Ideas

- MLR, where we compare coeffcient importances.
  - Interpret the p-values of coefficients.
  - Why are some significant with some fits, and not significant with other fits.
- Problem of Multiple Comparisons (See CSCI3022 NB23 for example)

In [ ]:

Module 3: Peer Reviewed Assignment

Outline:

The objectives for this assignment:

1. Learn how to read and interpret p-values for coefficients in R.
2. Apply Partial F-tests to compare different models.
3. Compute confidence intervals for model coefficients.
4. Understand model significance using the Overall F-test.
5. Observe the variability of coefficients using the simulated data.

General tips:

1. Read the questions carefully to understand what is being asked.
2. This work will be reviewed by another human, so make sure that you are clear and concise in what your explanations and answers.

Problem 1: Individual t-tests

The dataset below measures the chewiness (mJ) of different berries along with their sugar equivalent and salt (NaCl) concentration. Let's use these data to create a model to finally understand chewiness.

Here are the variables:

1. `nacl` : salt concentration (NaCl)
2. `sugar` : sugar equivalent
3. `chewiness` : chewiness (mJ)

Dataset Source: I. Zouid, R. Siret, F. Jourjion, E. Mehinagic, L. Rolle (2013). "Impact of Grapes Heterogeneity According to Sugar Level on Both Physical and Mechanical Berries Properties and their Anthocyanins Extractability at Harvest," Journal of Texture Studies, Vol. 44, pp. 95-103.

1. (a) Simple linear regression (SLR) parameters

In the below code, we load in the data and fit a SLR model to it, using `chewiness` as the response and `sugar` as the predictor. The summary of the model is printed. Let $\alpha = 0.05$.

Look at the results and answer the following questions:

- What is the hypothesis test related to the p-value `2.95e-09` ? Clearly state the null and alternative hypotheses and the decision made based on the p-value.
- Does this mean the coefficient is statistically significant?
- What does it mean for a coefficient to be statistically significant?

In [2]:
```
library(RCurl) #a package that includes the function getURL(), whic
h allows for reading data from github.
library(ggplot2)
url = getURL(paste0("https://raw.githubusercontent.com/bzaharatos
/",
                    "-Statistical-Modeling-for-Data-Science-Applica
tions/",
                    "master/Modern%20Regression%20Analysis%20/Datas
ets/berry_sugar_chewy.csv"))
chew.data = read.csv(text = url, sep = ",")

chew.lmod = lm(chewiness~sugar, data=chew.data)
summary(chew.lmod)
```

```
Loading required package: bitops
Registered S3 methods overwritten by 'ggplot2':
  method         from
  [.quosures     rlang
  c.quosures     rlang
  print.quosures rlang

Call:
lm(formula = chewiness ~ sugar, data = chew.data)

Residuals:
    Min      1Q  Median      3Q     Max
-2.4557 -0.5604  0.1045  0.5249  1.9559

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.662878   0.756610  10.128  < 2e-16 ***
sugar       -0.022797   0.003453  -6.603 2.95e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.9178 on 88 degrees of freedom
Multiple R-squared:  0.3313,    Adjusted R-squared:  0.3237
F-statistic: 43.59 on 1 and 88 DF,  p-value: 2.951e-09
```

- the hypothesis test related to the p-value `2.95e-09` is the full F-test. The null hypothesis is $H_0 : Y = \beta_0 + \varepsilon$; the alternative is $H_1 : \text{Some predictor is necessary.}$. The p-value is less than $\alpha = 0.05$, which means that we have some evidence against the null hypothesis.
- In the case of simple linear regression, this does mean that the parameter associated with sugar is statistically significant.
- A cofficient is statistically significant if the t-test associated with that coefficient has a p-value that is less than or equal to the pre-specified α. This suggests that, under the null hypothesis (if there is no relationship between chewiness and sugar), the data we observed or data more extreme would be very rare.

