Statistical Foundations for Engineers and Scientists

Eric M Reyes

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Contents

Preface

Engineers and scientists are routinely asked to make decisions based on observed data. That data will be subject to variability; learning to characterize variability and make decisions in the midst of variability is the idea behind statistics.

This text will introduce statistical concepts in the context of engineering, the physical, and the biological sciences. The text emphasizes statistical literacy (interpretation and clear communication of statistical methods, results, and concepts) and statistical reasoning (defining the need for data to address questions, modeling variability in a process, and choosing the appropriate methodology to address a question of interest). We describe approaches to collecting data, summarizing the information contained within the data, building a model to address a question of interest, using the data to estimate the unknowns in the model, assessing the model, and interpreting the results based on the model.

This text is applied, focusing primarily on knowing when various modeling strategies are appropriate and how to interpret their results. One goal is to provide a strong foundation in statistical ideas to enable readers to engage with research encountered in their field.

Part I

Unit I: Language and Logic of Inference

Chapter 1

The Statistical Process

Is driving while texting as dangerous as driving while intoxicated? Is there evidence that my measurement device is calibrated inappropriately? How much force, on average, can our concrete blocks withstand before failing? Regardless of your future career path, you will eventually need to answer a question. The discipline of statistics is about using data to address questions by converting that data into valuable information.

Statistics is the discipline of converting data into information.

It might be natural at this point to ask "do I really need an entire class about answering questions with data? Isn't this simple?" Sometimes, it is simple; other times, it can be far from it. Let's illustrate with the following example from Tintle et al. (2015).

Example 1.1: "Organ Donation"
Even though organ donations save lives, recruiting organ donors is difficult. Interestingly, surveys show that about 85% of Americans approve of organ donation in principle and many states offer a simple organ donor registration process when people apply for a driver's license. However, only about 38% of licensed drivers in the United States are registered to be organ donors. Some people prefer not to make an active decision about organ donation because the topic can be unpleasant to think about. But perhaps phrasing the question differently could affect a person's willingness to become a donor.

Johnson and Goldstein (2003) recruited 161 participants for a study, published in the journal *Science*, to address the question of organ donor recruitment. The participants were asked to imagine they had moved to a new state and were applying for a driver's license. As part of this application, the participants

were to decide whether or not to become an organ donor. Participants were presented with one of three different default choices:

- Some of the participants were forced to make a choice of becoming a donor or not, without being given a default option (the "neutral" group).
- Other participants were told that the default option was not to be a donor but that they could choose to become a donor if they wished (the "opt-in" group).
- The remaining participants were told that the default option was to be a donor but that they could choose not to become a donor if they wished (the "opt-out" group).

The study found that 79% of those in the neutral group, 42% of those in the opt-in group, and 82.0% of those in the opt-out group agreed to become donors.

The results of the study are presented in Figure 1.1. It seems obvious that using the "opt-in" strategy results in fewer people agreeing to organ donation. However, does the "opt-out" strategy, in which people are by default declared organ donors, result in more people agreeing to organ donation compared to the "neutral" strategy? On the one hand, a higher percentage did agree to organ donation under the "opt-out" (82% compared to 79%). However, since this study involved only a subset of Americans, is this enough evidence to claim the "opt-out" strategy is really superior compared to the "neutral" strategy in the broader population? The discipline of statistics provides a framework for addressing such ambiguity.

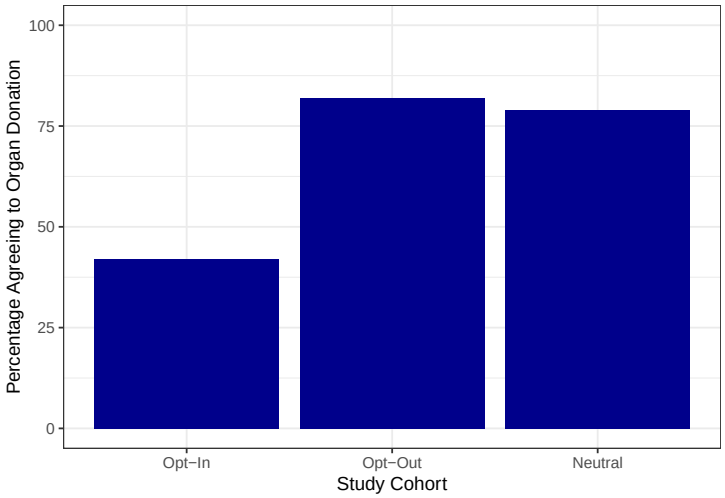


Figure 1.1: Summary of the responses for the Organ Donation Study described in Example **??**.

1.1 Overview of Drawing Inference

Let's begin by taking a step back and considering the big picture of how data is turned into information. Every research question we pose, at its heart, is trying to characterize a **population**, the group of subjects of ultimate interest.

Definition 1.1 (Population)**:**
The collection of subjects we would like to say something about.

In the Organ Donation study, the researchers would like to say something about Americans who are of the age to consent to organ donation; in particular, they would like to quantify how likely it is that someone from this group agrees to organ donation. Therefore, the population is *all Americans who are of the age to consent to organ donation.*

In general, the subjects in a population need not be people; in some studies, the population could be a collection of screws, cell phones, sheet metal... whatever characterizes the objects from which we would *like to* obtain measurements. We use the phrase "like to" because in reality it is often impossible (or impractical) to observe the entire population. Instead, we make observations on a subset of the population; this smaller group is known as the **sample**.

Definition 1.2 (Sample)**:**
The collection of subjects for which we actually obtain measurements (data).

For each subject within the sample, we obtain a collection of measurements forming our set of data. The goal of statistical modeling is to use the sample (the group we actually observe) to say something about the population of interest (the group we wish we had observed); this process is known as **statistical inference**. This process is illustrated in Figure 1.2.

Definition 1.3 (Statistical Inference)**:**
The process of using a sample to characterize some aspect of the underlying population.

1.2 Anatomy of a Dataset

Once we have our sample, we take measurements on each of the subjects within this sample. These measurements form the data. When we hear the word "data," most of us envision a large spreadsheet. In reality, data can take on many forms — spreadsheets, images, text files, unstructured text from a social media feed,

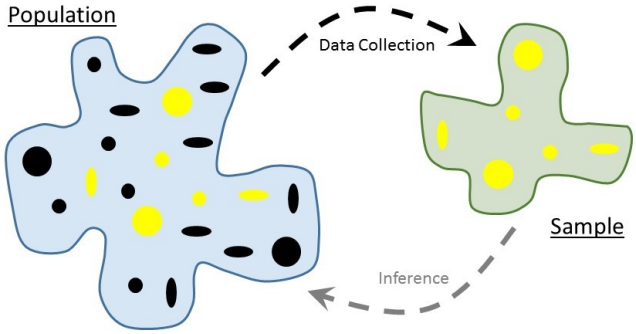


Figure 1.2: Illustration of the statistical process.

etc. Regardless of the form, all datasets contain information for each subject in the sample; this information, the various measurements, are called **variables**.

Definition 1.4 (Variable)**:**
A measurement, or category, describing some aspect of the subject.

Variables come in one of two flavors. **Categorical** variables are those which denote a grouping to which the subject belongs. Examples include marital status, brand, and experimental treatment group. **Numeric** variables are those which take on values for which ordinary arithmetic (e.g., addition and multiplication) makes sense. Examples include height, age of a product, and diameter. Note that sometimes numeric values are used to represent the levels of a categorical variable in a dataset; for example, 0 may indicate "No" and 1 may indicate "Yes" for a variable capturing whether a person is a registered organ donor. Therefore, just because a variable has a numeric value does not make it a numeric variable; the key here is that numeric variables are those for which arithmetic makes sense.

Definition 1.5 (Categorical Variable)**:**
Also called a "qualitative variable," a measurement on a subject which denotes a grouping or categorization.

Definition 1.6 (Numeric Variable)**:**
Also called a "quantitative variable," a measurement on a subject which takes on a numeric value and *for which ordinary arithmetic makes sense.*

While it may be natural to think of a dataset as a spreadsheet, not all spread-

Table 1.1: Example of a common data structure which does not represent tidy data. Data is from a hypothetical study comparing battery lifetimes (hours).

Brand A	Brand B
8.3	8.4
5.1	8.6
3.3	3.8
5.3	4.1
5.7	4.5
	4.0

sheets are created equal. Here, we consider datasets which have the following characteristics:

- Each column contains a unique variable.
- Each record (row in the dataset) corresponds to a different observation of the variables.
- If you have multiple datasets, they should include a column in the table that allows them to be linked (subject identifier).

These are characteristics of "tidy data." Even unstructured data such as images or text files must be processed, often converted to tidy data, prior to performing a statistical analysis. The above description eliminates a common method of storing data in engineering and scientific disciplines — storing each sample in a different column. To illustrate, suppose we conduct a study comparing the lifetime (in hours) of two brands of batteries. We measure the lifetime of five batteries of Brand A and six of Brand B. It is common to see a dataset like that in Table 1.1; the problem here is that the first record of the dataset contains information on two different observations. We have the lifetime from a battery of Brand A in the same row as the lifetime from a battery of Brand B. This violates the second condition of tidy data described above.

In order to adhere to the tidy structure, we can reformat this dataset as illustrated in Table 1.2. Here, each record represents a unique observation and each column is a different variable. We have also added a unique identifier.

It may take some time to get used to storing data in this format, but it makes analysis easier and avoids time spent managing the data later.

1.3 A Note on Codebooks

A dataset on its own is meaningless if you cannot understand what the values represent. *Before* you access a dataset, you should always review any available **codebooks**.

Table 1.2: Example of a tidy dataset, a good way of storing data. Data is from a hypothetical study comparing battery lifetimes (hours).

Battery	Brand	Lifetime
1	A	8.3
2	A	5.1
3	A	3.3
4	A	5.3
5	A	5.7
6	B	8.4
7	B	8.6
8	B	3.8
9	B	4.1
10	B	4.5
11	B	4.0

Definition 1.7 (Codebook)**:**
Also called a "data dictionary," these provide complete information regarding the variables contained within a dataset.

Some codebooks are excellent, with detailed descriptions of how the variables were collected and appropriate units. Other codebooks give only an indication of what each variable represents. Whenever you are working with previously collected data, reviewing a codebook is the first step; and, you should be prepared to revisit the codebook often throughout an analysis. When you are collecting your own dataset, constructing a codebook is essential for others to make use of your data.

Chapter 2

Case Study: Health Effects of the Deepwater Horizon Oil Spill

On the evening of April 20, 2010, the *Deepwater Horizon*, an oil drilling platform positioned off the coast of Louisiana, was engulfed in flames as the result of an explosion. The drilling rig, leased and operated by BP, had been tasked with drilling an oil well in water nearly 5000 feet deep. Eleven personnel were killed in the explosion. The following screenshot is from the initial coverage by the *New York Times*[1]:

The incident is considered the worst oil spill in US history, creating an environmental disaster along the Gulf Coast. In addition to studying the effects on the local environment, researchers have undertaken studies to examine the short and long-term health effects caused by the incident. As an example, it is reasonable to ask whether volunteers who were directly exposed to oil, such as when cleaning wildlife, are at higher risk of respiratory irritation compared to those volunteers who were helping with administrative tasks and therefore were not directly exposed to the oil. An article appearing in *The New England Journal of Medicine* (Goldstein, Osofsky, and Lichtveld 2011) reported the results from a health symptom survey performed in the Spring and Summer of 2010 by the National Institute for Occupational Safety and Health. Of 54 volunteers assigned to wildlife cleaning and rehabilitation, 15 reported experiencing "nose irritation, sinus problems, or sore throat." Of 103 volunteers who had no exposure to oil, dispersants, cleaners, or other chemicals, 16 reported experiencing "nose irritation, sinus problems, or sore throat."

