Parametric Shortcut: One-way ANOVA

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In this tutorial, we are going to explore using R to fit a One-way ANOVA model to two data sets using the parametric shortcut known as the One-way ANOVA F Test.

I'll be interweaving a couple of different examples throughout the text. The general structure to this tutorial is:

- Setting up `R` and Reading in Data
  - Loading Packages
  - Setting Options
  - Set Our Side Condition/Constraint
  - Loading Data
- Explore Your Data
- Discussion on whether ANOVA methods are appropriate
  - Incorporating Hasse diagrams
- Fitting the ANOVA Model
- Assessing the Assumptions of the Parametric Shortcut for One-way ANOVA
- Conducting the Omnibus Test
  - Pre-look decisions
  - Quick Look at Results
  - Making Professional Looking Tables
  - Interpreting Results
- Reporting Point Estimates
  - Formatting
  - Interpretations

Setting Up `R` and Reading in Data

There are two parts to this portion of the tutorial: getting `R` in order and reading in the data. If you are already familiar with these activities, you can skip ahead. HOWEVER, make sure you check out the code for setting up our constraint.

Getting `R` Ready

The first thing that we need to do is ensure that `R` is set up so that we can have success. For this particular tutorial, we will be using the following packages: `tidyverse`, `hasseDiagram`, `knitr`, `kableExtra`, `car`, `psych`, and `parameters`. You can load these packages into your session by running the following code in the Console or by placing this code into a code chunk in your R Markdown file:

```
# Demo code for loading packages for the tutorial
packages <- c("tidyverse", "hasseDiagram", "knitr",
              "kableExtra", "car", "psych", "parameters")
lapply(packages, library, character.only = TRUE)
```

Specifying R Options

While there are many options we can set, two options are particularly useful to set at the start: table formatting and on model constraint.

Table Formatting

To make professional looking tables in a R Markdown file, I recommend using the **knitr** and **kableExtra** packages. One thing to keep in mind is that by default, R does not like truly empty table cells (typically printing "NA"). Thus, to keep our tables as uncluttered as possible, we need to instruct R to leave empty table cells visually empty. We can do this with the following code:

```
# Demo code for controlling table options
# Tell Knitr to use empty space instead of NA in printed tables
options(knitr.kable.NA = "")
```

I typically place this code right after I load my packages.

Set Our Constraint

Recall that in order to ensure that we have estimable functions, we must set a side condition or constraint on our treatments:

$$\sum_{i}^{k} \alpha_i = 0$$

This is not what R does by default, but we can tell R to adopt this constraint with the following code:

```
## Demo code for setting the constraint
options(contrasts = c("contr.sum", "contr.poly"))
```

Again, I place this just after I set my table options. NOTE: you have to specify this option BEFORE you build any models in R.

Some Additonal Handy Tools

Over the years I have created some additional tools which can be useful as you perform ANOVA analyses. To access them, you must first load them into your R session/R Markdown document:

```
# Demo code for loading Neil's extra tools
source("https://raw.github.com/neilhatfield/STAT461/master/rScripts/ANOVATools.R")
```

This is typically the last line of code in my first code chunk of any R Markdown file for ANOVA.

Load Data

Once you have set the R options, now comes reading in data. For this tutorial, we're going to work with three different data sets: our Song Knowledge data, data from a honey study, and data from Example 3.2 Resin Lifetimes from the Oehlert textbook.

The following code demonstrates how we can read in the three data sets:

```
# Song Data
songData <- read.csv(
  file = "https://raw.github.com/neilhatfield/STAT461/master/dataFiles/songKnowledge2022.csv",
  header = TRUE,
  sep = ","
```

```
)
# Set year to an ordered factor
songData$year <- factor(
  x = songData$year,
  levels = c("sophomore", "junior", "senior")
)

# Honey Data--Manual Entry
honey <- data.frame(
  Amount = c(150, 50, 100, 85, 90, 95, 130, 50, 80),
  Varietal = rep(c("Clover", "Orange Blossom", "Alfalfa"), each = 3)
)
## Set Varietal to factor (no particular order)
honey$Varietal <- as.factor(honey$Varietal)

# Resin Lifetimes Data
resin <- read.table(
  file = "https://raw.github.com/neilhatfield/STAT461/master/dataFiles/resinLifetimes.dat",
  header = TRUE,
  sep = "" # Notice the change in separator
)
## Set temp to factor
resin$temp <- as.factor(resin$temp)

## Change the name of the y column to something more meaningful
names(resin)[which(names(resin) == "y")] <- "log10Lifetime"
```

Explore Your Data

At this point in time, you should engage in exploratory data analysis including creating professional looking data visualizations (I recommend using `ggplot2`) as well as looking at descriptive statistics by groups (I recommend using `psych`). For more details on both of these topics, see the starting guides for Data Visualizations and Descriptive Statistics I've posted.

Is ANOVA Even Appropriate?

Recall the base requirements for One-way ANOVA are:

- From Unit 2
  - you are working with a qualitative/categorical factor,
  - you are working with a quantitative response,
- From Unit 3
  - you are working with an additive model,
  - you have estimable effects, and
  - you have estimable errors/residuals.

The first two requirements (from Unit 2) you can check quickly in `R` by using the `str` ("structure") function or by clicking on the blue circle with a white triangle to the left of each data frame's name in the Environment tab of R Studio. This is ***not*** something that you put into any reports. Rather, this is something you should check for yourself. In essence, this is to make sure `R` is thinking about your data in the same way that you are.

```
# Checking the first two base requirements
str(songData)
```

```
## 'data.frame':    15 obs. of  2 variables:
##  $ year : Factor w/ 3 levels "sophomore","junior",..: 1 1 1 1 1 2 2 2 2 2 ...
##  $ score: int  2 9 8 5 10 10 12 9 5 9 ...
```

```
str(honey)
```

```
## 'data.frame':    9 obs. of  2 variables:
##  $ Amount  : num  150 50 100 85 90 95 130 50 80
##  $ Varietal: Factor w/ 3 levels "Alfalfa","Clover",..: 2 2 2 3 3 3 1 1 1
```

```
str(resin)
```

```
## 'data.frame':    37 obs. of  2 variables:
##  $ temp         : Factor w/ 5 levels "175","194","213",..: 1 1 1 1 1 1 1 1 2 2 ...
##  $ log10Lifetime: num  2.04 1.91 2 1.92 1.85 1.96 1.88 1.9 1.66 1.71 ...
```

What we want to see is that for our factor(s), `R` has the word "`Factor`" immediately after their (column) name. For our response, we want to see either "`num`" or "`int`" after their (column) name. If we see these AND they match our expectations of the data, then we can say that we've met these two requirements.

The last three base requirements (from Unit 3) stem from the Hasse diagram. Essentially, if you can build the Hasse diagram and have positive (i.e., non-zero and non-negative) degrees of freedom everywhere, then all three of these are satisfied.

Hasse diagrams can be included in your reports. The following is an example for how we might do so with the Honey study. For putting Hasse diagrams into your R Markdown files, I recommend using the Hasse Diagram App and copying the `R` code generated there.