1. (b) MLR parameters

Now let's see if the second predictor/feature `nacl` is worth adding to the model. In the code below, we create a second linear model fitting `chewiness` as the response with `sugar` and `nacl` as predictors.

Look at the results and answer the following questions:

- Which, if any, of the slope parameters are statistically significant?
- Did the statistical significance of the parameter for `sugar` stay the same, when compared to 1 (a)? If the statistical signficance changed, explain why it changed. If it didn't change, explain why it didn't change.

In [11]:
```
chew.lmod.2 = lm(chewiness ~ ., data=chew.data)
summary(chew.lmod.2)
```

```
Call:
lm(formula = chewiness ~ ., data = chew.data)

Residuals:
    Min      1Q  Median      3Q     Max 
-2.3820 -0.6333  0.1234  0.5231  1.9731 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -7.1107    13.6459  -0.521    0.604
nacl          0.6555     0.6045   1.084    0.281
sugar        -0.4223     0.3685  -1.146    0.255

Residual standard error: 0.9169 on 87 degrees of freedom
Multiple R-squared:  0.3402,    Adjusted R-squared:  0.325 
F-statistic: 22.43 on 2 and 87 DF,  p-value: 1.395e-08
```

- None of the parameters of the model are statistically significant.
- The statistical significance of the parameter for `sugar` did not stay the same, when compared to 1 (a). It changed because a second predictor was added to the model, changing the variability in y being explained by the structural part of the model.

Note that the main issue with these data are that `sugar` and `nacl` are highly correlated (see the correlation matrix for the model matrix below) . This creates a serious problem for estimating the model parameters. One indication of the problem is that both t-tests are statistically insignificant but the full F-test is statistically significant. This problem is called collinearity and is explored in a later module.

In [10]:
```
cor(model.matrix(chew.lmod.2)[,-1])
```

	nacl	sugar
nacl	1.0000000	0.9999562
sugar	0.9999562	1.0000000

1. (c) Model Selection

Determine which of the two models we should use. Explain how you arrived at your conclusion and write out the actual equation for your selected model.

```
In [12]: anova(chew.lmod, chew.lmod.2)
```

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
88	74.12640	NA	NA	NA	NA
87	73.13801	1	0.9883882	1.175719	0.2812249

Based on the full F-test, the simple linear regression model should be used.

1. (d) Parameter Confidence Intervals

Compute 95% confidence intervals for each parameter in your selected model. Then, in words, state what these confidence intervals mean.

```
In [13]: confint(chew.lmod)
```

	2.5 %	97.5 %
(Intercept)	6.15927388	9.16648152
sugar	-0.02965862	-0.01593536

Problem 2: Variability of Slope in SLR

In this exercise we'll look at the variability of slopes of simple linear regression models fitted to realizations of simulated data.

Write a function, called `sim_data()`, that returns a simulated sample of size $n = 20$ from the model $Y = 1 + 2.5X + \epsilon$ where $\epsilon \overset{iid}{\sim} N(0, 1)$. We will then use this generative funciton to understand how fitted slopes can vary, even for the same underlying population.