[1] http://www.nytimes.com/2010/04/22/us/22rig.html?rref=collection%2Ftimestopic%2FOil%20Spills&action=click&contentCollection=timestopics&region=stream&module=stream_unit&version=search&contentPlacement=1&pgtype=collection

Search Continues After Oil Rig Blast

By CAMPBELL ROBERTSON APRIL 21, 2010

The rig burned Wednesday about 50 miles southeast of Venice, La. Firefighting efforts were causing it to take on water and list. Gerald Herbert/Associated Press

NEW ORLEANS — An explosion on an oil drilling rig off the coast of southeast Louisiana left at least 3 people critically injured and 11 others missing as of Wednesday night.

Figure 2.1: *New York Times* coverage of the *Deepwater Horizon* oil spill.

While a larger fraction of volunteers cleaning wildlife *in the study* reported respiratory symptoms compared to those who were not directly exposed to irritants, would we expect similar results if we were able to interview all volunteers? What about during a future oil spill? Is there evidence that more than 1 in 5 volunteers who clean wildlife will develop respiratory symptoms? What is a reasonable value for the increased risk of respiratory symptoms for those volunteers with direct exposure compared to those without?

In the first part of this text, we use this motivating example as the context for discussing how research questions should be framed, methods for data collection, summarizing and presenting data clearly, quantifying the variability in an estimate, and quantifying the degree to which the data disagrees with a proposed model. We capture these ideas in what we call the *Five Fundamental Ideas of Inference*. We will also see that any statistical analysis moves between the components of what we call the *Distributional Quartet*. These two frameworks allow us to describe the language and logic of inference, serving as a foundation for the statistical thinking and reasoning needed to address more complex questions encountered later in the text.

Chapter 3

Asking the Right Questions

The discipline of statistics is about turning data into information in order to address some question. While there may be no such thing as a stupid question, there are ill-posed questions — those which cannot be answered as stated. Consider the Deepwater Horizon Case Study. It might seem natural to ask "if a volunteer cleans wildlife, will she develop adverse respiratory symptoms?" Let's consider the data. Of the 54 volunteers assigned to wildlife cleaning and rehabilitation, 15 reported experiencing adverse respiratory symptoms ("nose irritation, sinus problems, or sore throat"); while some volunteers developed symptoms, others did not. It seems the answer to our question is then "it depends" or "maybe." This is an example of an *ill-posed question*. Such questions exist because of *variability*, the fact that every subject in the population does not behave in exactly the same way. In our example not every volunteer had the same reaction when directly exposed to oil.

It is variability that creates a need for statistics; in fact, you could think of statistics as the study and characterization of variability. We must therefore learn to ask the *right* questions — those which can be answered in the presence of variability.

Definition 3.1 (Variability)**:**
The notion that measurements differ from one observation to another.

The presence of variability makes some questions ill-posed; statistics concerns itself with how to address questions in the presence of variability.

3.1 Characterizing a Variable

Recall that the goal of statistical inference is to say something about the population; as a result, any question we ask should then be centered on this larger group. The first step to constructing a well-posed question is then to identify the population of interest for the study. For the Deepwater Horizon Case Study, it is unlikely that we are only interested in these 54 observed volunteers assigned to wildlife cleaning. In reality, we probably want to say something about volunteers for any oil spill. The 54 volunteers in our dataset form the sample, a subset from all volunteers who clean wildlife following an oil spill. Our population of interest is comprised of all volunteers who clean wildlife following an oil spill.

When identifying the population of interest, be specific! Suppose you are trying to estimate the average height of trees. Are you really interested in *all* trees? Or, are you interested in Maple trees within the city limits of Terre Haute, Indiana?

Since we expect that the reaction to oil exposure — the primary variable of interest for this study, sometimes called the **response** — to vary from one individual to another, we cannot ask a question about the *value* of the reaction (whether they experienced symptoms or not). Instead, we want to characterize the **distribution** of the response.

Definition 3.2 (Response)**:**
The primary variable of interest within a study. This is the variable you would either like to explain or estimate.

Definition 3.3 (Distribution)**:**
The pattern of variability corresponding to a set of values.

Notice that in this case, the response is a categorical variable; describing the distribution of such a variable is equivalent to describing how individuals are divided among the possible groups. With a finite number of observations, we could present the number of observations (**frequeny**) within each group. For example, of the 54 volunteers, 15 experienced adverse symptoms and 39 did not. This works well within the sample; however, as our population is infinitely large (all volunteers cleaning wildlife following an oil spill), reporting the frequencies is not appropriate. In this case, we report the fraction of observations (**relative frequency**) falling within each group; this helps convey information about the distribution of this variable.

Definition 3.4 (Frequency)**:**

The number of observations falling into a particular level of a categorical variable.

Definition 3.5 (Relative Frequency)**:**
Also called the "proportion," the fraction of observations falling into a particular level of a categorical variable.

Numeric quantities, like the proportion, which summarize the distribution of a variable within the population are known as **parameters**.

Definition 3.6 (Parameter)**:**
Numeric quantity which summarizes the distribution of a variable within the population *of interest. Generally denoted by Greek letters in statistical formulas.*

While the *value* of a variable may vary across the population, the *parameter* is a single fixed constant which summarizes the variable for that population. For example, the grade received on an exam varies from one student to another in a class; but, the *average exam grade* is a fixed number which summarizes the class as a whole. Well-posed questions can be constructed if we limit ourselves to questions about the parameter. The second step in constructing well-posed questions is then to identify the parameter of interest.

The questions we ask generally fall into one of two categories:

- Estimation: what *proportion* of volunteers who clean wildlife following an oil spill will experience adverse respiratory symptoms?
- Hypothesis Testing: is it reasonable to expect that no more than 1 in 5 volunteers who clean wildlife following an oil spill will experience adverse respiratory symptoms?

Definition 3.7 (Estimation)**:**
Using the sample to approximate the value of a parameter from the underlying population.

Definition 3.8 (Hypothesis Testing)**:**
Using a sample to determine if the data is consistent with a working theory or if there is evidence to suggest the data is not consistent with the theory.

Since we do not get to observe the population (we only see the sample), we cannot observe the value of the parameter. That is, we will never know the true proportion of volunteers who experience symptoms. However, we can determine what the data suggests about the population (that is what inference is all about).

Parameters are unknown values and can, in general, never be known.

It turns out, the vast majority of research questions can be framed in terms of a parameter. This is the first of what we consider the *Five Fundamental Ideas of Inference*.

Fundamental Idea:

Fundamental Idea I: A research question can often be framed in terms of a parameter which characterizes the population. Framing the question should then guide our analysis.

We now have a way of describing a well-posed question, a question which can be addressed using data. Well posed questions are about the population and can be framed in terms of a parameter which summarizes that population. We now describe how these questions are typically framed.

3.2 Framing the Question

In engineering and scientific applications, many questions fall under the second category of model consistency. Examining such questions is known as **hypothesis testing**, which is a form of model comparison in which data is collected to help the researcher choose between two competing theories for the parameter of interest. In this section, we consider the terminology surrounding specifying such questions.

For the Deepwater Horizon Case Study suppose we are interested in addressing the following question:

> Is there evidence that more than 1 in 5 volunteers who clean wildlife following an oil spill will develop adverse respiratory symptoms?

The question itself is about the population (all volunteers assigned to clean wildlife following an oil spill) and is centered on a parameter (the proportion who develop adverse respiratory symptoms). That is, this is a well-posed question that can be answered with appropriate data. The overall process for addressing these types of questions is similar to conducting a trial in a court of law. In the United States, a trial has the following essential steps:

1. Assume the defendant is innocent.
2. Present evidence to establish guilt, to the contrary of innocence (prosecution's responsibility).
3. Consider the weight of the evidence presented (jury's responsibility).

4. Make a decision. If the evidence is "beyond a reasonable doubt," the jury declares the defendant guilty; otherwise, the jury declares the defendant not guilty.

The process of conducting a hypothesis test has similar essential steps:

1. Assume the opposite of what we want the data to show (develop a working theory).
2. Gather data and compare it to the proposed model from step (1).
3. Quantify the likelihood of our data from step (2) under the proposed model.
4. If the likelihood is small, conclude the data is not consistent with the working model (there is evidence for what we want to show); otherwise, conclude the data is consistent with the working model (there is no evidence for what we want to show).

Notice that a trial focuses not on proving guilt but on disproving innocence; similarly, in statistics, we are able to establish evidence *against* a specified theory. This is one of several subtle points in hypothesis testing. We will discuss these subtleties at various points throughout the text and revisit the overall concepts often. Here, we focus solely on that first step — developing a working theory that we want to *disprove*.

Consider the above question for the Deepwater Horizon Case Study. We want to find evidence that the proportion experiencing adverse symptoms exceeds 0.20 (1 in 5). Therefore, we would like to *disprove* (or provide evidence *against*) the statement that the proportion experiencing adverse symptoms is no more than 0.20. This is known as the **null hypothesis**; the opposite of this statement, called the **alternative hypothesis**, captures what we would like to establish.

Definition 3.9 (Null Hypothesis)**:**
The statement (or theory) that we would like to disprove. *This is denoted* H_0*, read "H-naught" or "H-zero."*

Definition 3.10 (Alternative Hypothesis)**:**
The statement (or theory) capturing what we would like to provide evidence for*; this is the opposite of the null hypothesis. This is denoted* H_1 *or* H_a*, read "H-one" and "H-A" respectively.*

For the Deepwater Horizon Case Study, we write:

> H_0 : The proportion of volunteers assigned to clean wildlife following an oil spill who experience adverse respiratory symptoms is no more than 0.20.
> H_1 : The proportion of volunteers assigned to clean wildlife following an oil spill who experience adverse respiratory symptoms exceeds 0.20.

Each hypothesis is a well-posed statement (about a parameter characterizing the entire population), and the two statements are exactly opposite of one another meaning only one can be a true statement.

When framing your questions, be sure your null hypothesis and alternative hypothesis are exact opposites of one another, and ensure the "equality" component *always* goes in the null hypothesis.

We can now collect data and determine if it is consistent with the null hypothesis (a statement similar to "not guilty") or if the data provides evidence against the null hypothesis and in favor of the alternative (a statement similar to "guilty").

Often these statements are written in a bit more of a mathematical structure in which a Greek letter is used to represent the parameter of interest. For example, we might write

> Let θ be the proportion of volunteers (assigned to clean wildlife following an oil spill) who experience adverse respiratory symptoms.
> $H_0 : \theta \leq 0.20$
> $H_1 : \theta > 0.20$

In the above statements, θ represents the parameter of interest; the value 0.20 is known as the **null value**.

Definition 3.11 (Null Value)**:**
The value associated with the equality component of the null hypothesis; it forms the threshold or boundary between the two hypothesis. Note: not all questions of interest require a null value be specified.

Hypothesis testing is a form of statistical inference in which we quantify the evidence *against* a working theory (captured by the null hypothesis). We essentially argue that the data supports the alternative if it is not consistent with the working theory.

This section has focused on developing the null and alternative hypothesis when our question of interest is best characterized as one of comparing models or evaluating a particular statement. If our goal is estimation, a null and alternative hypothesis are not applicable. For example, we might have the following goal:

> Estimate the proportion of volunteers (assigned to clean wildlife following an oil spill) who experience adverse respiratory symptoms.

In this version of our research "question" there is no statement which needs to be evaluated. We are interested in estimation, not hypothesis testing and thus there is no corresponding null and alternative hypothesis.