Hasse Diagram Example-Honey Study

In investigating the effect of the type of varietal (species of flower) has on the production of excess honey, we constructed the Hasse diagram in Figure 1. With our nine hives of the same species of bee, we can see that we have sufficient degrees of freedom to estimate the effects for our three levels of varietal and have degrees of freedom for our error term. Given that we're measuring our response (excess honey) in pounds, along with the additive model shown in Figure 1, a one-way ANOVA model is a valid approach.

```
# DEMO CODE

# Hasse Diagram for the Honey Study
modelLabels <- c("1 Make Honey 1", "3 Varietal 2", "9 (Hives) 6")
modelMatrix <- matrix(
  data = c(FALSE, FALSE, FALSE, TRUE, FALSE, FALSE, TRUE, TRUE, FALSE),
  nrow = 3,
  ncol = 3,
  byrow = FALSE
)
hasseDiagram::hasse(
 data = modelMatrix,
 labels = modelLabels
)
```

Your Turn

Try creating the code (either on your own or via the app) for the Hasse diagrams for the Song Knowledge and the Resin Lifetime studies (see p. 32 of Oehlert).

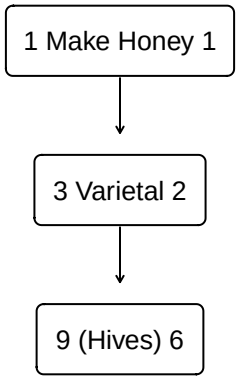


Figure 1: Hasse Diagram for Honey Study

Fit the ANOVA Model

In order to check out the assumptions of the Parametric Shortcut (a.k.a. "the ANOVA F Test"), we first need to fit the ANOVA model in `R`. This will enable us to access the residuals in an easy way. I must give a word of caution here: don't look at the results of the model just yet. You must first assess all of the assumptions so that you can build your trust in the results.

To fit our ANOVA model, we will primarily use the `aov` function that is part of base `R`. (You can also use the `lm` function with the same arguments.) We will want to save our model to a named object so that we can call them at later times. Here is how we would build/fit the model:

```
# Demo code for building ANOVA models
## Song Knowledge study
songModel <- aov(
  formula = score ~ year,
  data = songData,
  na.action = "na.omit"
)

## Honey study
honeyModel <- aov(
  formula = Amount ~ Varietal,
  data = honey,
  na.action = "na.omit"
)

## Resin Lifetime study
resinModel <- aov(
  formula = log10Lifetime ~ temp,
  data = resin,
  na.action = "na.omit"
)
```

Notice that in all three examples, we used the same three arguments to `aov`: `formula`, `data`, and `na.action`.

- The `formula` argument is how we express our model. In essence, you put in all of our factors/terms. `R` automatically knows to account for the first and last nodes of our Hasse diagrams (the action screen and measurement units).
  - The structure of the formulas are `responseName ~ factorName` for one-way ANOVA.
- The `data` argument is where you tell `aov` the name of the data frame you want to use.
- The `na.action` argument is a safety precaution. You are instructing `R` that if there is an observation with missing values, then `R` is to omit that observation from the model. (You may leave this argument off if you desire and are willing to run the risk of problems.)

Assessing Assumptions

Before we look at the results of fitting the ANOVA model, we must first assess the assumptions. `R` automatically does the parametric shortcut test when we call the results of fitting the model–regardless of whether the parametric shortcut is actually valid. Thus, we need to be convinced that we've met the assumptions of the test well enough to trust the results.

For the parametric shortcut (a.k.a. "the ANOVA F test"), there are three assumptions:

1) Our residuals need to follow a Gaussian distribution,
2) We have homoscedasticity among the residuals, and
3) We have Independent Observations

For the first two assumptions, we will need to access the residuals from our model. We can do this in two different ways: `songModel$residuals` or `residuals(honeyModel)`. Either method will give the same set of things.

Remember, we want to ***assess not test*** our assumptions. Thus, we will be relying on specific data visualizations (and some descriptive statistics) to help us. All of which can go into your reports.

Assessing the Gaussian Assumption

The first assumption is that our residuals follow a Gaussian ("normal") distribution, A QQ plot is the tool of choice; one of the better versions of this plot comes from the `car` package. The following code demonstrates creating QQ Plots for the Song Knowledge and Honey studies:

```
# Demo code for making QQ plots
## Chunk options for side-by-side plots
### fig.show="hold", out.width="100%", fig.height=3.5
## R option for side-by-side plots
par(mfrow = c(1,2), mar = c(4, 4, 0.1, 0.1))

## Song Knowledge study
car::qqPlot(
  x = songModel$residuals,
  distribution = "norm",
  envelope = 0.90,
  id = FALSE,
  pch = 20,
  ylab = "Residuals"
)

# QQ plot for Honey Residuals
car::qqPlot(
  x = residuals(honeyModel),
  distribution = "norm",
  envelope = FALSE,
  id = TRUE,
  pch = 1,
  ylab = "Residuals"
)
```

```
## [1] 2 1
```

You'll notice that in the `qqPlot` function there are several arguments that allow you to customize the plots. The two arguments that are required are `x` (where you'll call the residuals) and `distribution` (where you will use `"norm"`).

The `id`, `pch`, and `ylab` arguments are meant to improve the visual display of the graph.

- The `id` argument will label the two points with the most extreme vertical distances from the solid blue reference line. These labels can be distracting, thus I recommend using `id = FALSE`.