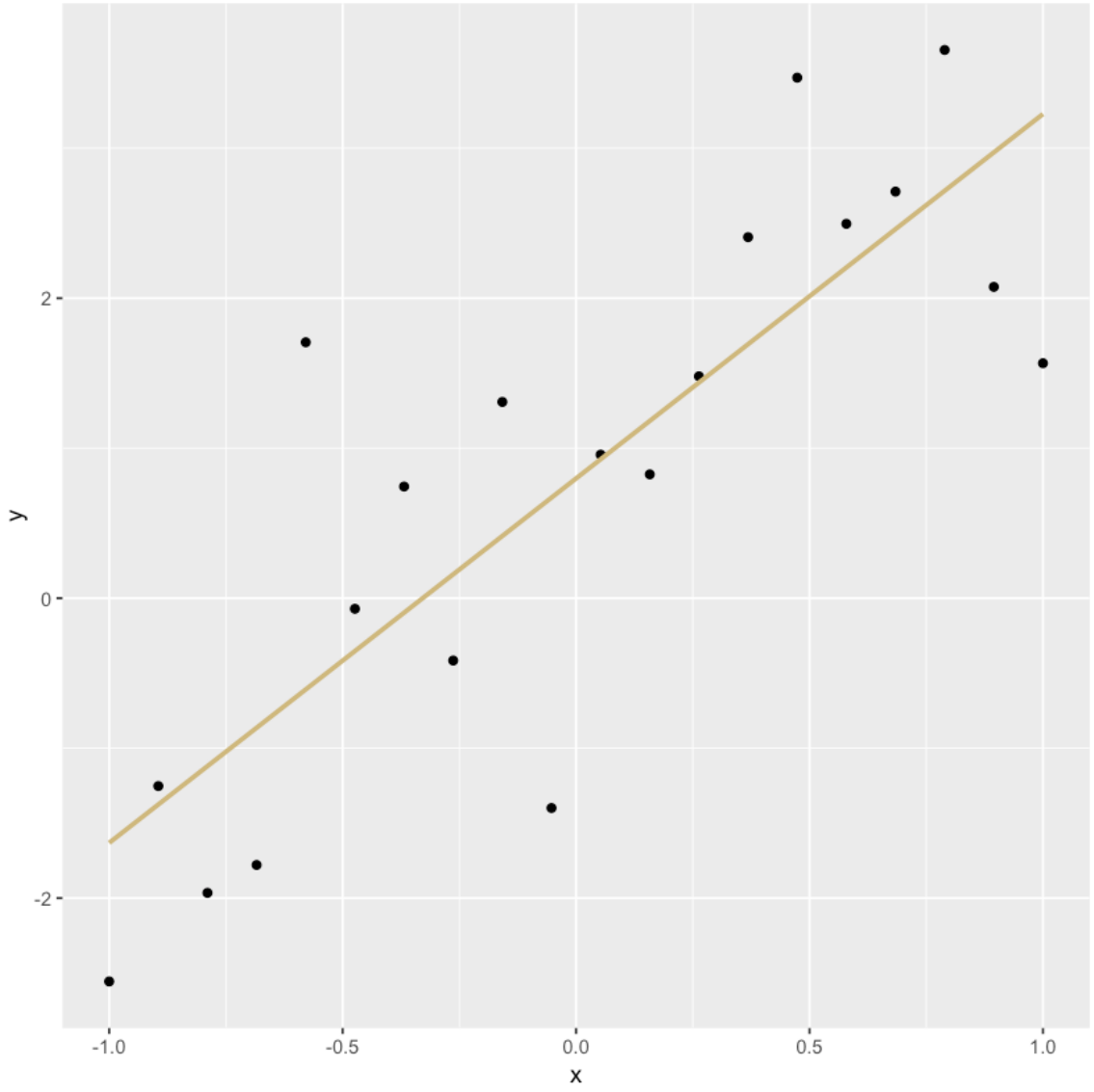
In [43]:
```
sim_data <- function(n=20, var=1, beta.0=1, beta.1=2.5){
    # BEGIN SOLUTION HERE
    x = seq(-1, 1, length.out = n); beta0 = 1; beta1 = 2.5; e = rno
rm(n, 0, sqrt(var))
    y = beta0 + beta1*x + e
    # END SOLUTION HERE
    data = data.frame(x=x, y=y)
    return(data)
}
```

2. (a) Fit a slope

Execute the following code to generate 20 data points, fit a simple linear regression model and plot the results.

Just based on this plot, how well does our linear model fit the data?

In [44]:
```
data = sim_data()
lmod = lm(y~x, data=data)
ggplot(aes(x=x, y=y), data=data) +
    geom_point() +
    geom_smooth(method="lm", formula=y~x, se=FALSE, color="#CFB87
C")
```



The model appears to fit the data reasonably well!