Process for Framing a Question In order to frame a research question, consider the following steps:

1. Identify the population of interest.
2. Identify the parameter(s) of interest.
3. Determine if you are interested in estimating the parameter(s) or quantifying the evidence against some working theory.
4. If you are interested in testing a working theory, make the null hypothesis the working theory and the alternative the exact opposite statement (what you want to provide evidence for).

Chapter 4

Gathering the Evidence (Data Collection)

Consider again the goal of statistical inference — to use a sample as a snapshot to say something about the underlying population (Figure 4.1). This generally provokes unease in people, leading to a distrust of statistical results. In this section we attack that distrust head on.

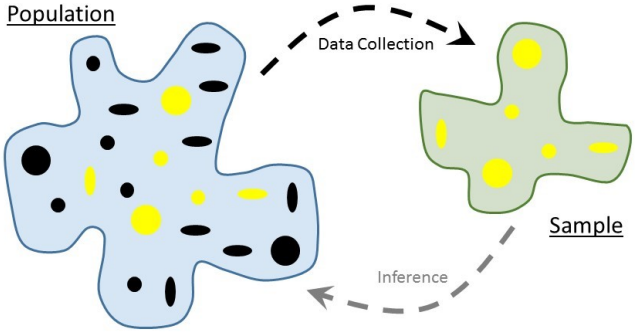


Figure 4.1: Illustration of the statistical process (reprinted from Chapter 1).

4.1 What Makes a Sample Reliable

If we are going to have some amount of faith in the statistical results we produce, we must have data in which we can place our trust. *The Treachery of Images* (Figure 4.2) is a canvas painting depicting a pipe, below which the artist wrote

the French phrase "This is not a pipe." Regarding the painting, the artist said

> The famous pipe. How people reproached me for it! And yet, could you stuff my pipe? No, it's just a representation, is it not? So if I had written on my picture "This is a pipe," I'd have been lying!

Figure 4.2: *The Treachery of Images* by René Magritte.

Just as a painting is a representation of the object it depicts, so a sample should be a representation of the population under study. This is the primary requirement if we are to rely on the resulting data.

In order for a statistical analysis to be reliable, the sample must be *representative* of the population under study.

We need to be careful to not get carried away in our expectations. What constitutes "representative" really depends on the question, just as an artist chooses his depiction based on how he wants to represent the object. Let's consider the following example.

Example 4.1: "School Debt"
In addition to a degree, college graduates also tend to leave with a large amount of debt due to college loans. In 2012, a graduate with a student loan had an average debt of $29,400; for graduates from private non-profit institutions, the average debt was $32,300[1].

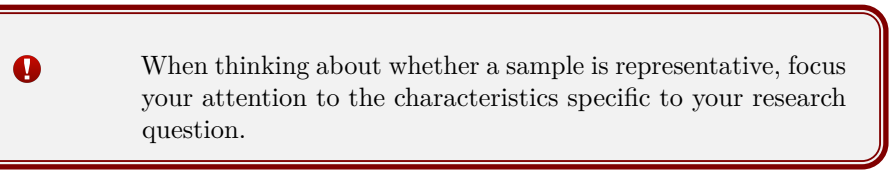
[1] http://ticas.org/sites/default/files/pub_files/Debt_Facts_and_Sources.pdf

Suppose we are interested in determining the average amount of debt in student loans carried by a graduating senior from Rose-Hulman Institute of Technology, a small private non-profit engineering school. There are many faculty at Rose-Hulman who choose to send their children to the institute. Since I am also on the faculty, I know many of these individuals. Suppose I were to ask each to report the amount of student loans their children carried upon graduation from Rose-Hulman. I compile the 25 responses and compute the average amount of debt. Further, I report that based on this study, there is significant evidence that the average debt carried by a graduate of Rose-Hulman is far below the $32,300 reported above (great news for this year's graduating class)! Why might we be hesitant to trust these results?

Many objections to statistical results stem from a distrust of whether the data (the sample) is really representative of the population of interest. Rose-Hulman, like many other universities, has a policy that the children of faculty may attend their university (assuming admittance) tuition-free. We would therefore expect their children to carry much less debt than the typical graduating senior. There is a mismatch between the group we would like to study and the data we have collected.

This example provides a nice backdrop for discussing what it means to be representative. First, let's define our population; in this case, we are interested in graduating seniors from Rose-Hulman. The variable of interest is the amount of debt carried in student loans; the parameter of interest is then the *average* amount of debt in student loans carried by graduating seniors of Rose-Hulman. However, the sample consists of only graduating seniors of Rose-Hulman who have a parent employeed by the university.

With regard to the grade point average of the students in our sample, it is probably similar to all graduating seniors. The starting salary of the students in our sample is probably similar to all graduating seniors; the fraction of mechanical engineering majors versus math majors is probably similar. So, in many regards the sample is representative of the population; however, it fails to be representative with regard to the variable of interest. This is our concern. The amount of debt carried by students in our sample is not representative of that debt carried by all graduating seniors from the university.



Does that mean the sample is useless? Yes and no. The sample collected cannot be used to answer our initial question of interest. No statistical method can fix bad data; statistics adheres to the "garbage-in, garbage-out" phenomena. If the data is bad, no analysis will undo that. However, while the sample cannot

be used to answer our initial question, it could be used to address a different question:

> What is the average amount of debt in student loans carried by graduating seniors from Rose-Hulman whose parent is a faculty member at the university?

For this revised question, the sample may indeed be representative. If we are working with previously collected data, we must consider the population to which our results will generalize. That is, for what population is the given sample representative? If we are collecting our data, we need to be sure we collect data in such a way that the data is representative of our target population. Let's first look at what *not* to do.

4.2 Poor Methods of Data Collection

Example **??** is an example of a "convenience sample," when the subjects in the sample are chosen simply due to ease of collection. Examples include surveying students only in your sorority when you are interested in all females who are part of a sorority on campus; taking soil samples from only your city when you are interested in the soil for the entire state; and, obtaining measurements from only one brand of phone, because it was the only one you could afford on your budget, when you are interested in studying all cell phones on the market. A convenience sample is unlikely to be representative if there is a relationship between the ease of collection and the variable under study. This was true in the School Debt example; the relationship of a student to a faculty member was directly related to the amount of debt they carried. As a result, the resulting sample was not representative of the population.

When conducting a survey with human subjects, it is common to only illicit responses from volunteers. Such "volunteer samples" tend to draw in those with extreme opinions. Consider product ratings on Amazon. Individual ratings tend to cluster around 5's and 1's. This is because those customers who take time to submit a review (which is voluntary) tend to be those who are really thrilled with their product (and want to encourage others to purchase it) and those who are really disappointed with their purchase (and want to encourage others to avoid it). Such surveys often fail to capture those individuals in the population who have "middle of the road" opinions.

We could not possibly name all the poor methods for collecting a sample; but, poor methods all share something in common — it is much more likely the resulting sample is not representative. Failing to be representative results in **biased** estimates of the parameter.

Definition 4.1 (Bias)**:**
A set of measurements is said to be biased if they are consistently *too high*

(or too low). Similarly, an estimate of a parameter is said to be biased if it is consistently *too high (or too low).*

To illustrate the concept of bias, consider shooting at a target as in Figure 4.3. We can consider the center of our target to be the parameter we would like to estimate within the population. The values in our sample (the strikes on the target) will vary around the parameter; while we do not expect any one value to hit the target precisely, a "representative" sample is one in which the values tend to be clustered about the parameter (unbiased). When the sample is not representative, the values in the sample tend to cluster off the mark (biased). Notice that to be unbiased, it may be that not a single value in the sample is perfect, but aggregated together, they point in the right direction. So, bias is not about an individual measurement being an "outlier," (more on those in a later chapter) but about repeatedly shooting in the wrong direction.

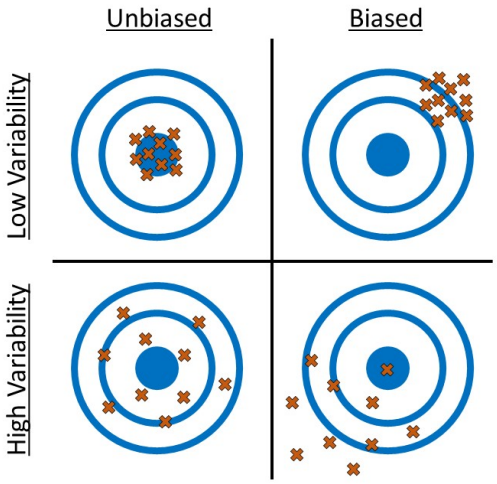


Figure 4.3: Illustration of bias and variability.

There is a difference between *accuracy* and *precision*. Generally, *accuracy* refers to location (and therefore bias); we say a process is accurate when it is unbiased. *Precision* refers to the variability.

Biased results are typically due to poor sampling methods that result in a sample which is not representative of the target population.

The catch (there is always a catch) is that we will never *know* if a sample is actually representative or not. We can, however, employ methods that help to minimize the chance that the sample is biased.

4.3 Preferred Methods of Sampling

No method guarantees a perfectly representative sample; but, we can take measures to reduce or eliminate bias. A useful strategy is to employ *randomization*. This is sum[illegible]nental Idea:

Fundamental Idea:

Fundamental Idea II: If data is to be useful for making conclusions about the population, a process referred to as drawing inference, proper data collection is crucial. Randomization can play an important role ensuring a sample is representative and that inferential conclusions are appropriate.

Consider the School Debt example again. Suppose instead of the strategy described there, we had done the following:

> We constructed a list of all graduating seniors from the university. We placed the name of each student on an index card; then, we thoroughly shuffled the cards and chose the top 25 cards. For these 25 individuals, we recorded the amount of debt in student loans each carried.

This essentially describes using a lottery to select the sample. This popular method is known as taking a **simple random sample**. By conducting a lottery, we make it very unlikely that our sample consists of only students with a very small amount of student debt (as occurred when we used a convenience sample).

Definition 4.2 (Simple Random Sample)**:**
Often abbreviated SRS, this is a sample of size n such that every *collection of size n is equally likely to be the resulting sample. This is equivalent to a lottery.*

There are situations in which a simple random sample does not suffice. Again, consider our School Debt example. The Rose-Hulman student body is predominantly domestic, with only about 3% of the student body being international

students. But, suppose we are interested in comparing the average debt carried between international and domestic students. It is very likely, by chance alone, that in a simple random sample of 25 students none will be international. Instead of a simple random sample, we might consider taking a sample of 13 domestic students and a sample of 12 international students; this is an example of a **stratified random sample**. This approach is useful when there is a natural grouping of interest within the population.

Definition 4.3 (Stratified Random Sample)**:**
A sample in which the population is first divided into groups, or strata, based on a characteristic of interest; a simple random sample is then taken within each group.

There are countless sampling techniques used in practice. The two described above can be very useful starting points for developing a custom method suitable for a particular application. Their benefit stems from their use of randomization.

This section is entitled "Preferred Methods" because while these methods are ideal, they are not always practical. Consider the Deepwater Horizon Case Study; conceptually, we can take a simple random sample of the volunteers for our study. However, as with any study involving human subjects, researchers would be required to obtain consent from each subject in the study. That is, a volunteer has the right to refuse to participate in the study. Therefore, it is unlikely that a simple random sample as described above could be obtained. Again, the key is to obtain a *representative* sample; while random selection may be a nice tool for accomplishing this, we may need to appeal to the composition of the sample itself to justify its use. *Based on the characteristics of those willing to participate in the study, do we feel the study participants form a representative group of all volunteers?* That is the essential question. This is often why studies report a table summarizing subject demographics such as age, gender, etc. It is also why it is extremely important for researchers to describe how subjects were selected so that readers may make the judgement for themselves whether the sample is representative.