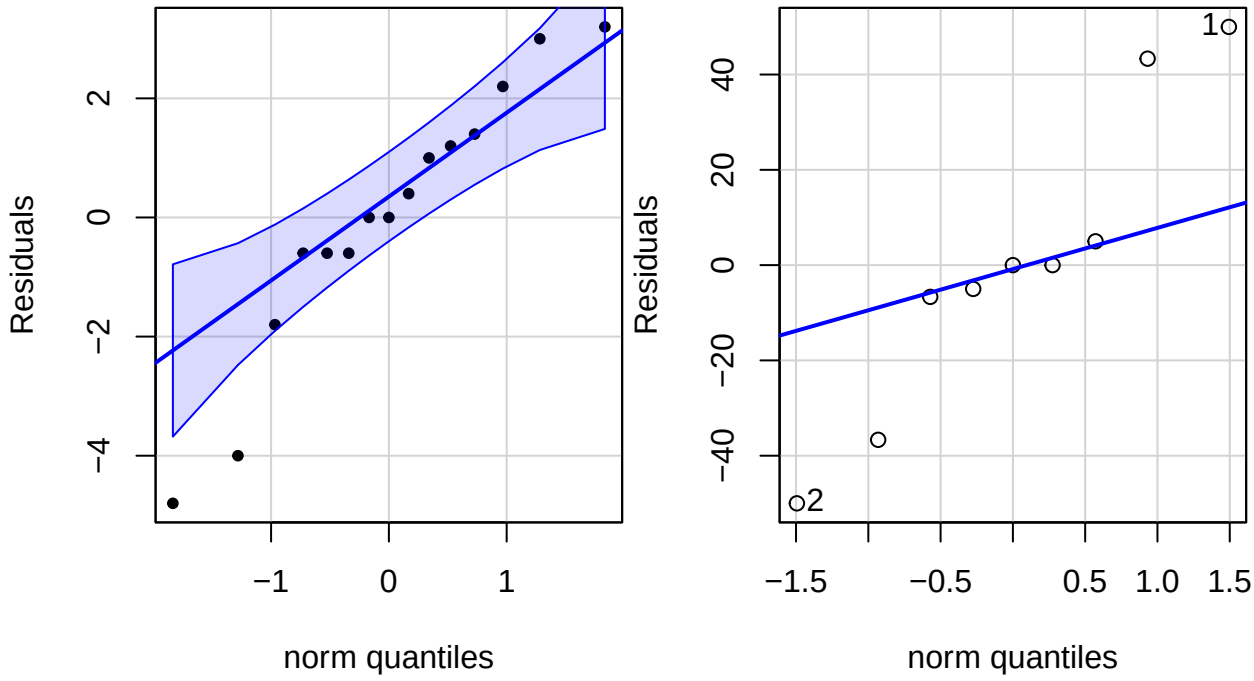


Figure 2: QQ Plot Residuals for Song Knowledge (left) and Honey (right) Studies

  - You'll also notice that there is an errant `## [1] 2 1` in this document. This is consequence of setting `id = TRUE`. And will not make your reports look professional.

- The `pch` (plotting character) controls the type of dot used. The default value is 1 for an open circle; solid dots are typically better. Thus, you'll want to use `pch = 19` or `pch = 20` for solid dots; the 19 version is slightly larger in size than 20.
- The `ylab` is a way to make the label for the vertical axis a bit nicer. You can use `ylab = "Residuals"` for your plots.

The `envelope` argument is particularly useful when assessing the Gaussian assumption for ANOVA. To turn off the envelope you use `envelope = FALSE`. To add the envelope, you used `envelope = num` where `num` is your chosen confidence level such as 0.90 for the Song Knowledge context. This helps in our assessment as any points that are away from the line but yet still inside the envelope aren't of much concern. This lets us focus on residuals which are truly far from the blue reference line. The level of confidence we use has a direct impact on how concerned we should be for violations of the Gaussian assumption. For 90%, then we are okay with at most ~10% of the observed residuals being outside the envelope. This decision banks upon us capitalizing that balanced designs have moderate robustness to violating the Gaussian assumption.

For the Song Knowledge QQ Plot (left of Figure 2), we can see that 2 residuals are outside the envelope; 2 is close enough to 10% of 15 (i.e., 1.5) for us to proceed (perhaps cautiously) with the Gaussian assumption being satisfied.

Take a look that the QQ Plot for the Honey Study (right of Figure 2). How would you judge the Gaussian assumption? Notice that the lack of envelope makes the judgement a bit harder. However, we can note that there are four observations (out of 9) whose residuals are quite far from the blue reference line. This suggests that our residuals do not follow a Gaussian distribution.

Your Turn

Try replicating the QQ plot code for the Resin Lifetime study. How would you assess the Gaussian assumption?

Secondary Tool

Another tool that you can use for assessing the Gaussian assumption are two descriptive statistics: *Sample Skewness* and *Sample Excess Kurtosis*. These are generated by the `psych` package's `describe` function (i.e., `psych::describe(songModel$residuals)`. You can also call them directly with `psych::skew(songModel$residuals)` and `psych::kurtosi(songModel$residuals)`. Ideally, we want the value of *Sample Skewness* and *Sample Excess Kurtosis* to be as close to zero as possible.

For the Song Knowledge context, the value of *Sample Skewness* is -0.6 and the value of *Sample Excess Kurtosis* is -1.17. These values are questionable but when partnered with the QQ plot and our knowledge of the study design, they are cautiously acceptable.

For the Honey study, the value of *Sample Skewness* is 0.11 and the value *Sample Excess Kurtosis* is -1.17. Using these values in conjunction with the QQ plot re-affirms that we should question whether we've satisfied the Gaussian assumption with the honey data.

Assessing Homoscedasticity

The second assumption for the parametric shortcut is that of homoscedasticity. This assumption deals with there being the same or similar amounts of variation within each group. For this assumption, you can make use of the values of the *Sample Arithmetic Standard Deviation* or *Sample Arithmetic Variance* IF you are looking by groups. The `describeBy` function from the `psych` package is your friend here. However, there is also visual method which you can use: the strip chart.

A strip chart is a variation on a scatter plot. If you have done regression, you might have looked at a scatter plot of residuals by fitted values. A strip chart is the same idea. However, rather than having many different fitted values, we'll only have the same number as groups. This is what creates the strips. For this visualization, we will use the `ggplot2` package rather than the output of the `plot` function. (We always want to aim for professional looking plots.)

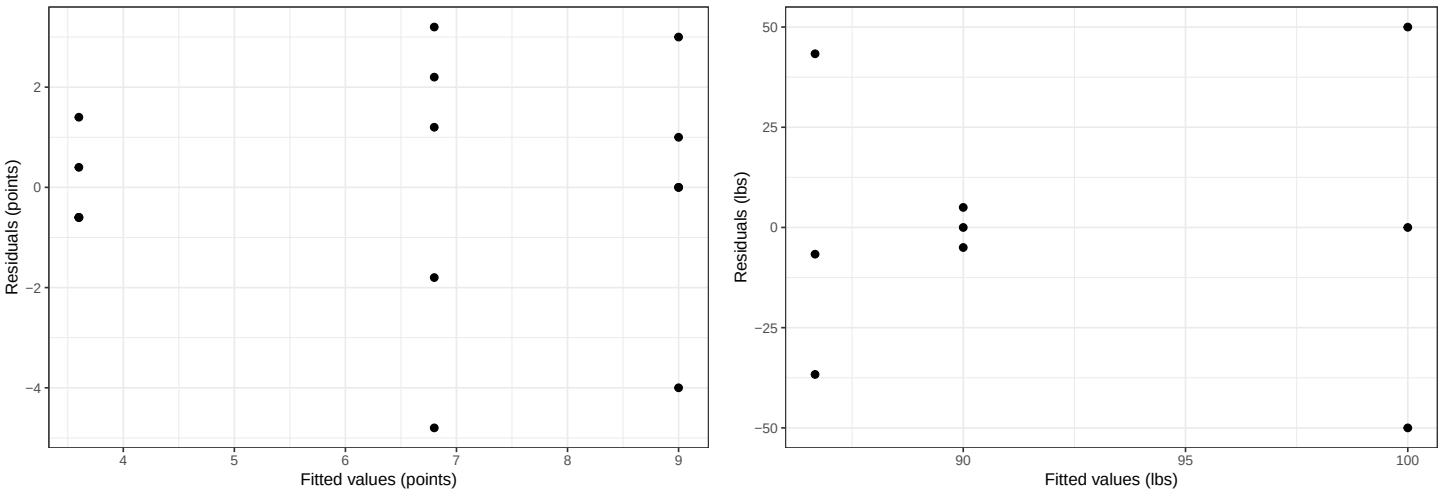
```
# Demo code for making strip charts
# Chunk options for side-by-side
### fig.subcap=c("Song Knowledge Study", "Honey Study"), fig.ncol=2,
### out.width="50%"
## There are no special par calls needed with this approach (only good for PDF outputs)

# Strip chart for Song Knowledge Residuals
ggplot(
  data = data.frame(
    residuals = songModel$residuals,
    fitted = songModel$fitted.values
  ),
  mapping = aes(x = fitted, y = residuals)
) +
  geom_point(size = 2) +
  theme_bw() +
  xlab("Fitted values (points)") +
  ylab("Residuals (points)")

# Strip chart for Honey Residuals
ggplot(
  data = data.frame(
    residuals = residuals(honeyModel),
    fitted = fitted(honeyModel)
  ),
  mapping = aes(x = fitted, y = residuals)
) +
  geom_point(size = 2) +
  theme_bw() +
  xlab("Fitted values (lbs)") +
  ylab("Residuals (lbs)")
```

When we look at strip charts for assessing homoscedasticity, we're primarily focused two aspects: comparing the lengths of the strips and if there are any patterns.

