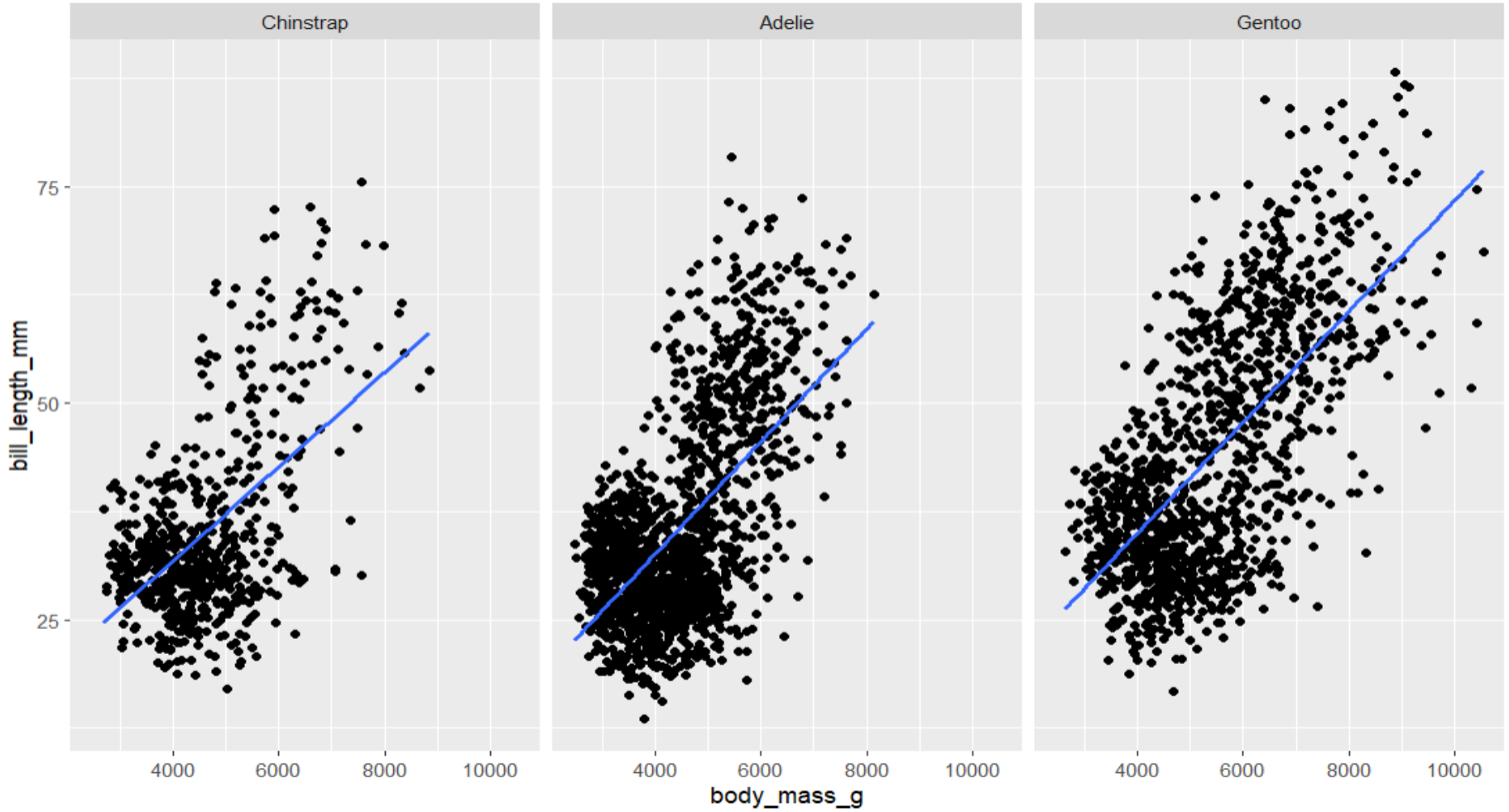
Linear Regression Interpretation 5

```
Call:
lm(formula = bill_length_mm ~ sex * species, data = peng)

Residuals:
    Min      1Q  Median      3Q     Max
-25.363  -8.939  -3.260   7.657  42.837

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)           33.7825     0.6733  50.173  < 2e-16 ***
sexmale                2.6932     0.9955   2.705  0.00686 **
speciesAdelie          0.3751     0.8046   0.466  0.64114
speciesGentoo          8.3807     0.8424   9.949  < 2e-16 ***
sexmale:speciesAdelie -0.1121     1.1764  -0.095  0.92407
sexmale:speciesGentoo  1.1471     1.2180   0.942  0.34635
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 12.38 on 3424 degrees of freedom
Multiple R-squared:  0.1185,    Adjusted R-squared:  0.1172
F-statistic: 92.06 on 5 and 3424 DF,  p-value: < 2.2e-16
```