4.4 Two Types of Studies

Thinking about how the data was collected helps us determine how the results generalize beyond the sample itself (to what population the results apply). When our question of interest is about the relationship between two variables (as most questions are), we must also carefully consider the study design. Too often separated from the statistical analysis that follows, keeping the study design in mind should guide the analysis as well as inform us about the conclusions we can draw.

In order to illustrate how study design can impact the results, consider the

following example.

Example 4.2: "Kangaroo Care"
At birth, infants have low levels of Vitamin K, a vitamin needed in order to form blood clots. Though rare, without the ability for her blood to clot, an infant could develop a serious bleed. In order to prevent this, the American Academy of Pediatrics recommends that all infants be given a Vitamin K shot shortly after birth in order to raise Vitamin K levels. As with any shot, there is typically discomfort to the infant, which can be very discomforting to new parents.

Kangaroo Care is a method of holding a baby which emphasizes skin-to-skin contact. The child, who is dressed only in a diaper, is placed upright on the parent's bare chest; a light blanket is draped over the child. Suppose we are interested in determining if utilizing the method while giving the child a Vitamin K shot reduces the discomfort in the infant, as measured by the total amount of time the child cries following the shot. Contrast the following two potential study designs:

(A) We allow the attending nurse to determine whether Kangaroo Care is initiated prior to giving the Vitamin K shot. Following the shot, we record the total time (in seconds) the child cries.
(B) We flip a coin. If it comes up heads, the nurse should have the parents implement Kangaroo Care prior to giving the Vitamin K shot; if it comes up tails, the nurse should give the Vitamin K shot without implementing Kagaroo Care. Following the shot, we record the total time (in seconds) the child cries.

Note, in both study designs (A) and (B), we only consider term births which have no complications to avoid situations that might alter the timing of the Vitamin K shot or the ability to implement Kangaroo Care.

Note that there are some similarities in the two study designs:

- The underlying population is the same for both designs — infants born at term with no complications.
- There are two groups being compared in both designs — the "Kangaroo Care" group and the "no Kangaroo Care" group.
- The response (variable of interest) is the same in both designs — the time (in seconds) the infant cries.
- There is action taken by the researcher in both designs — a Vitamin K shot is given to the child.

There is one prominent difference between the two study designs:

- For design (A), the choice of Kangaroo Care is left up to the nurse (self-selected); for design (B), the choice of Kangaroo is *assigned* to the nurse by the researcher, and this selection is made *at random*.

Design (A) is an example of an **observational study**; design (B) is a **controlled experiment**.

Definition 4.4 (Observational Study)**:**
A study in which each subject "self-selects" into one of groups being compared in the study. The phrase "self-selects" is used very loosely here and can include studies in which the groups are defined by an inherent characteristic or the groups are chosen haphazardly.

Definition 4.5 (Controlled Experiment)**:**
A study in which each subject is randomly *assigned to one of the groups being compared in the study.*

It is common to think that anytime the environment is "controlled" by the researcher that a controlled experiment is taking place, but the defining characteristic is the random assignment to groups (sometimes referred to as the *factor* under study or *treatment* groups). In the example above, both study designs involved a controlled setting (the delivery room of a hospital) in which trained staff (the nurse) deliver the shot. However, only design (B) is a controlled experiment because the researchers randomly determined into which group the infant would be placed.

To understand the impact of random allocation, suppose that we had conducted a study using design (A); further, the results suggest that those infants who were given a shot while using Kangaroo Care cried for a shorter time period, on average. Can we conclude that it was the Kangaroo Care that led to the shorter crying time? Maybe. Consider the following two potential explanations for the resulting data:

(1) Kangaroo Care is very effective; as a result, those children who were given Kangaroo Care had reduced crying time, on average, following the Vitamin K shot.
(2) It turns out that those nurses who chose to implement Kangaroo Care (remember, they have a choice under design (A) whether they implement the method) were also the nurses with a gentler bedside manner. Therefore, these nurses tended to be very gentle when giving the Vitamin K shot whereas the nurses who chose not to implement Kangaroo Care tended to just jab the needle in when giving the shot. As a result, the reduced crying time is not a result of the Kangaroo Care but the manner in which the shot was given.

The problem is that we are unable to determine which of the explanations is correct. Given the data we have collected, we are unable to tease out the effect of the Kangaroo Care from that of the nurse's bedside manner. As a result, we are able to say we observed an *association* between the use of Kangaroo Care and reduced crying time, but we are unable to conclude that Kangaroo Care

caused a reduction in the crying time (that is, there may not be a *relationship* between the two variables). In this hypothetical scenario, the nurse's bedside manner is called a **confounder**.

Definition 4.6 (Confounding)**:**
When the effect of a variable on the response is mis-represented due to the presence of a third, potentially unobserved, variable known as a confounder.

Confounders can mask the relationship between the factor under study and the response. There is a documented association between ice cream sales and the risk of shark attacks. As ice cream sales increase, the risk of a shark attack also tends to increase. This does not mean that if a small city in the Midwest increases its ice cream sales that the citizens are at higher risk of being attacked by a shark. As Figure 4.4 illustrates, there is a confounder — temperature. As the temperatures increase, people tend to buy more ice cream; as the temperature increases, people tend to go to the beach increasing the risk of a shark attack. Two variables can appear to be related as a result of a confounder.

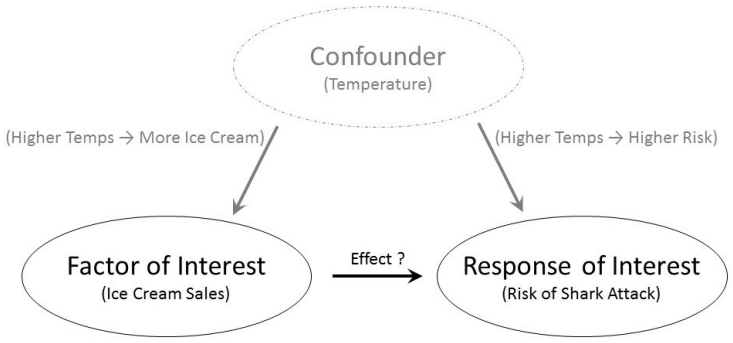


Figure 4.4: Illustration of a confounding variable. The confounder, related to both the factor and the treatment can make it appear as though there is a causal relationship when none exists.

Confounders are variables that influence *both* the factor of interest and the response.

Observational studies are subject to confounding; thus, controlled experiments are often considered the gold standard in research because they allow us to infer cause-and-effect relationships from the data. Why does the random allocation make such an impact? Because it removes the impact of confounders. Let's return to the hypothetical Vitamin-K study. Suppose there are nurses with a

gentle bedside manner and those who are a little less gentle. If the infants are randomly assigned to one of the two treatment groups, then for every gentle nurse who is told to implement Kangaroo Care while giving the shot, there tends to be a gentle nurse who is told to not implement Kangaroo Care. Similarly, for every mean nurse who is told to implement Kangaroo Care while giving a shot, there tends to be a mean nurse who is told to not implement Kangaroo Care. This is illustrated in Figure 4.5. For an observational study, the treatment groups can be unbalanced; for example, the figure illustrates a case in which there is a higher fraction (11/12 compared to 1/4) of friendly nurses in the Kangaroo Care group compared to the No Kangaroo Care group. For the controlled experiment however, the treatment groups tend to be balanced; there is approximately the same fraction of friendly nurses in both groups. Random assignment is the great equalizer. It tends to result in groups which are similar in all respects; therefore, any differences we observe between the groups *must* be due to the grouping and not an underlying confounding variable.

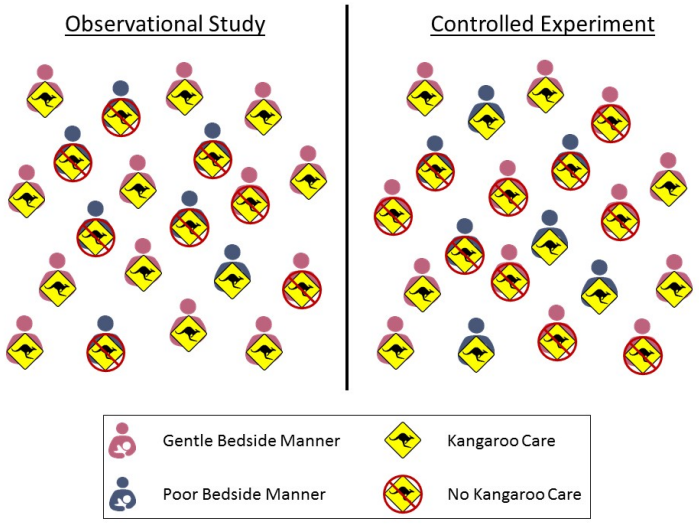


Figure 4.5: Illustration of the impact of random assignment in study design. For the observational study, the treatment groups are unbalanced. For the controlled experiment, the treatment groups are balanced.

Randomly assigning subjects to groups balances the groups with respect to any confounders; that is, the groups being compared are similar. Therefore, any differences between the two groups can be attributed to the grouping factor itself, leading to cause-and-effect conclusions.

While controlled experiments are a fantastic study design, we should not discount the use of observational studies. Consider the Deepwater Horizon Case Study; suppose we are interested in the following question:

> Is there evidence that volunteers who are directly exposed to oil have an increased risk of developing adverse respiratory symptoms compared to those who are not directly exposed to oil?

The response is whether a volunteer develops adverse respiratory symptoms; the factor of interest is whether the volunteer has direct exposure to oil. We could conduct a controlled experiment by randomly determining which volunteers are assigned to wildlife clean up and which are assigned to administrative tasks, for example. However, it may be that volunteer tasks need to be determined by skillset or by greatest need at the time the person volunteers. It may not be feasible to randomly assign volunteers to specific positions. Or, it could be that the data was obtained after the fact; that is, the data is not the result of a planned study in which case random assignment is not possible because volunteers self-selected into positions in the past. If random assignment is not possible, it does not mean the data is useless. But, it does mean we will need to be sure we address the potential confounding when performing the analysis and discussing the results.

The big idea is that in order to make causal conclusions, we must be able to state that the groups being compared are balanced with respect to any potential confounders; random assignment is one technique for accomplishing this.

Chapter 5

Presenting the Evidence (Summarizing Data)

If you open any search engine and look up "data visualization," you will quickly be overwhelmed by a host of pages, texts, and software filled with tools for summarizing your data. Here is the bottom line: a good visualization is one that helps you answer your question of interest. It is both that simple and that complicated

Fundamental Idea:

Fundamental Idea III: The use of data for decision making requires that the data be summarized and presented in ways that address the question of interest.

Whether simple or complex, all graphical and numerical summaries should help turn the data into usable information. Pretty pictures for the sake of pretty pictures are not helpful. In this section, we will consider various simple graphical and numerical summaries to help build a case for addressing the question of interest.

5.1 Characteristics of a Distribution (Summarizing a Single Variable)

Remember that because of *variability*, the key to asking good questions is to not ask questions about individual values but to characterize the underlying *distribution* (see Definition 3.3). Therefore, characterizing the underlying distribution is also the key to a good visualization or numeric summary. For the Deepwater Horizon Case Study, the response (whether a volunteer experienced adverse

respiratory symptoms) is categorical. As we stated previously, summarizing the distribution of a categorical variable reduces to showing how individual subjects fall into the various groups. Figure 5.1 displays a *bar chart* summarizing the rate of respiratory symptoms for volunteers cleaning wildlife.