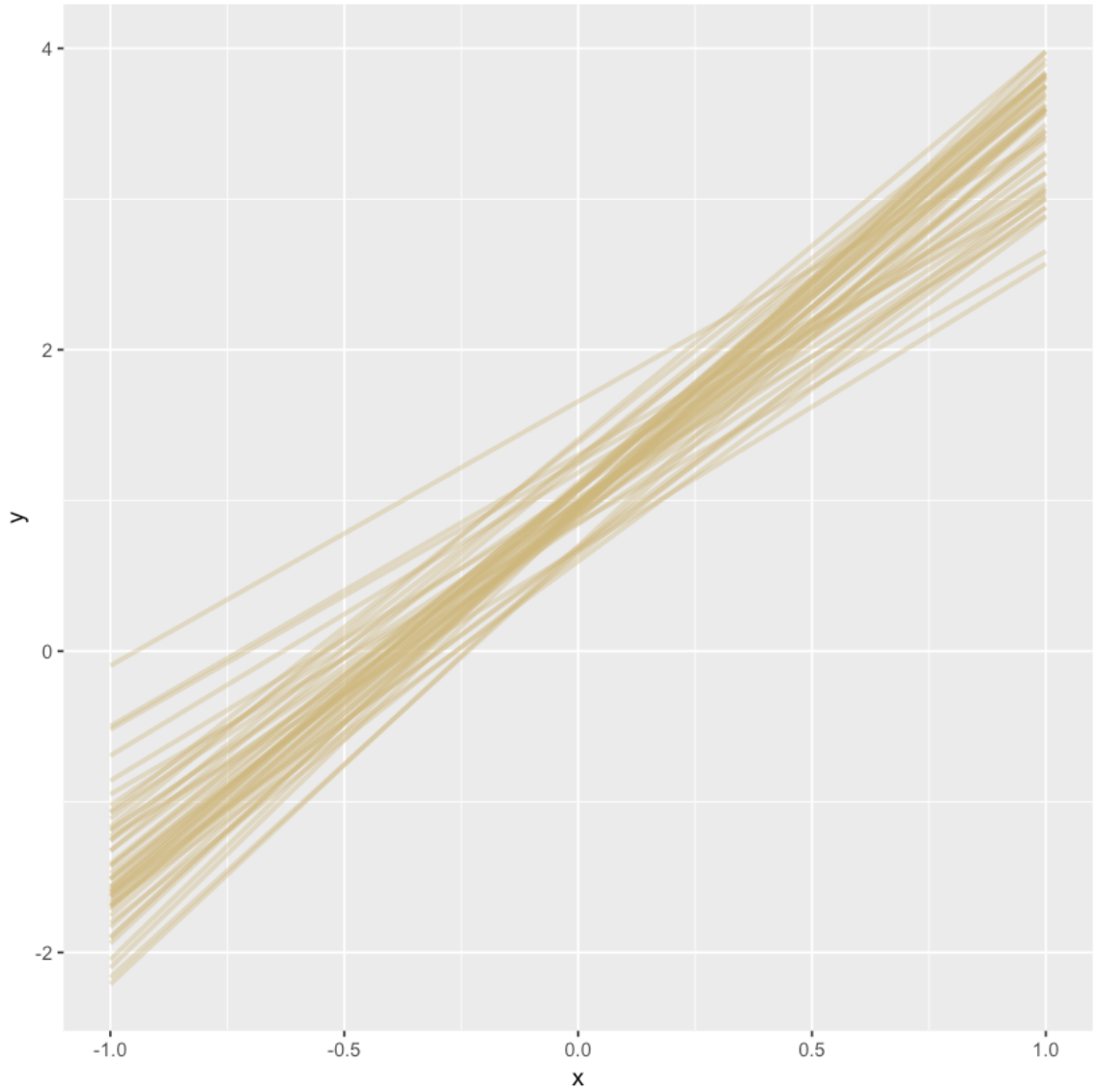
2. (b) Do the slopes change?