Let's first focus on the Song Knowledge portion of Figure 3. We have three strips of 5 points (note: three points for the lowest fitted value are all on top of each other). The lengths of these strips are such that the first strip is well under half of either of the others. This is a rule of thumb that we want to look out for: if any group has more than twice the length of another group, we should start worrying about homoscedasticity. If we turn our attention to the Honey portion of Figure 3, we can see the same kind of worry. Having a single group with different amount of variation is not a terminal violation, especially if we have a balanced design. However, we will want to proceed with caution.



(a) Song Knowledge Study

(b) Honey Study

Figure 3: Strip Chart Examples

A bigger issue for homoscedasticity is that of patterns in a strip chart. The most common pattern to look out for is a megaphone or funnel shape. We have a (right-opening) megaphone if the length of the strips get larger as you move from the left to the right along the horizontal axis. We have a funnel (left-opening megaphone) if the length of the strips gets smaller as you move from left to right. Keep an eye out for other patterns or shapes. These indicate deeper issues that result in violating the homoscedasticity assumption.

Turning back to Figure 3, we need to keep in mind that having only three strips makes judging patterns challenging. When I look at the Song Knowledge strip chart, I see a bit of a megaphone shape; but the last strip narrows instead of expands. When I look at the Honey strip chart, I see a bow tie (wide on the outsides, narrow in the middle).

Taking the two pieces together, I'm mildly cautious for the Song Knowledge data satisfying the homoscedasticity assumption. For the Honey study, I'm closer to saying we've violated the homoscedasticity assumption. (In practice, I would recommend looking at performing some kind of transformation on the data and refitting the model.)

Your Turn

Try replicating the strip chart code for the Resin Lifetime study. How would you assess the Homoscedasticity assumption?

Assessing Independence of Observations

The last assumption is not only the most important but the hardest to check. I want to stress that this assumption is about the ***Independence of Observations***. There are many kinds of independence in Statistics (e.g., independence of attributes), thus you need to clearly articulate which kind of independence you're talking about here.

Knowledge of Study Design and Sample

The first method we have available to us is not graphical or statistical in nature. Rather, we focus on what we know about the study design, how the data were collected, and the make up of the sample (i.e., the measurement units). For example, did we take precautions to draw a random sample for our measurement units? Did we take a convenience sample? Did we end up getting a chunk of closely related family members? Think through all possible ways that we could end up with measurement units directly impacting each other and then check the study to see if any of those methods could have/did slip through our guards.

For the Song Knowledge study, while all students present that day took part, the 15 students in our sample were selected via `R`'s `sample` function in a stratified manner. Given this set up, we can proceed with some confidence that we have satisfied the assumption of Independent Observations.

Graphical and Statistical Methods

In order to use graphical and/or statistical methods, we must know the order in which measurements were taken or how they were arranged spatially. In the case of the Song Knowledge study, we do not have this information, thus we **can not** use these methods.

Index Plots For the Honey data, we know that the order of the values reflects the measurement order (provided you entered the data in the same way as I did). Since we know ordering, we can make use of a visualization known as a index plot (Figure 4).

```
# Demo code for index plots

# Index Plot for Honey Residuals
ggplot(
  data = data.frame(
    residuals = honeyModel$residuals,
    index = 1:length(honeyModel$residuals)
  ),
  mapping = aes(x = index, y = residuals)
) +
  geom_point(size = 1.5) +
  geom_line() +
  theme_bw() +
  geom_hline(
    yintercept = 0,
    linetype = "dashed",
    color = "red"
  ) +
  xlab("Measurement order") +
  ylab("Residuals")
```

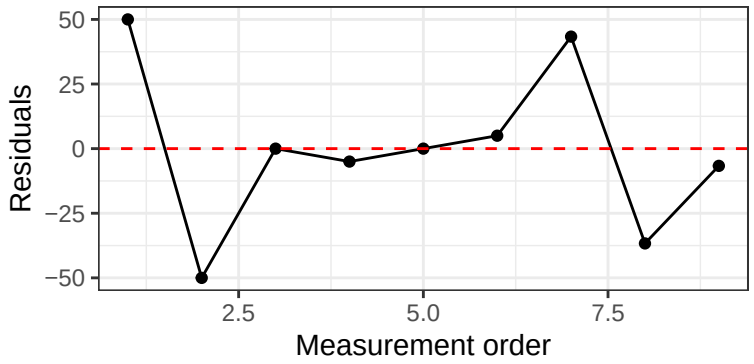


Figure 4: Index Plot for Honey Residuals

What we're looking for is a pattern. A "cloud" of points or the lack of any pattern is what we're hoping for. If instead we see something that reminds us of things we saw in college algebra, pre-calculus, trig, calculus, or another math classes, then we have a problem. For the Honey data, I do not see any indication of a pattern.

Durbin-Watson In addition to the index plots, we can also use the Durbin-Watson statistic to measure the level of autocorrelation (or serial correlation) in our data. Again, we must know the measurement order of our data.

If there is no autocorrelation (i.e., independent observations), then the DW statistic should be around 2. A ***rough*** Rule of Thumb is that DW values that are less than 1.5 or greater than 2.5 are causes for concern. However, the DW statistic is sensitive to things such as long runs of the same treatment/group in the data. This means that there is a lot of wiggle room in this rule of thumb. Only use the DW statistic in conjunction with the index plot AND your knowledge of the study. Use `car::durbinWatsonTest(honeyModel)$dw` to get the value of the Durbin-Watson statistic.

For the Honey data, the value of the Durbin-Watson statistic is 2.57, which is fairly close to the 2.5 cutoff, so I'm not concerned about violations of the Independence of Observations assumptions.

Your Turn

Use the information in Oehlert about the Resin Lifetime example as well as fact that the data appear in measurement order in the DAT file to assess the assumption of Independent Observations. What do you come up with?

Conducting the Parametric Shortcut (ANOVA *F* Test)

There are a couple of things that we will want to make sure that we have before we actually look at the results of the ANOVA F test. First, we need to make a set of choices related to our decision rule. Second, we need to assess the assumptions of the shortcut.

Decision Rule

For this shortcut we will make use of a p-value decision rule. This is standard practice for ANOVA problems. However, we need to be sure that we've made two choices before we look at the results.