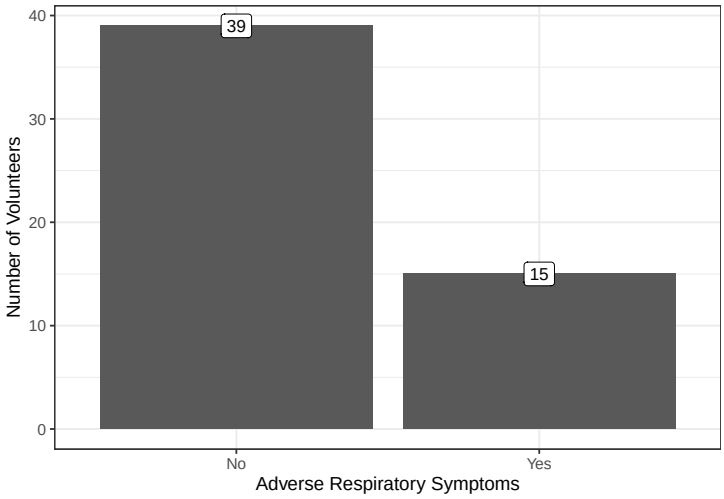


Figure 5.1: Frequency of adverse respiratory symptoms for volunteers cleaning wildlife following the Deepwater Horizon oil spill.

In general, it does not matter whether the frequency or the relative frequencies are reported; however, if the relative frequencies are plotted, some indication of the sample size should be provided with the figure either as an annotation or within the caption. From the above graphic, we see that nearly 28% of volunteers assigned to wildlife experienced adverse respiratory symptoms; the graphic helps address our question, even if not definitively.

When you are summarizing only categorical variables, a bar chart is sufficient. Statisticians tend to agree that bar charts are preferable to pie charts (see this whitepaper and this blog for further explanation).

While a single type of graphic (bar charts) are helpful for looking at categorical data, summarizing the distribution of a numeric variable requires a bit more thought. Consider the following example.

Example 5.1: "Paper Strength"
While electronic records have become the predominant means of storing information, we do not yet live in a paperless society. Paper products are still

Table 5.1: Breaking length (km) for first 5 specimens in the Paper Strength study.

Specimen	Breaking Length
1	21.312
2	21.206
3	20.709
4	19.542
5	20.449

used in a variety of applications ranging from printing reports and photography to packaging and bathroom tissue. In manufacturing paper for a particular application, the strength of the resulting paper product is a key characteristic.

There are several metrics for the strength of paper. A conventional metric for assessing the inherent (not dependent upon the physical characteristics, such as the weight of the paper, which might have an effect) strength of paper is the *breaking length*. This is the length of a paper strip, if suspended vertically from one end, that would break under its own weight. Typically reported in kilometers, the breaking length is computed from other common measurements. For more information on paper strength measurements and standards, see the following website: http://www.paperonweb.com

A study was conducted at the University of Toronto to investigate the relationship between pulp fiber properties and the resulting paper properties (Lee 1992). The breaking length was obtained for each of the 62 paper specimens, the first 5 measurements of which are shown in Table 5.1. The complete dataset is available online at the following website: https://vincentarelbundock.github.io/Rdatasets/doc/robustbase/pulpfiber.html

While there are several questions one might ask with the available data, here we are primarily interested in characterizing the breaking length of these paper specimens.

Figure 5.2 presents the breaking length for all 62 paper specimens in the sample through a *dot plot* in which the breaking length for each observed specimen is represented on a number line using a single dot.

With any graphic, we tend to be drawn to three components:

- *where* the values tend to be,
- *how tightly* the values tend to be clustered there, and
- *the way* the values tend to cluster.

Notice that about half of the paper specimens in the sample had a breaking length longer than 21.26 km. Only about 25% of paper specimens had a breaking length less than 19.33 km. These are measures of *location*. In particular, these

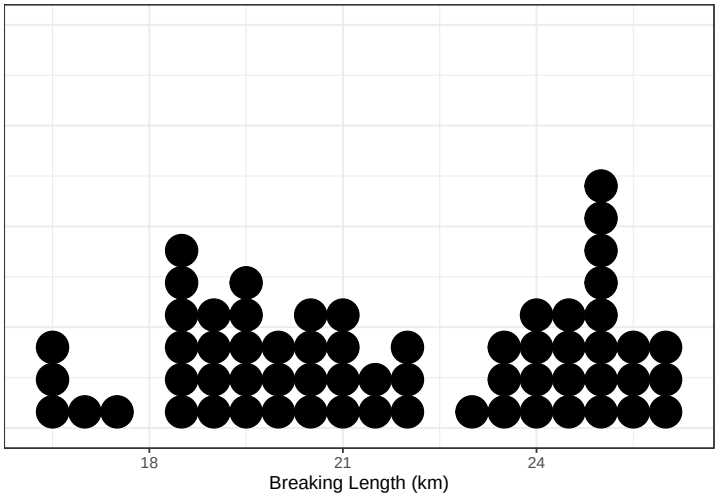


Figure 5.2: Breaking Length (km) for 62 paper specimens.

are known as **percentiles**, of which the **median**, **first quartile** and **third quartile** are commonly used examples.

Definition 5.1 (Percentile)**:**
The k-th percentile is the value q such that $k\%$ of the values in the distribution are less than or equal to q. For example,

- *25% of values in a distribution are less than or equal to the 25-th percentile (known as the "first quartile" and denoted Q_1).*
- *50% of values in a distribution are less than or equal to the 50-th percentile (known as the "median").*
- *75% of values in a distribution are less than or equal to the 75-th percentile (known as the "third quartile" and denoted Q_3).*

The **average** is also a common measure of location. The breaking length of a paper specimen is 21.72 km, on average. In this case, the average breaking length and median breaking length are very close; this need not be the case. The average is not describing the "center" of the data in the same way as the median; they capture different properties.

Definition 5.2 (Average)**:**
Also known as the "mean," this measure of location represents the balance point for the distribution. It is denoted by $\bar{x}$.

For a sample of size n, it is computed by

$$\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i$$

where x_i rerpesents the i-th value in the sample.

When referencing the average for a population, the mean is also called the "Expected Value," and is often denoted by μ.

Clearly, the breaking length is not equivalent for all paper specimens; that is, there is variability in the measurements. Measures of *spread* quantify the variability of values within a distribution. Common examples include the **standard deviation** (related to **variance**) and **interquartile range**. For the Paper Strength example, the breaking length varies with a standard deviation of 2.88 km; the interquartile range for the breaking length is 5.2 km.

The standard deviation is often reported more often than the variance since it is on the same scale as the original data; however, as we will see later, the variance is useful from a mathematical perspective for derivations. Neither of these values has a natural interpretation; instead, larger values of these measures simply indicate a higher degree of variability in the data.

Definition 5.3 (Variance)**:**
A measure of spread, this roughly captures the average distance values in the distribution are from the mean.

For a sample of size n, it is computed by

$$s^2 = \frac{1}{n-1}\sum_{i=1}^{n} (x_i - \bar{x})^2$$

where $\bar{x}$ is the sample mean and x_i is the i-th value in the sample. The division by $n-1$ instead of n reduces the bias in the statistic.

The symbol σ^2 is often used to denote the variance in the population.

Definition 5.4 (Standard Deviation)**:**
A measure of spread, this is the square root of the variance.

Definition 5.5 (Interquartile Range)**:**
The distance between the first and third quartiles. This measure of spread indicates the range over which the middle 50% of the data is spread.

The measures we have discussed so far are illustrated in Figure 5.3. While some authors suggest the summaries you choose to report depends on the shape of the distribution, we argue that it is best to report the values that align with the question of interest. It is the question that should be shaped by the beliefs about the underlying distribution.

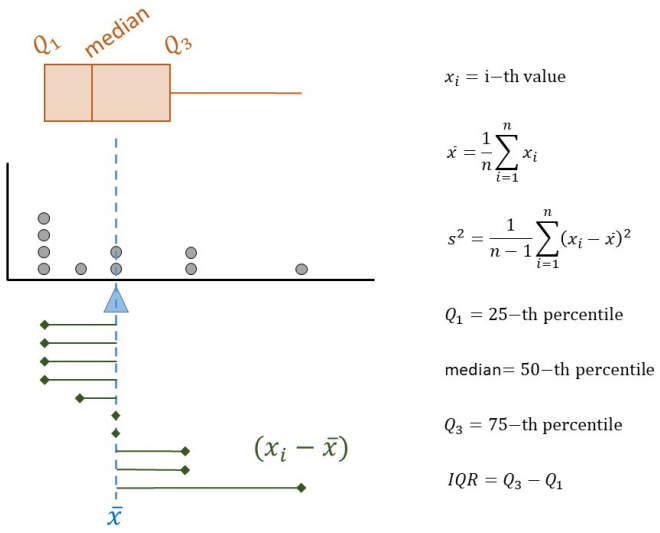


Figure 5.3: Illustration of measures of location and spread for a distribution of values.

Finally, consider the *shape* of the distribution of breaking length we have observed. The breaking length tends to be clustered in two locations; we call this *bimodal* (each mode is a "hump" in the distribution). Other terms used to describe the shape of a distribution are *symmetric* and *skewed*. Symmetry refers to cutting a distribution in half (at the median) and the lower half being a mirror image of the upper half; skewed distributions are those which are not symmetric.

Observe then that the dot plot above gives us some idea of the location, spread, and shape of the distribution, in a way that the table of values could not. This makes it a useful graphic as it is characterizing the **distribution of the sample** we have observed. This is one of the four components of what we call the *Distributional Quartet*.

Definition 5.6 (Distribution of the Sample)**:**
The pattern of variability in the observed values of a variable.

When the sample is not large, a dot plot is reasonable. Other common visualizations for a single variable include:

- *jitter plot*: similar to a dot plot, each value observed is represented by a dot; the dots are "jittered" (shifted randomly) in order to avoid overplotting when many subjects share the same value of the response.
- *box plot*: a visual depiction of five key percentiles; the plot includes the minimum, first quartile, median, third quartile, and maximum value observed. The quartiles are connected with a box, the median cuts the box into two components.
- *histogram*: can be thought of as a grouped dot plot in which subjects are "binned" into groups of similar values. The height of each bin represents the number of subjects falling into that bin.
- *density plot*: a smoothed histogram in which the y-axis has been standardized so that the area under the curve has value 1. The y-axis is not interpretable directly, but higher values simply mean more likely to occur.

To illustrate these graphics, the breaking length for the Paper Strength example is summarized using various methods in Figure 5.4. The latter three visualizations are more helpful when the dataset is very large and plotting the raw values actually hides the distribution. There is no right or wrong graphic; it is about choosing the graphic which addresses the question and adequately portrays the distribution.

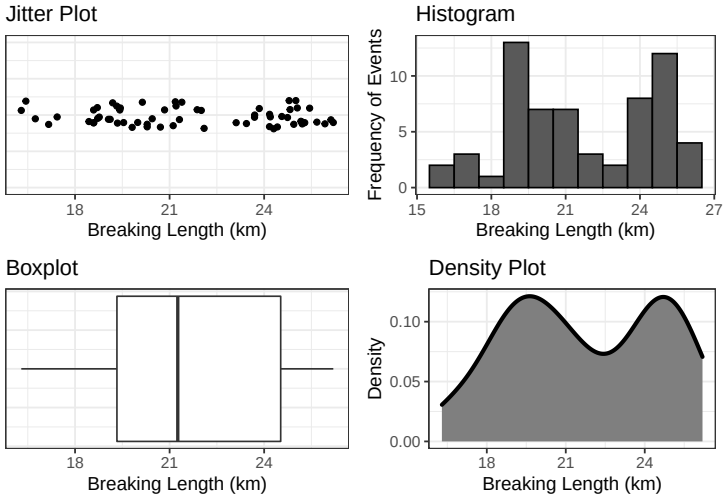


Figure 5.4: Four graphical summaries of the breaking length for the Paper Strength example.