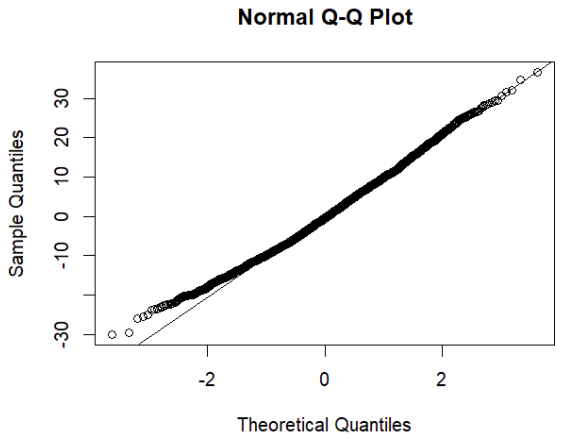


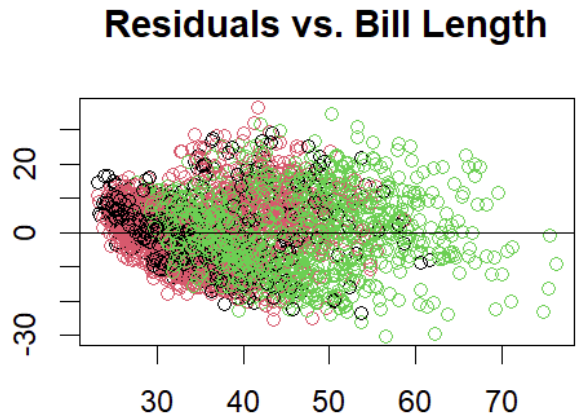
Species, Body Mass, and Bill Length



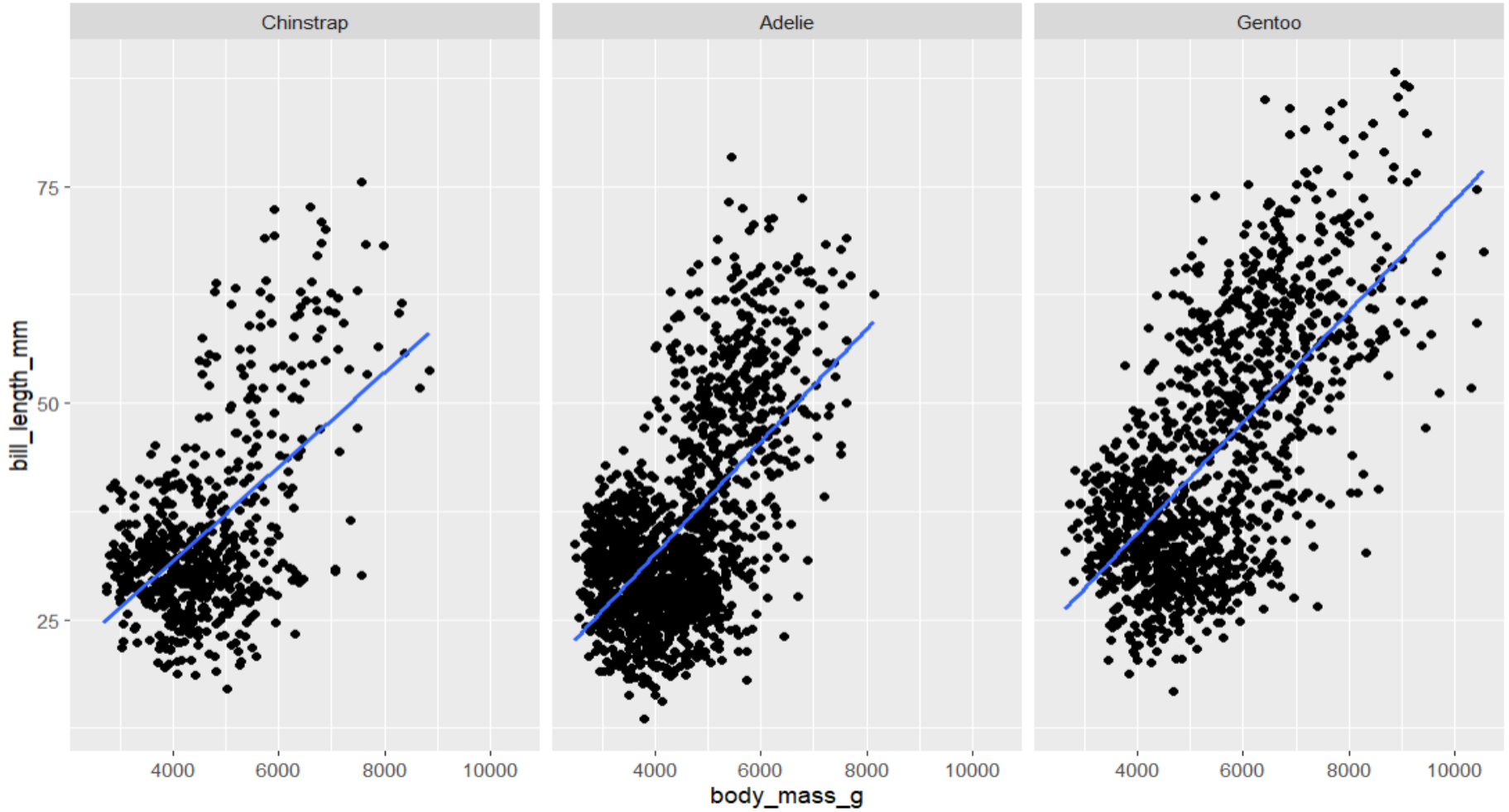
Linear Regression Interpretation 6

```
Call:
lm(formula = bill_length_mm ~ body_mass_g + species, data = peng)

Residuals:
    Min      1Q  Median      3Q     Max
-30.066  -7.172  -0.502   6.618  36.679

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)    6.0538147  0.7391125   8.191 3.63e-16 ***
body_mass_g    0.0062924  0.0001361  46.227  < 2e-16 ***
speciesAdelie  1.4052469  0.4643997   3.026   0.0025 **
speciesGentoo  3.8924911  0.4935059   7.887 4.11e-15 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 9.788 on 3426 degrees of freedom
Multiple R-squared:  0.4485,    Adjusted R-squared:  0.448
F-statistic: 928.8 on 3 and 3426 DF,  p-value: < 2.2e-16
```