Now we want to see how the slope of our line varies with different random samples of data. Call our data genaration funciton 50 times to gather 50 independent samples. Then we can fit a SLR model to each of those samples and plot the resulting slope. The function below performs this for us.

Experiment with different variances and report on what effect that has to the spread of the slopes.

In [51]:
```
gen_slopes <- function(num.slopes=50, var=1, num.samples=20){
    g = ggplot()
    # Repeat the sample for the number of slopes
    for(ii in 1:num.slopes){
        # Generate a random sampling of data
        data = sim_data(n=num.samples, var=var)
        # Add the slope of the best fit linear model to the plot
        g = g + stat_smooth(aes(x=x, y=y), data=data, method="lm",
geom="line",
                            se=FALSE, alpha=0.4, color="#CFB87C", s
ize=1)
    }
    return(g)
}
```

In [52]:
```
gen_slopes()
```



As σ^2 increases, so does the variability in the slope terms.

2. (c) Distributions of Slopes

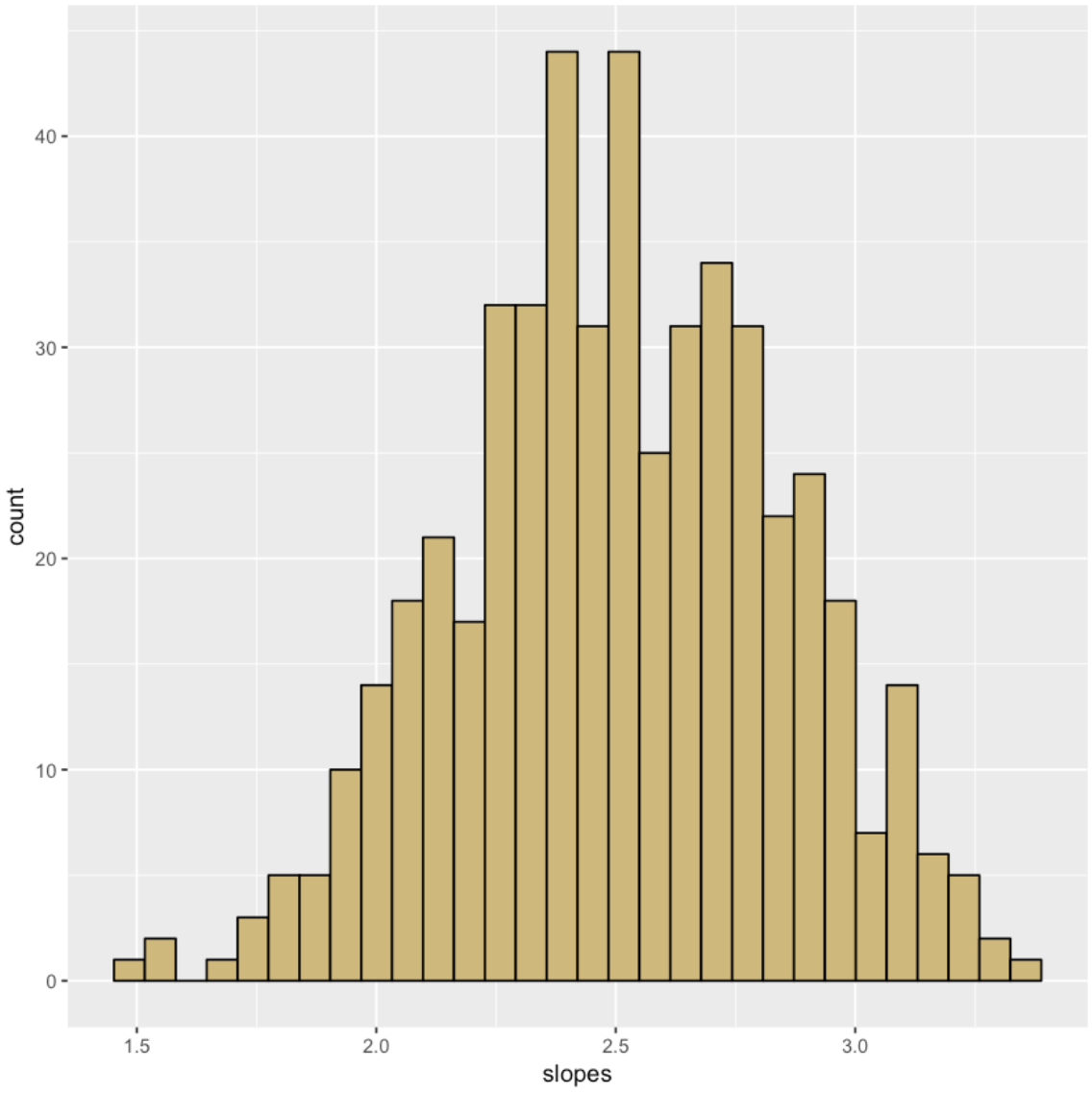
As we see above, the slopes are somewhat random. That means that they follow some sort of distribution, which we can try to discern. The code below computes `num_samples` independent realizations of the model data, computes the SLR model, and generates a histogram of the resulting slopes.