First, we need to be sure that we've set our chosen which Type I error rate we're going to use (more on this later) and set the Type I risk level, $\mathcal{E}_I$.

Second, we need to decide what our *Unusualness Threshold*, UT, is going to serve as the way to decide whether we reject or fail to reject the null hypothesis. The Unusualness Threshold (also called "Level of Significance") is the maximum percentage of the time we anticipate seeing "unusual events" given the null hypothesis. This is a probability value and we're free to choose the value provided that $UT \leq \mathcal{E}_I$. (There are some subtle distinctions between the ideas of Unusualness Threshold/Level of Significance and Type I risk that we won't get into.)

For this tutorial, I'm going to use $\mathcal{E}_I = 0.05$ and $UT = 0.03$.

Assessment of Assumptions

We will proceed cautiously with the Song Knowledge data. We will NOT proceed with the parametric shortcut for the Honey data. Remember, the parametric shortcut is robust to moderate and minor violations of assumptions. In the case of the Honey study, I have stronger concerns about two of the three assumptions, so I would not want to use this shortcut without taking additional steps (beyond this tutorial).

I also feel that we can proceed (cautiously) with the Resin Lifetimes data.

Quick Look Method

Technically, you've already done the parametric shortcut (ANOVA F test). When you used the *aov* command, `R` took the shortcut automatically. Thus, all we need to do is look at the results. If you are just looking for yourself, the "quick look" method is great. However, this method is absolutely **TERRIBLE** for reports. To quickly look at the results you use either the `summary` or `anova` functions on your model objects (the outputs of the `aov` call):

```
# Demo code
# Summary example with Song Knowledge
summary(songModel)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## year         2  73.73   36.87   6.144 0.0145 *
## Residuals   12  72.00    6.00
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Anova example with Resin Lifetime
anova(resinModel)
```

```
## Analysis of Variance Table
##
## Response: log10Lifetime
##           Df Sum Sq Mean Sq F value    Pr(>F)
## temp       4 3.5376 0.88441  96.363 < 2.2e-16 ***
## Residuals 32 0.2937 0.00918
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The `anova` function is special wrapper of the `summary` function that adds just a bit more information about the design. However, we can do MUCH better.

Professional ANOVA Tables

There are two kinds of professional looking ANOVA tables. The first is a classical table that is essentially the output of the `summary`/`anova` call (sans the significance codes) in a table format. However, these are *lacking*. The modern ANOVA table incorporates effect sizes (practical significance) into the table along with statistical significance.

To make these modern tables, we will need the `parameters` package along with `knitr` and `kableExtra` packages.

```r
# Demo Code
# Create professional looking, modern ANOVA table for Song Knowledge
parameters::model_parameters(
  model = songModel,
  omega_squared = "raw",
  eta_squared = "raw",
  epsilon_squared = "raw"
) %>%
  knitr::kable(
  digits = 4,
  col.names = c(
    "Source", "SS", "df", "MS", "F", "p-value",
    "Omega Sq.", "Eta Sq.", "Epslion Sq."),
  caption = "ANOVA Table for Song Knowledge Study",
  format = "latex",
  booktabs = TRUE,
  align = c("l", rep("c", 8))
  ) %>%
  kableExtra::kable_styling(
    font_size = 10,
    latex_options = c("HOLD_position")
  )
```

Table 1: ANOVA Table for Song Knowledge Study

Source	SS	df	MS	F	p-value	Omega Sq.	Eta Sq.	Epslion Sq.
year	73.7333	2	36.8667	6.1444	0.0145	0.4069	0.5059	0.4236
Residuals	72.0000	12	6.0000					

Interpretation of Table 1 We can see that a STAT461 undergradute's year in school accounts for 6.14 times as much variation as the residuals in Table 1. Since our p-value is less than UT ($0.0145 < 0.03$), we will reject the null hypothesis and decide to act as if a STAT461 undergraduate student's year in college does impact their song knowledge score. In particular, their year in school accounts for around 40% of the variation in their score.

```r
# Demo Code
# Create professional looking modern ANOVA table for Resin Lifetimes
parameters::model_parameters(
  model = resinModel,
  omega_squared = "raw",
  eta_squared = "raw",
  epsilon_squared = "raw"
) %>%
  knitr::kable(
  digits = 4,
  col.names = c(
    "Source", "SS", "df", "MS", "F", "p-value",
    "Omega Sq.", "Eta Sq.", "Epslion Sq."),
  caption = "ANOVA Table for Resin Lifetimes Study",
  format = "latex",
  booktabs = TRUE,
  align = c("l", rep("c", 8))
  ) %>%
  kableExtra::kable_styling(
    font_size = 10,
    latex_options = c("HOLD_position")
  ) %>%
  kableExtra::footnote(
    general = "Computer rounding has made the p-value look like zero.",
    general_title = "Note. ",
    footnote_as_chunk = TRUE
  )
```

Table 2: ANOVA Table for Resin Lifetimes Study

Source	SS	df	MS	F	p-value	Omega Sq.	Eta Sq.	Epslion Sq.
temp	3.5376	4	0.8844	96.363	0	0.9116	0.9233	0.9138
Residuals	0.2937	32	0.0092					

Note. Computer rounding has made the p-value look like zero.

Interpretation of Table 2 From Table 2, we can see that we will reject the null hypothesis that the temperature impacts lifetime of the resin. The operating temperature accounts for ~96 times as much variation in the log_{10} lifetimes for the resin as the residuals. From a practical standpoint, the operating temperature accounts for essentially 91% of all variation in lifetimes.

Notice that both Table 1 and Table 2 look much more professional than the raw output we got from using `summary` and `anova`. Further, by using this approach with the `model_parameters` function, we've gotten our three estimates of effect size for the model (i.e., practical significance).

There is a downside in this approach: the p-value in Table 2 has been made to look equal to zero. We know that while p-values may be essentially equal to zero, they are never actually zero. We added a footnote to Table 2. However, we could attempt to fix this issue using the following function:

```r
# Set up the p-value rounding function.
pvalRound <- function(x){
  ifelse(
    test = x < 0.0001,
    yes = "< 0.0001",
    no = x
  )
}
```

```
# Demo Code to fix p-value rounding issues
# Professional looking modern ANOVA table with fixed p-value
parameters::model_parameters(
  model = resinModel,
  omega_squared = "raw",
  eta_squared = "raw",
  epsilon_squared = "raw"
) %>%
  dplyr::mutate(
    p = ifelse(
      test = is.na(p),
      yes = NA,
      no = pvalRound(p)
    )
  ) %>%
  knitr::kable(
  digits = 4,
  col.names = c(
    "Source", "SS", "df", "MS", "F", "p-value",
    "Omega Sq.", "Eta Sq.", "Epslion Sq."),
  caption = "ANOVA Table for Resin Lifetimes Study",
  format = "latex",
  booktabs = TRUE,
  align = c("l", rep("c", 8))
  ) %>%
  kableExtra::kable_styling(
    font_size = 10,
    latex_options = c("HOLD_position")
  )
```

Table 3: ANOVA Table for Resin Lifetimes Study

Source	SS	df	MS	F	p-value	Omega Sq.	Eta Sq.	Epslion Sq.
temp	3.5376	4	0.8844	96.363	< 0.0001	0.9116	0.9233	0.9138
Residuals	0.2937	32	0.0092					

Either table (Table 2 or Table 3) is sufficient. You only need to worry about fixing a p-value looking like 0 IF you have a p-value that is sufficiently close to zero (i.e., less than 0.0001). While 0.0001 is a fairly common threshold, you could update the `pvalRounding` function to use another threshold such as 0.001. I do not recommend going smaller than 0.0001 though.

Reporting Point Estimates

One of the last things that we're going to do in this tutorial is get the point estimates for our Grand Mean and treatment effects.

Make sure that you've told R to use the Sum to Zero constraint before proceeding.

To get these point estimates, we will use the `dummy.coef` function. To make the results look professional, we'll again make use the `knitr` and `kableExtra` packages.