The numeric summaries of a distribution are known as **statistics**. While parameters characterize a variable at the population level, statistics characterize a variable at the sample level.

Definition 5.7 (Statistic)**:**

Numeric quantity which summarizes the distribution of a variable within a sample.

Why would we compute numerical summaries in the sample if we are interested in the population? Remember the goal of this discipline is to use the sample to say something about the underlying population. As long as the sample is representative, the distribution of the sample should reflect the **distribution of the population**; therefore, summaries of the sample should be close to the analogous summaries of the population (statistics estimate their corresponding parameters). Now we see the real importance of having a representative sample; it allows us to say that what we observe in the sample is a good proxy for what is happening in the population.

Definition 5.8 (Distribution of the Population)**:**
The pattern of variability in values of a variable at the population level. Generally, this is impossible to know, but we might model it.

That is, the mean in the sample should approximate (estimate) the mean in the population; the standard deviation of the sample should estimate the standard deviation in the population; and, the shape of the sample should approximate the shape of the population, etc. The sample is acting as a representation in all possible ways of the population.

A representative sample reflects the population; therefore, we can use statistics as estimates of the population parameters.

We would never use $\bar{x}$ to represent a parameter like the mean of the population. The symbol $\bar{x}$ (or $\bar{y}$, etc.) represents observed values being averaged together. Since the values are observed, we must be talking about the sample, and therefore $\bar{x}$ represents a statistic. A similar statement could be made for s^2 (sample variance) compared to σ^2 (population variance). In reality, the symbols themselves are not important. The importance is on their representation. Statistics are observed while parameters are not.

5.2 Summarizing Relationships

The summaries discussed above are nice for examining a single variable. In general, research questions of interest typically involve the relationship between

two or more variables. Most graphics are two-dimensional (though 3-dimensional graphics and even virtual reality are being utilized now); therefore, summarizing a rich set of relationships may require the use of both axes as well as color, shape, size, and even multiple plots in order to tell the right story. We will explore these various features in upcoming units of the text. Here, we focus on the need to tell a story that answers the question of interest instead of getting lost in making a graphic. Consider the following question from the Deepwater Horizon Case Study:

> What is the increased risk of developing adverse respiratory symptoms for volunteers cleaning wildlife compared to those volunteers who do not have direct exposure to oil?

Consider the graphic in Figure 5.5; this is *not* a useful graphic. While it compares the number of volunteers with symptoms in each group, we cannot adequately address the question because the research question involves comparing the rates for the two groups.

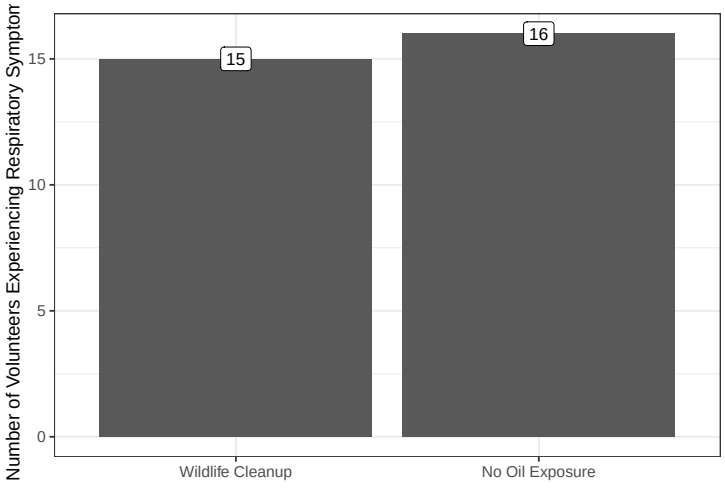


Figure 5.5: Illustration of a poor graphic; the graphic does not give us a sense of the rate within each group in order to make a comparison.

Instead, Figure 5.6 compares the rates within each group. Notice that since we are reporting relative frequencies, we also report the sample size for each group.

From the graphic, it becomes clear that within the sample a higher fraction of volunteers cleaning wildlife experienced adverse symptoms compared with those without oil exposure. In fact, volunteers cleaning wildlife were 1.79 times more likely to experience adverse respiratory symptoms.

The key to a good summary is understanding the question of interest and addressing this question through a useful characterization of the variability.

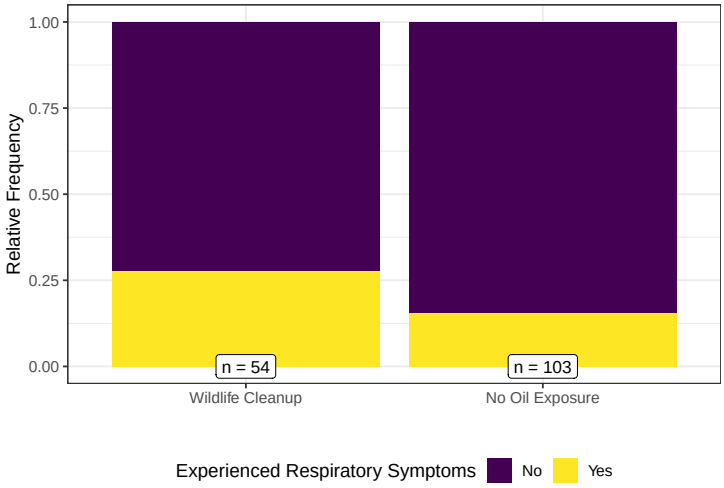


Figure 5.6: Comparison of the rate of adverse respiratory symptoms among volunteers assigned to different tasks.

Chapter 6

Assessing the Evidence (Quantifying the Variability in Estimates)

Again, the goal of statistical inference is to use the sample as a snapshot of the underlying population (Figure 6.1). There are generally three reasons people distrust this process:

1. Fear that the sample does not represent what is going on in the population.
2. Fear that we cannot make a conclusion with a sample of size n (wanting more data).
3. Fear that one study is not enough to make a conclusion.

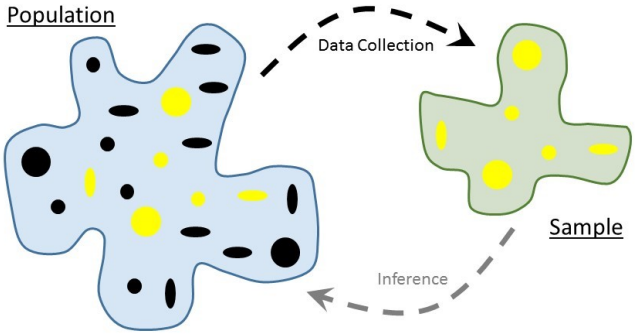


Figure 6.1: Illustration of the statistical process (reprinted from Chapter 1).

We have already tackled the first fear in Chapter 4; if we are to trust statistical results, we must collect data that is representative of the underlying population. The second and third fears above are tied together, though maybe not obviously. Before launching into a slightly more formal discussion, consider the following thought experiment.

Example 6.1: "Free Throws"
Your friend Dave lives for his Wednesday "pick-up" basketball games at the gym. One afternoon, while waiting for a few more players to arrive Dave shoots 10 free throws, of which he makes 3.

I imagine no one is ready to claim *definitively* that Dave has a 30% success rate from the free throw line. So, what can we say? Well, if this set of 10 free throws is representative of Dave's free throw performance, then we would say that 30% is an *estimate* for his success rate; that is, the statistic 30% is a good guess at the unknown parameter (overall success rate). There are two ways we might improve our "trust" in this estimate. First, we might consider a larger sample size (make Dave shoot more free throws); let's continue along these lines for a moment.

Example 6.2: "Free Throws (cont.)"
Joe has also been waiting for a few more players to arrive; however, Joe shoots 100 free throws (clearly he has more time on his hands) of which he makes 30.

Again, we probably wouldn't claim *definitively* that Joe has a 30% success rate from the free throw line. And again, assuming this set of 100 free throws is representative of his overall performance, we would say 30% is an *estimate* for his success rate. But, we might also say we have more "trust" in our guess for Joe's overall performance compared with our guess for Dave's. The more shots we observe, the more we seem to "trust" our estimate. This idea is known as the **Law of Large Numbers**.

Definition 6.1 (Law of Large Numbers)**:**
For our purposes, this essentially says that as a sample size gets infinitely large, a statistic will become arbitrarily close (extremely good approximation) of the parameter it estimates.

There are two drawbacks with the Law of Large Numbers. First, it does not tell us how "close" a statistic is to the parameter for any specific sample size; second, we cannot take an infinitely large sample. And, for populations which are infinitely large (like all the free throws Dave could ever shoot, for example), any sample size could be considered small relative to the size of the population. For our thought experiment, it is probably not feasible to have Dave or Joe

shoot thousands of free throws, for example. Our goal then becomes to somehow quantify the "trust" we have in our estimates *given the sample size we have available*. That is, given that we only saw Dave shoot 10 free throws, can we quantify our "trust" in that 30% estimate of his free throw success? We need some way of measuring "trust," and we do that through a notion of statistical "confidence."

In statistics, our "trust" is tied to the estimate's repeatability — "if we were to repeat the study, how much would we expect our estimate to change?"

We will formalize the notion of statistical confidence shortly, but for now, linking our trust in an estimate to its repeatability gets at the last fear. We know that if we repeat a study, the results will change; our job is to quantify (keeping the sample size in mind) the degree to which the results will change. That is, we need to quantify the *variability* in the estimate across repeated studies (known as sampling variability; we told you statistics was all about variability). This is characterized by the **sampling distribution**.

Definition 6.2 (Sampling Distribution)**:**
The distribution of a statistic *across repeated samples.*

This is perhaps the most important of the *Distributional Quartet*; it is the holy grail of statistical inference. Once we have the sampling distribution, inference is straight-forward.

Fundamental Idea:

Fundamental Idea IV: Variability is inherent in any process, and as a result, our estimates are subject to sampling variability. However, these estimates often vary across samples in a predictable way; that is, they have a distribution that can be modeled.

6.1 Conceptualizing the Sampling Distribution

The sampling distribution of a statistic is one of the most fundamental, and yet one of the most abstract, concepts in statistics. Its name is even confusing; the "distribution of the sample" (Definition 5.6) and the "sampling distribution" (Definition 6.2) are two different things. Let's first focus on getting ahold of this abstract concepts.

For the Deepwater Horizon Case Study, consider the following question:

> What proportion of volunteers assigned to clean wildlife will develop adverse respiratory symptoms?

In the sample, we observed 15 out of 54 such volunteers (27.8% or a proportion of 0.278). This proportion is a good estimate of the rate of adverse symptoms in the population (assuming the sample is representative, of course).

Now, imagine randomly selecting 54 *new* volunteers from the population (repeating the study). For this new sample, it would be possible to determine the fraction of volunteers that experienced adverse symptoms; we would expect this value to be a bit different than what we obtained in the first sample since the two samples consist of different subjects. Since this second sample is also representative, however, it also provides a good estimate of the parameter. That is, we now have two good estimates of the same parameter.

Now, we could take a third random sample of 54 volunteers and compute the fraction in this third sample which experienced adverse symptoms. This third sample also provides a good (and potentially unique) estimate of the parameter. We could continue this process m times, for some large number m, as illustrated in Figure 6.2.