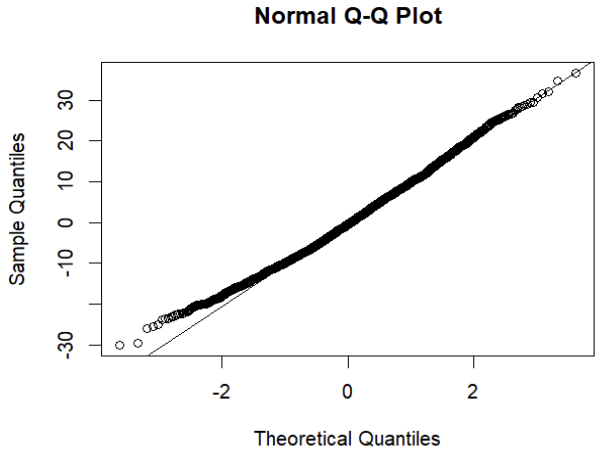
Species, Body Mass, and Bill Length

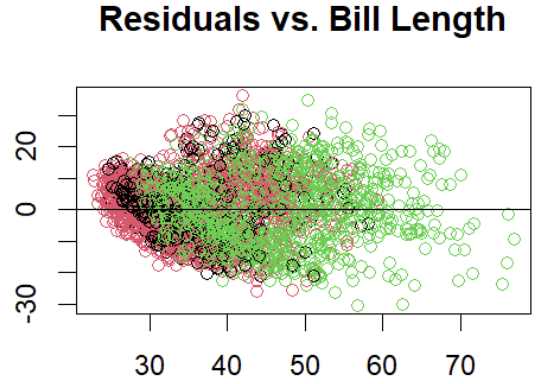


Species, Body Mass, and Bill Length Plotted Together

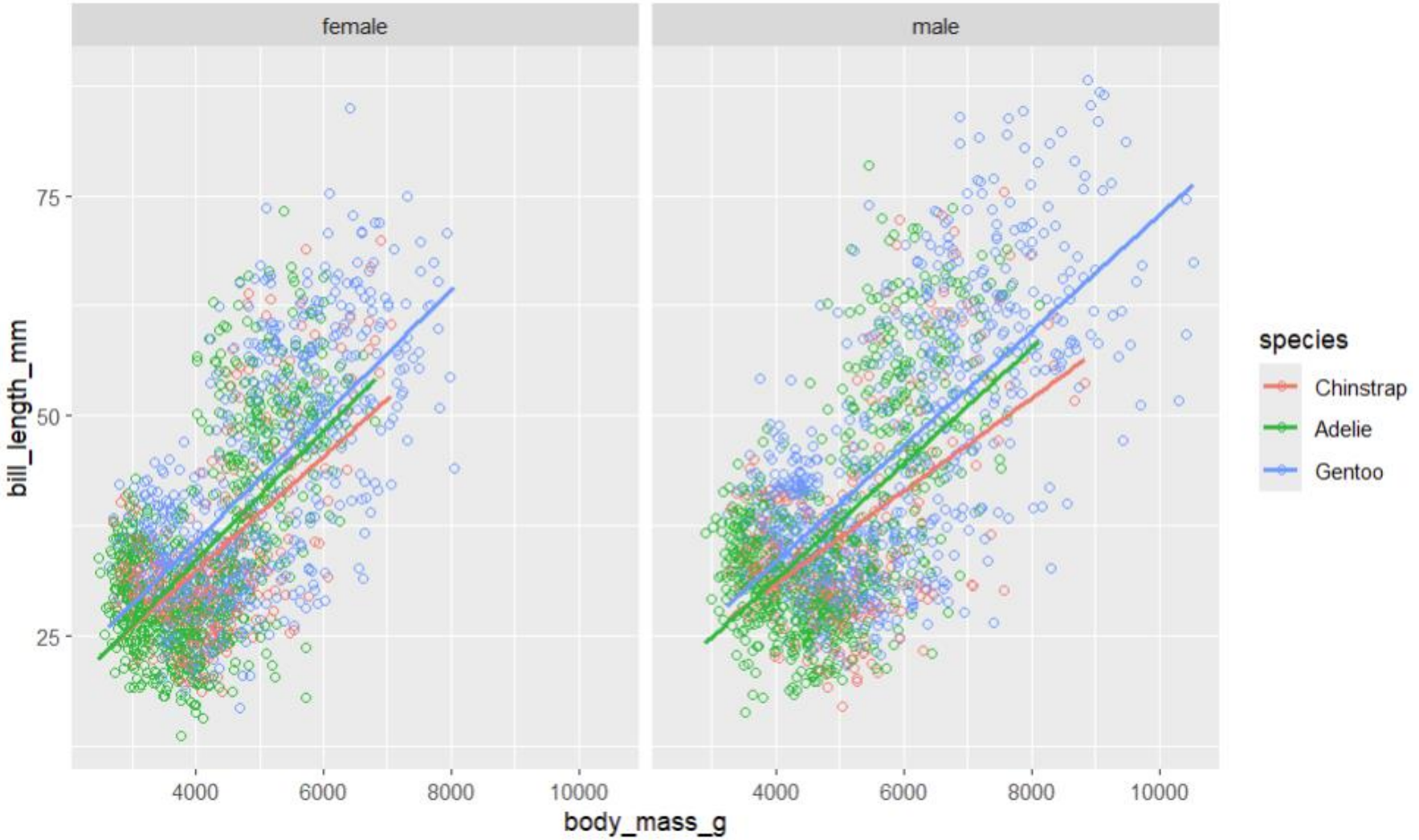
Linear Regression Interpretation 7

```
Call:
lm(formula = bill_length_mm ~ body_mass_g * species, data = peng)

Residuals:
    Min      1Q  Median      3Q     Max
-30.283  -7.176  -0.478   6.561  36.471

Coefficients:
                             Estimate Std. Error t value Pr(>|t|)
(Intercept)                10.0121114  1.6732204   5.984 2.41e-09 ***
body_mass_g                 0.0054323  0.0003534  15.370  < 2e-16 ***
speciesAdelie              -3.4802666  1.9832206  -1.755   0.0794 .
speciesGentoo              -0.6645410  1.9867524  -0.334   0.7380
body_mass_g:speciesAdelie   0.0010686  0.0004233   2.525   0.0116 *
body_mass_g:speciesGentoo   0.0009701  0.0004014   2.417   0.0157 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 9.781 on 3424 degrees of freedom
Multiple R-squared:  0.4497,    Adjusted R-squared:  0.4489
F-statistic: 559.5 on 5 and 3424 DF,  p-value: < 2.2e-16
```





Species, Body Mass, and Bill Length separated by Sex



Questions?