```
# Demo making a profession table of coefficients/point estimates
## If you want to quickly look, just enter dummy.coef(songModel) into the console

# Song Knowledge Data
pointEst <- dummy.coef(songModel)
pointEst <- unlist(pointEst)
names(pointEst) <- c("Grand Mean", "Sophomores", "Juniors",
```

```
                    "Seniors")

data.frame("Estimate" = pointEst) %>%
  knitr::kable(
  digits = 2,
  caption = "Point Estimates from the Song Knowledge Study",
  format = "latex",
  booktabs = TRUE,
  align = "c"
  ) %>%
  kableExtra::kable_styling(
    font_size = 12,
    latex_options = c("HOLD_position")
  )
```

Table 4: Point Estimates from the Song Knowledge Study

	Estimate
Grand Mean	6.47
Sophomores	0.33
Juniors	2.53
Seniors	-2.87

If you just call `dummy.coef(songModel)` in the console, you'll see a value labelled `(Intercept)`; this is the value of the *Grand Sample Arithmetic Mean*. The other values should be labelled by factor name and level name. These point estimates are what will fill our various screens (plus the residuals).

Keep in mind that the estimates in Table 4 are *rates*. Thus, for the Song Knowledge study, we would interpret this value as 6.47 points per student; our entire sample accumulated 6.47 times as many points as sampled students.

We can also see the factor level (treatment) effects ($\widehat{\alpha_i}$) estimates. For Juniors, they accumulated an additional 2.53 points per student where as the Sophomores only accumulated 0.33 points per student and the Seniors accumulated -2.87 points per student. This suggests that Seniors performing worse that baseline ($GSAM$).

Your Turn

Attempt to come up with the code that makes the following table for the Resin Lifetime study. Additionally, practice interpreting these point estimates.

Table 5: Point Estimates from the Resin Lifetime Study

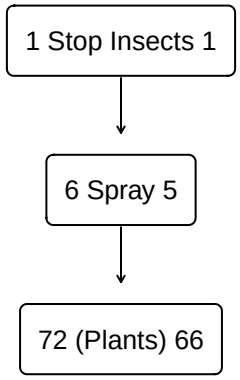
	Estimate
Grand Mean	1.44
175ºC	0.49
194ºC	0.19
213ºF	-0.06
231ºF	-0.24
250ºF	-0.38

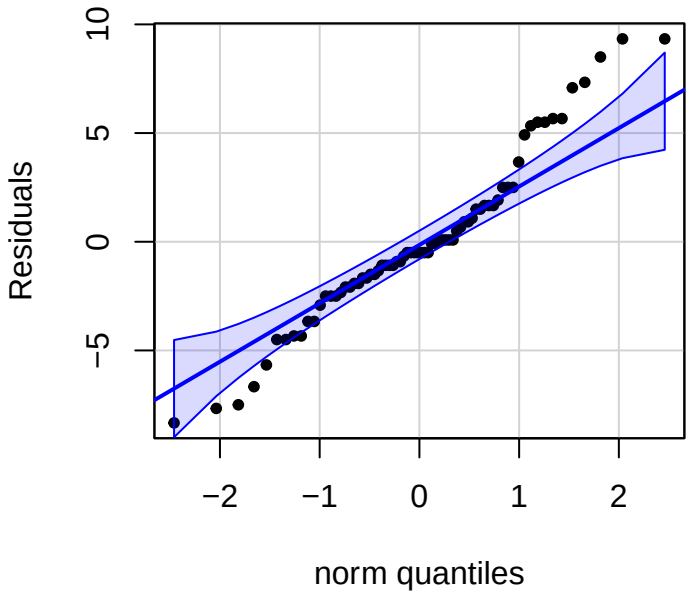
Putting Everything Together–Your Turn

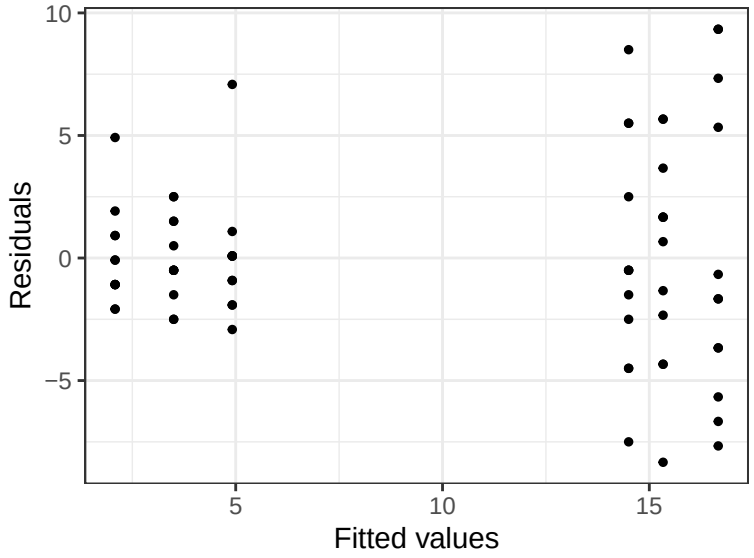
Now is an opportunity for you to get some practice. I'm going to use the data frame `InsectSprays`, which is built into R. You may load this data into your session with the command `data("InsectSprays")`.

A bit of background: the original researchers were exploring the effectiveness of various sprays on reducing the number of instances of particular type of insect for a crop. Each observation is randomly sampled plant from a field. NOTE: we do not know the measurement order.

Explore these data and build the elements that you would include a report as shown above. I'm going to provide several outputs, but no narrative. Use these as reminders for what to do. If you get stuck, check out the code appendix to see the code that I used.







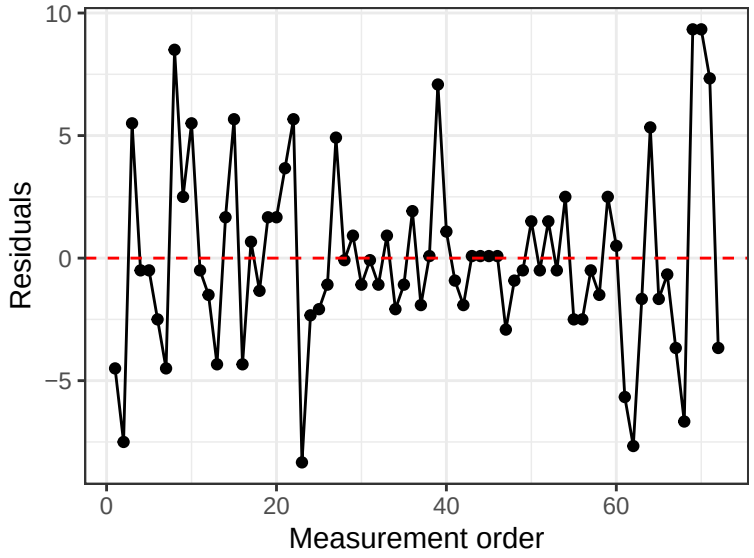


Table 6: ANOVA Table for Insect Spray Study

Source	SS	df	MS	F	p-value	Omega Sq.	Eta Sq.	Epslion Sq.
spray	2668.833	5	533.7667	34.7023	< 0.0001	0.7006	0.7244	0.7036
Residuals	1015.167	66	15.3813					

Table 7: Point Estimates from the Insect Spray Study

	Estimate
Grand Mean	9.50
Spray A	5.00
Spray B	5.83
Spray C	-7.42
Spray D	-4.58
Spray E	-6.00
Spray F	7.17

Code Appendix