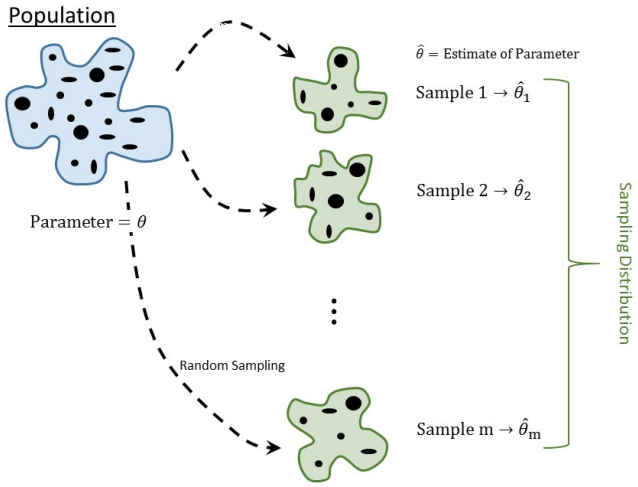


Figure 6.2: Illustration of repeatedly sampling from a population.

Consider what we are describing. With each representative sample, we have constructed an estimate of the parameter. What we have kept from each replicate sample is *not* the values of the variables themselves (whether the volunteers experienced adverse respiratory symptoms); instead, we have retained the *statistic* from each of m completely different studies. So, which of these m estimates do we trust? *All of them.* Since each sample is representative of the population,

each estimate is a good (not perfect) estimate of the parameter. Since we have all these estimates, we could think about pooling the information from all of them; describing the way in which these estimates change from one sample to another is the sampling distribution.

Notice that the sampling distribution is not describing a variable; it is describing a *statistic*. In order to construct a sampling distribution, we go through the following steps:

1. Take a sample; record variables of interest.
2. Compute the statistic which estimates the parameter and retain this value.
3. Repeat steps 1 and 2 a large number of times.
4. Examine the statistics collected.

So, the sampling distribution is not a plot of the raw values of a variable on individual subjects but a plot of statistics which summarize entire samples. That is, the unit of observation has changed. While a sample consists of individual subjects from the population, the sampling distribution consists of individual samples from the population.

Re-read the description of a sampling distribution several times, and return to it often as you read through the text. It takes a while for this to sink in, but if you truly grasp this one concept, the remainder of statistical inference becomes much more accessible.

6.2 Example of a Sampling Distribution

Since this idea is so critical to grasping statistical inference, we are going to walk through the process of generating a sampling distribution for a known data generating process.

Example 6.3: "Dice Experiment"
Consider an ordinary six-sided die; we are interested in the proportion of times that rolling the die will result in a 1. Putting this in the language of the statistics, we have the following:

- The *population* of interest is all rolls of the die. Notice that this population is infinitely large as we could roll the die forever.
- The *variable* is the resulting value from the roll. Since this can take on only one of six values, this is a categorical variable.
- The *parameter* of interest is the proportion of rolls that result in a 1.

Our goal is to construct the sampling distribution of the *sample proportion* of rolls that result in a 1 when the die is rolled 20 times.

What makes this example unique is that we know the value of the parameter. Because of the physical properties of a die, we know that the probability a roll results in a 1 is $\theta = 1/6$. So, statistical inference is not needed here. This example simply provides a simple vehicle for studying sampling distributions. Also, before going on, notice that the sampling distribution is for the statistic (the *sample proportion*) and not the parameter; and, it is constructed for a fixed sample size (in this case, $n = 20$ rolls). Going back to the steps for creating a sampling distribution described in the previous section, we have the following steps:

1. Roll a die 20 times, each time recording the resulting value.
2. Compute the proportion of times (out of the 20) the resulting value was a 1 and retain this value.
3. Repeat steps 1 and 2 a large number of times (let's say 500).
4. Plot the resulting values; there should be 500 proportions that we are keeping.

Notice that we are actually rolling a die 10000 times (20 rolls repeated 500 times); we only keep 500 values (one proportion for each set of 20 rolls). This is something you could physically do at home. For example, the first sample might look like that in Figure 6.3.

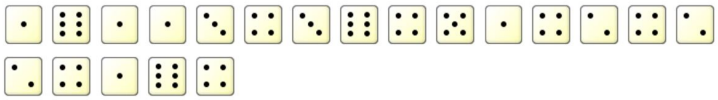


Figure 6.3: Potential sample of rolling a die 20 times.

For this particular sample, the proportion in the sample (our statistic of interest) would be 0.25 (5/20). That is the value we would record. We then repeat this 499 more times. You could try a few out yourself using an online simulator. Figure 6.4 shows the resulting proportions for when we simulated this process with 500 samples, each sample consisting of 20 rolls.

With modern computing power, there is no need to restrain ourselves to repeating the study 500 times. A simple computer program could replicate rolling the study (20 rolls of a die) thousands of times. Figure 6.5 is the sampling distribution for the proportion of rolls that result in a 1 based on a sample of size 20, repeating the study 50000 times.

Notice that the sampling distribution is centered around the true value of the parameter ($\theta = 1/6$). In general, the sampling distribution of a statistic, when taken from a random sample, is centered on the true value of the parameter. This is the unbiased nature of the data coming out; random samples are representative of the population. Similarly, note that while no one sample (remember, each value in the distribution represents a statistic from a sample of 20 values) is perfect, none of the samples produced values which were really far from the true

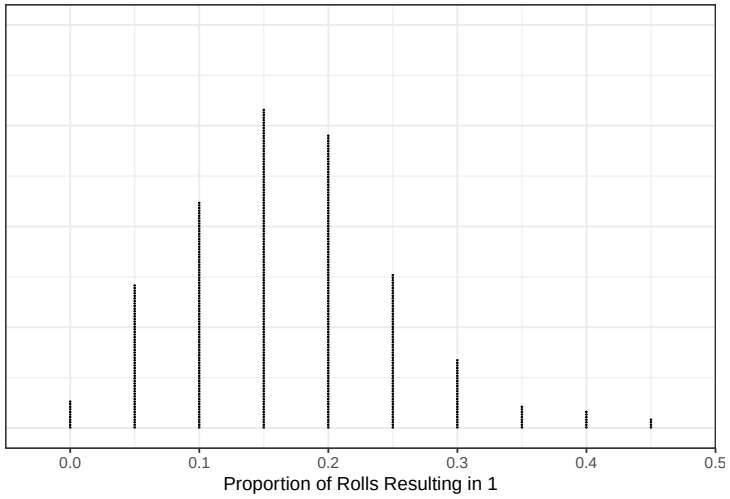


Figure 6.4: Sampling distribution for the proportion of 20 rolls of a die which result in a 1. The distribution is based on repeating the sampling process 500 times.

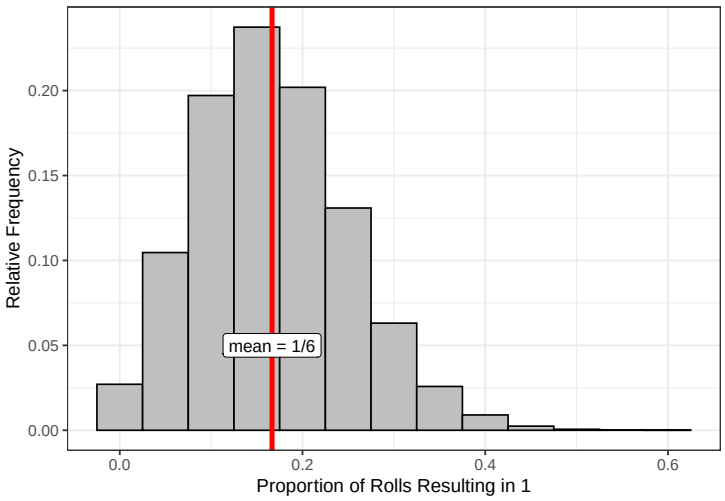


Figure 6.5: Sampling distribution for the proportion of 20 rolls of a die which result in a 1. The distribution is based on repeating the sampling process 50000 times.

parameter. That is, a representative sample may not be perfect, but it will give a *reasonable* estimate of the parameter. Notice that these properties hold even though we had a relatively small sample size (only rolling the die $n = 20$ times).

The size of the sample is not as important as whether it is representative. A small representative sample is better for making inference than a large sample which is biased.

One of the most useful things about the sampling distribution is that it gives us an idea of how much we might expect our statistic to change from one sample to another. Based on Figure 6.5, we could say that if we roll a die 20 times, the proportion of rolls which result in a 1 is most likely to be between 0.05 and 0.30 (so somewhere between 1 and 6 ones out of the 20 rolls). It would be *extremely* rare to have 12 of the 20 rolls result in a 1 (notice how small the bar is on the 0.6 proportion). The sampling distribution is therefore giving us an idea of the variability in our statistic.

Remember, our goal was to account for the variability in the statistic (how much it changes from one sample to another) *while accounting for the sample size*. How is this done? When forming the sampling distribution, we repeated the study. For each replication, we obtained a new sample that *had the same size as the original*. So, the sample size is baked into the sampling distribution. To see the impact of taking a larger sample, consider rolling a six-sided die 60 times instead of 20 times. When we build the sampling distribution, each replication will then involve repeating the process with 60 new rolls. Figure 6.6 shows the sampling distribution of the proportion of 60 rolls which result in a 1, using 50000 replications. Notice that the distribution is still centered on the true parameter $\theta = 1/6$. The primary difference between this figure and the last is that when we increased the sample size, the sampling distribution narrowed.

We all have this intuition that "more data is better." In truth, we should say "more *good* data is better." By "better," we mean that the statistic is less variable. Notice that we have to be careful here. We are not saying that the *sample* has less variability; we are saying the *statistic* has less variability. That is, we do not expect our estimate to change as much from one sample to the next. From Figure 6.6, we have that if we roll the die 60 times, we expect the proportion of 1's to be somewhere between 0.1 and 0.25 (somewhere between 6 and 15 ones out of the 60 show up). The proportion is varying much less from one sample to the next compared to when we rolled the die only 20 times.

Larger samples result in *statistics* which are less variable. This shows itself in the sense that the sampling distribuiton is narrower.

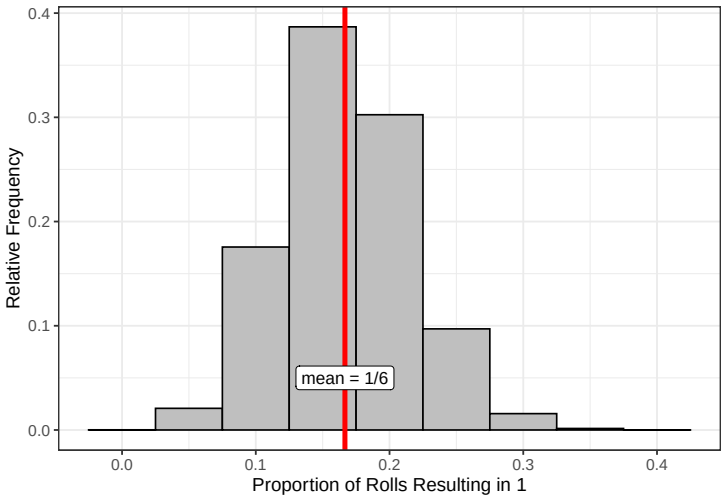


Figure 6.6: Sampling distribution for the proportion of 60 rolls of a die which result in a 1. The distribution is based on repeating the sampling process 50000 times.

Students often believe that a large sample reduces the variability in the data. That is not true; a large sample reduces the variability in the *statistic*.

We repeat a warning here that we stated when introducing the concept of *bias*. There is a difference between *accuracy* and *precision*. Generally, *accuracy* refers to location (and therefore bias); we say an estimate is accurate accurate when it is unbiased. *Precision* refers to the variability; we say an estimate is more precise when it has less variability. With regard to sampling distributions, accuracy refers to the center of the sampling distribution while precision refers to its spread.