Again, experiment with different variances for the simulated data and record what you notice. What do you notice about the shapes of the resulting histograms?

In [60]:
```
hist_slopes <- function(num.slopes=500, var=1, num.samples=20){
    slopes = rep(0, num.slopes)
    # For num.slopes, compute a SLR model slope
    for(i in 1:num.slopes){
        # Simulate the desired data
        data = sim_data(var=var, n=num.samples)
        # Fit an SLR model to the data
        lmod = lm(y~x, data=data)
        # Add the slopes to the vector of slopes
        slopes[i] = lmod$coef[2]
    }
    # Plot a histogram of the resulting slopes
    g = ggplot() + aes(slopes) + geom_histogram(color="black", fill
="#CFB87C")
    return(g)
}
```

In [61]:
```
hist_slopes()
```

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



The histograms are *roughly* bell shaped. As σ^2 increases, so does the width of the bell curve.

2. (d) Confidence Intervals of Slopes

What does that all mean? It means that when we fit a linear regression model, our parameter *estimates* will not be equal to the true parameters. Instead, the estimates will vary from sample to sample, and form a distribution. This is true for any linear regression model with any data - not just simulated data - as long as we assume that there is a large population that we can resample the response from (at fixed predictor values). Also note that we only demonstrated this fact with the slope estimate, but the same principle is true for the intercept, or if we had several slope parameters.

This simulation shows that there is a chance for a linear regression model to have a slope that is very different from the true slope. But with a large sample size, n, or small error variance, σ^2, the distribution will become narrower. Confidence intervals can help us understand this variability. The procedure that generates confidence intervals for our model parameters has a high probability of covering the true parameter. And, the higher n is, for a fixed σ^2, or the smaller σ^2 is, for a fixed n, the narrower the confidence interval will be!

Draw a single sample of size $n = 20$ from `sim_data()` with variance $\sigma^2 = 1$. Use your sample to compute a 95% confidence interval for the slope. Does the known slope for the model (which we can recall is 2.5) fall inside your confidence interval? How does the value of σ^2 affect the CI width?

In [65]:
```
df = sim_data(var = 1)
lm_sim = lm(y ~ x, data = df)
confint(lm_sim)
```

	2.5 %	97.5 %
(Intercept)	0.5203094	1.515409
x	1.6084691	3.247904

Yes, the known slope falls within the confidence interval, which we expect to happen in 95% of the simulations. If we increase σ^2, we will increase the width of the CI.