```
# Setting Document Options
knitr::opts_chunk$set(
  echo = FALSE,
  warning = FALSE,
  message = FALSE,
  fig.align = "center"
)

packages <- c("tidyverse", "hasseDiagram", "knitr",
              "kableExtra", "car", "psych", "parameters")
lapply(packages, library, character.only = TRUE)

# Tell Knitr to use empty space instead of NA in printed tables
options(knitr.kable.NA = "")

# Set constraint
options(contrasts = c("contr.sum", "contr.poly"))

# Load extra tools
source("https://raw.github.com/neilhatfield/STAT461/master/rScripts/ANOVATools.R")

# Demo code for loading packages for the tutorial
packages <- c("tidyverse", "hasseDiagram", "knitr",
              "kableExtra", "car", "psych", "parameters")
lapply(packages, library, character.only = TRUE)

# Demo code for controlling table options
# Tell Knitr to use empty space instead of NA in printed tables
options(knitr.kable.NA = "")

## Demo code for setting the constraint
options(contrasts = c("contr.sum", "contr.poly"))

# Demo code for loading Neil's extra tools
source("https://raw.github.com/neilhatfield/STAT461/master/rScripts/ANOVATools.R")

# Song Data
songData <- read.csv(
  file = "https://raw.github.com/neilhatfield/STAT461/master/dataFiles/songKnowledge2022.csv",
  header = TRUE,
  sep = ","
)
# Set year to an ordered factor
songData$year <- factor(
  x = songData$year,
  levels = c("sophomore", "junior", "senior")
)

# Honey Data--Manual Entry
honey <- data.frame(
  Amount = c(150, 50, 100, 85, 90, 95, 130, 50, 80),
  Varietal = rep(c("Clover", "Orange Blossom", "Alfalfa"), each = 3)
)
## Set Varietal to factor (no particular order)
honey$Varietal <- as.factor(honey$Varietal)

# Resin Lifetimes Data
```

```r
resin <- read.table(
  file = "https://raw.github.com/neilhatfield/STAT461/master/dataFiles/resinLifetimes.dat",
  header = TRUE,
  sep = "" # Notice the change in separator
)
## Set temp to factor
resin$temp <- as.factor(resin$temp)

## Change the name of the y column to something more meaningful
names(resin)[which(names(resin) == "y")] <- "log10Lifetime"

# Checking the first two base requirements
str(songData)
str(honey)
str(resin)

# DEMO CODE

# Hasse Diagram for the Honey Study
modelLabels <- c("1 Make Honey 1", "3 Varietal 2", "9 (Hives) 6")
modelMatrix <- matrix(
  data = c(FALSE, FALSE, FALSE, TRUE, FALSE, FALSE, TRUE, TRUE, FALSE),
  nrow = 3,
  ncol = 3,
  byrow = FALSE
)
hasseDiagram::hasse(
 data = modelMatrix,
 labels = modelLabels
)

# Demo code for building ANOVA models
## Song Knowledge study
songModel <- aov(
  formula = score ~ year,
  data = songData,
  na.action = "na.omit"
)

## Honey study
honeyModel <- aov(
  formula = Amount ~ Varietal,
  data = honey,
  na.action = "na.omit"
)

## Resin Lifetime study
resinModel <- aov(
  formula = log10Lifetime ~ temp,
  data = resin,
  na.action = "na.omit"
)

# Demo code for making QQ plots
## Chunk options for side-by-side plots
### fig.show="hold", out.width="100%", fig.height=3.5
## R option for side-by-side plots
par(mfrow = c(1,2), mar = c(4, 4, 0.1, 0.1))
```

```r
## Song Knowledge study
car::qqPlot(
  x = songModel$residuals,
  distribution = "norm",
  envelope = 0.90,
  id = FALSE,
  pch = 20,
  ylab = "Residuals"
)

# QQ plot for Honey Residuals
car::qqPlot(
  x = residuals(honeyModel),
  distribution = "norm",
  envelope = FALSE,
  id = TRUE,
  pch = 1,
  ylab = "Residuals"
)

# Demo code for making strip charts
# Chunk options for side-by-side
### fig.subcap=c("Song Knowledge Study", "Honey Study"), fig.ncol=2,
### out.width="50%"
## There are no special par calls needed with this approach (only good for PDF outputs)

# Strip chart for Song Knowledge Residuals
ggplot(
  data = data.frame(
    residuals = songModel$residuals,
    fitted = songModel$fitted.values
  ),
  mapping = aes(x = fitted, y = residuals)
) +
  geom_point(size = 2) +
  theme_bw() +
  xlab("Fitted values (points)") +
  ylab("Residuals (points)")

# Strip chart for Honey Residuals
ggplot(
  data = data.frame(
    residuals = residuals(honeyModel),
    fitted = fitted(honeyModel)
  ),
  mapping = aes(x = fitted, y = residuals)
) +
  geom_point(size = 2) +
  theme_bw() +
  xlab("Fitted values (lbs)") +
  ylab("Residuals (lbs)")

# Demo code for index plots

# Index Plot for Honey Residuals
ggplot(
  data = data.frame(
    residuals = honeyModel$residuals,
    index = 1:length(honeyModel$residuals)
```

```
  ),
  mapping = aes(x = index, y = residuals)
) +
  geom_point(size = 1.5) +
  geom_line() +
  theme_bw() +
  geom_hline(
    yintercept = 0,
    linetype = "dashed",
    color = "red"
  ) +
  xlab("Measurement order") +
  ylab("Residuals")
# Demo code
# Summary example with Song Knowledge
summary(songModel)

# Anova example with Resin Lifetime
anova(resinModel)

# Demo Code
# Create professional looking, modern ANOVA table for Song Knowledge
parameters::model_parameters(
  model = songModel,
  omega_squared = "raw",
  eta_squared = "raw",
  epsilon_squared = "raw"
) %>%
  knitr::kable(
  digits = 4,
  col.names = c(
    "Source", "SS", "df", "MS", "F", "p-value",
    "Omega Sq.", "Eta Sq.", "Epslion Sq."),
  caption = "ANOVA Table for Song Knowledge Study",
  format = "latex",
  booktabs = TRUE,
  align = c("l", rep("c", 8))
  ) %>%
  kableExtra::kable_styling(
    font_size = 10,
    latex_options = c("HOLD_position")
  )

# Demo Code
# Create professional looking modern ANOVA table for Resin Lifetimes
parameters::model_parameters(
  model = resinModel,
  omega_squared = "raw",
  eta_squared = "raw",
  epsilon_squared = "raw"
) %>%
  knitr::kable(
  digits = 4,
  col.names = c(
    "Source", "SS", "df", "MS", "F", "p-value",
    "Omega Sq.", "Eta Sq.", "Epslion Sq."),
  caption = "ANOVA Table for Resin Lifetimes Study",
  format = "latex",
  booktabs = TRUE,
```

```
  align = c("l", rep("c", 8))
  ) %>%
  kableExtra::kable_styling(
    font_size = 10,
    latex_options = c("HOLD_position")
  ) %>%
  kableExtra::footnote(
    general = "Computer rounding has made the p-value look like zero.",
    general_title = "Note. ",
    footnote_as_chunk = TRUE
  )

# Set up the p-value rounding function.
pvalRound <- function(x){
  ifelse(
    test = x < 0.0001,
    yes = "< 0.0001",
    no = x
  )
}


# Demo Code to fix p-value rounding issues
# Professional looking modern ANOVA table with fixed p-value
parameters::model_parameters(
  model = resinModel,
  omega_squared = "raw",
  eta_squared = "raw",
  epsilon_squared = "raw"
) %>%
  dplyr::mutate(
    p = ifelse(
      test = is.na(p),
      yes = NA,
      no = pvalRound(p)
    )
  ) %>%
  knitr::kable(
  digits = 4,
  col.names = c(
    "Source", "SS", "df", "MS", "F", "p-value",
    "Omega Sq.", "Eta Sq.", "Epslion Sq."),
  caption = "ANOVA Table for Resin Lifetimes Study",
  format = "latex",
  booktabs = TRUE,
  align = c("l", rep("c", 8))
  ) %>%
  kableExtra::kable_styling(
    font_size = 10,
    latex_options = c("HOLD_position")
  )

# Demo making a profession table of coefficients/point estimates
## If you want to quickly look, just enter dummy.coef(songModel) into the console

# Song Knowledge Data
pointEst <- dummy.coef(songModel)
pointEst <- unlist(pointEst)
names(pointEst) <- c("Grand Mean", "Sophomores", "Juniors",
```

```
                    "Seniors")

data.frame("Estimate" = pointEst) %>%
  knitr::kable(
  digits = 2,
  caption = "Point Estimates from the Song Knowledge Study",
  format = "latex",
  booktabs = TRUE,
  align = "c"
  ) %>%
  kableExtra::kable_styling(
    font_size = 12,
    latex_options = c("HOLD_position")
  )

# Demo making a profession table of coefficients/point estimates

# Resin Lifetime Data
pointEst <- dummy.coef(resinModel)
pointEst <- unlist(pointEst)
names(pointEst) <- c("Grand Mean", "175ºC", "194ºC",
                "213ºF", "231ºF", "250ºF")

data.frame("Estimate" = pointEst) %>%
  knitr::kable(
  digits = 2,
  caption = "Point Estimates from the Resin Lifetime Study",
  format = "latex",
  booktabs = TRUE,
  align = "c"
  ) %>%
  kableExtra::kable_styling(
    font_size = 12,
    latex_options = c("HOLD_position")
  )

# Putting Everything Together--Your Turn Code-------------------------------------------------------------

# Hasse Diagram for Insect Spray Study
modelLabels <- c("1 Stop Insects 1", "6 Spray 5", "72 (Plants) 66")
modelMatrix <- matrix(
  data = c(FALSE, FALSE, FALSE, TRUE, FALSE, FALSE, TRUE, TRUE, FALSE),
  nrow = 3,
  ncol = 3,
  byrow = FALSE
)
hasseDiagram::hasse(
 data = modelMatrix,
 labels = modelLabels
)

# Load Data
data("InsectSprays")

# Fit Model
isModel <- aov(
  formula = count ~ spray,
  data = InsectSprays
)
```

```r
# Assess Gaussian Assumption with a QQ Plot
car::qqPlot(
  x = isModel$residuals,
  distribution = "norm",
  envelope = 0.90,
  id = FALSE,
  pch = 20,
  ylab = "Residuals"
)

# Supplement with Skewness and Kurtosis
isRSkew <- psych::skew(isModel$residuals)
isRKurt <- psych::kurtosi(isModel$residuals)

# Use a strip plot to assess homoscedasticity
ggplot(
  data = data.frame(
    residuals = isModel$residuals,
    fitted = isModel$fitted.values
  ),
  mapping = aes(x = fitted, y = residuals)
) +
  geom_point(size = 1) +
  theme_bw() +
  xlab("Fitted values") +
  ylab("Residuals")

# RED HERRING
# We don't know measurement order so this plot does not actually
# provide any assistance to us.

# Index Plot for Resin Residuals
ggplot(
  data = data.frame(
    residuals = isModel$residuals,
    index = 1:length(isModel$residuals)
  ),
  mapping = aes(x = index, y = residuals)
) +
  geom_point(size = 1.5) +
  geom_line() +
  theme_bw() +
  geom_hline(
    yintercept = 0,
    linetype = "dashed",
    color = "red"
  ) +
  xlab("Measurement order") +
  ylab("Residuals")

dw <- car::durbinWatsonTest(resinModel)$dw

# Insect Sprays ANOVA Table
parameters::model_parameters(
  model = isModel,
  omega_squared = "raw",
  eta_squared = "raw",
  epsilon_squared = "raw"
) %>%
```

```
  dplyr::mutate(
    p = ifelse(
      test = is.na(p),
      yes = NA,
      no = pvalRound(p)
    )
  ) %>%
  knitr::kable(
  digits = 4,
  col.names = c(
    "Source", "SS", "df", "MS", "F", "p-value",
    "Omega Sq.", "Eta Sq.", "Epslion Sq."
    ),
  caption = "ANOVA Table for Insect Spray Study",
  format = "latex",
  booktabs = TRUE,
  align = c("l", rep("c", 8))
  ) %>%
  kableExtra::kable_styling(
    font_size = 12,
    latex_options = c("HOLD_position")
  )

# Point Estimates for Insect Sprays
pointEst <- dummy.coef(isModel)
pointEst <- unlist(pointEst)
names(pointEst) <- c("Grand Mean", "Spray A", "Spray B",
                     "Spray C", "Spray D", "Spray E", "Spray F")

data.frame("Estimate" = pointEst) %>%
  knitr::kable(
  digits = 2,
  caption = "Point Estimates from the Insect Spray Study",
  format = "latex",
  booktabs = TRUE,
  align = "c"
  ) %>%
  kableExtra::kable_styling(
    font_size = 12,
    latex_options = c("HOLD_position")
  )
```