6.3 Modeling the Sampling Distribution

Let's return to the Deepwater Horizon Case Study. In particular, suppose we are tyring to address the following question:

> What proportion of volunteers assigned to clean wildlife will develop adverse respiratory symptoms?

We have an estimate for this proportion ($\widehat{p} = 0.278$) based on the observed sample. Based on the discussion in the previous section, we know the sampling distribution of this proportion can help us quantify the variability in the estimate. Figure 6.7 represents the sampling distribution of this proportion. From the graphic, we would not expect the proportion of volunteers who experience adverse respiratory symptoms to move much beyond 0.15 and 0.4 if we were to repeat the study; it would almost certainly not move beyond 0.1 and 0.5 if we were to repeat the study.

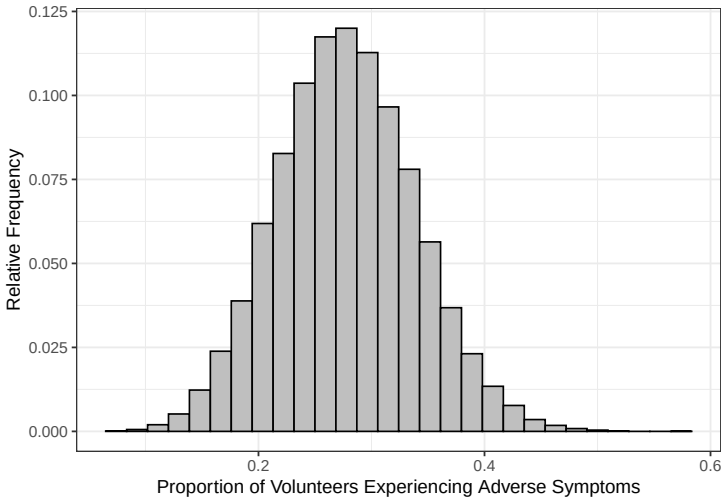


Figure 6.7: Sampling distribution for the proportion of volunteers assigned to wildlife who will develop adverse symptoms based on a sample of 54 volunteers.

Now, you might ask "wait, where did this sampling distribution come from? There is no way you actually repeated the study 50000 times, right?" Right. In the previous section, we described building the sampling distribution through repeated sampling. But, in practice, this is never practical; if it were, we would have just conducted a bigger sample to begin with. Generally, cost is the limiting factor in choosing a sample size; so, we only have a limited set of data to work with. The sampling distribution is critical to making inference, but we cannot take multiple samples to make it. Where does that leave us? The answer. . . modeling. Our goal is to construct a *model* of the sampling distribution that we can use to make inference.

There are three general techniques for modeling the sampling distribution of a statistic:

1. Build an empirical model.
2. Build an exact analytical model using probability relations.
3. Build an approximate analytical model using probability limit theorems.

We will focus on the first approach; the latter two approaches are discussed in the last unit of the text. Our emphasis is on the conceptual understanding of a sampling distribution and its model. While these latter two approaches differ in their technique, the use of the resulting model is the same. We choose to focus on the first approach because it requires less background and reinforces the conceptual understanding of a sampling distribution discussed above. The idea in constructing an empirical model is to mimic the discussion above regarding the construction of a sampling distribution. Our description references Figure 6.8 often.

We are limited by our resources; because of time and money constraints, we cannot resample from the population (crossed off resamples in Figure 6.8). So, we pretend for a moment that our original sample (colored in green in the figure) is the population for a moment. Our idea is to randomly sample from this original sample, creating a *resample* (colored in orange in the figure). Forgive the non-technical terms here, but since the orange "blob" is a random sample from the green "blob," then it is representative of the green blob. Therefore, if we construct an estimate $\widehat{\theta}^*$ from the orange blob (the star denotes a statistic from a resample), then it should be close to the statistic $\widehat{\theta}$ from the green blob; but, since this green blob is representative of the population, $\widehat{\theta}$ should be close to the true parameter θ. Therefore, we have that

$$\widehat{\theta}^* \approx \widehat{\theta} \approx \theta \Rightarrow \widehat{\theta}^* \approx \theta$$

That is, each resample produces a statistic which is a good estimate of the parameter from the underlying population. The benefit here is that the resamples are from the original sample, not the population, and can therefore be constructed in the computer. And, given today's computing power, we are not limited by time or money (10000 resamples can often be taken in a matter of seconds). If you want to see this process in action, we encourage you to check out the free online app located at http://www.lock5stat.com/StatKey/bootstrap_1_cat/bootstrap_1_cat.html.

Again, the idea is to mimic in the computer the resampling that we were unable to do in real life. This process is known as the **bootstrap** procedure.

Definition 6.3 (Bootstrap)**:**
A method of modeling the sampling distribution by repeatedly resampling from the original data.

A couple of notes on the actual implementation of a bootstrap procedure:

1. Each resample (known as a *bootstrap resample*) is the same size as the original sample.
2. Each resample is taken *with replacement*; that means the values from the original sample can show up multiple times. Think of "catch and release"

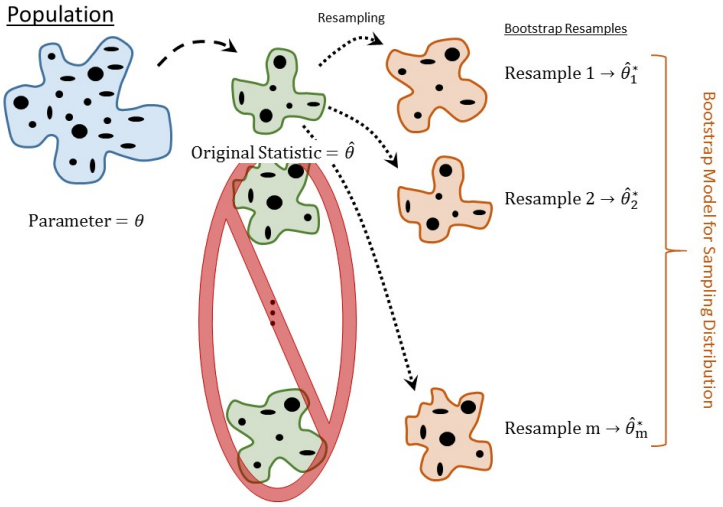


Figure 6.8: Illustration of modeling the sampling distribution via the Bootstrap.

fishing.

3. Typically, between 3000 and 10000 bootstrap resamples are taken.

We will avoid actual computation throughout the text, but several resources are available for implementing the bootstrap procedure (and its many variants) in various computer programming languages and software packages.

> **!** Students often believe that the bootstrap "creates more data." This is not true. Instead, the boostrap resamples from the existing data. This highlights the need to have a representative sample when performing analysis.

As an example, for the Deepwater Horizon Case Study, we performed the following steps to create Figure 6.7:

1. Select 54 volunteers at random (with replacement) from the original sample of 54 volunteers who had been assigned to clean wildlife.
2. For our bootstrap resample, we compute the proportion of those individuals who had experienced adverse respiratory symptoms; this is our *bootstrap statistic*.
3. We repeated steps 1 and 2 several thousand times, retaining the bootstrap statistics from each bootstrap resample.
4. We plotted the distribution of the bootstrap statistics.

6.4 Using a Model for the Sampling Distributions (Confidence Intervals)

In Chapter 5 we discussed specific statistics, numerical estimates of our parameters. Returning to our question for the Deepwater Horizon Case Study — "What proportion of volunteers assigned to clean wildlife will develop adverse respiratory symptoms?" — we have such an estimate: $\widehat{p} = 0.278$. However, there is something unsatisfying about this estimate... it fails to acknowledge the variability in the statistic which we know exists. We would like to leverage the information contained in our model for the sampling distribution to provide an estimate which incorporates the variability in this statistic.

From Figure 6.7, we observed that we would not expect the proportion of volunteers who had experienced adverse symptoms to move much beyond 0.15 to 0.4 if we were to repeat the study. How does this help us in performing inference? Remember that each value in the bootstrap model for the sampling distribution is an estimate of the underlying parameter. So, we can think of the above model as showing us what good estimates of the parameter look like. Another way of saying it: the model for the sampling distribution shows us the *reasonable* (or *plausbile*) values of the parameter. Here, by "reasonable," we mean values of the parameter for which the data is *consistent*. Consider the following statements (which are equivalent):

- Based on our sample of 54 volunteers, it is reasonable that the proportion of volunteers assigned to clean wildlife who would experience adverse respiratory symptoms is between 0.15 and 0.4.
- Our sample of 54 volunteers is consistent with between 15% and 40% of all volunteers assigned to clean wildlife experiencing adverse respiratory symptoms.

We have just conducted inference for "estimation" type questions. We are able to provide an estimate for the parameter which acknowledges that the data is not perfect and there is variability in sampling procedures. That variability incorporated itself into constructing an estimate that is an interval instead of a single point.

The above interval was chosen arbitrarily by just looking at the sampling distribution and capturing the peak of the distribution. If we want to be more formal, we might try to capture the middle 95% of values. This is known as a **confidence interval**.

Definition 6.4 (Confidence Interval)**:**
An interval (range of values) estimate of a parameter that incorporates the variability in the statistic. The process of constructing a k% confidence interval results in them containing the parameter of interest in k% of repeated studies. The value of k is called the confidence level*.*

We have not formally defined "confidence," linking it to the behavior of a statistic across repeated samples. We have "higher confidence" when our process results in capturing the true parameter in a higher percentage of repeated studies.

If we were to capture the middle 95% of statistics in our model of the sampling distribution, a 95% confidence interval, we would obtain an interval of (0.167, 0.407), as shown in Figure 6.9.

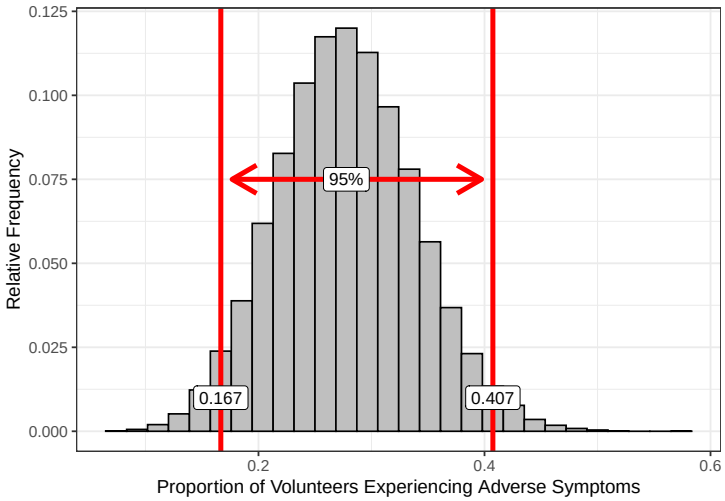


Figure 6.9: Construction of a confidence interval via bootstrapping for the proportion of volunteers assigned to wildlife who will develop adverse symptoms based on a sample of 54 volunteers.

The following is a general procedure for constructing confidence intervals:

1. Choose a confidence level k.
2. Construct a model for the sampling distribution of the statistic.
3. Grab the middle k% of values from the model in step (2).

Notice that the definition of a confidence interval, and this general procedure, apply regardless of the technique used for constructing the model of the sampling distribution.

Confidence intervals are often misinterpreted; this comes from their dependence on repeated sampling. When thinking about confidence intervals, think about playing a game of ring toss: you toss a ring in hopes of landing on top of a target. The target is the parameter characterizing the population. The confidence

interval is like a ring. Since the confidence interval is constructed from a model of the sampling distribution, it changes with each sample; that is, the confidence interval itself is a statistic. Just like in ring toss where the ring moves with each toss, the confidence interval moves with each sample. However, the target stays fixed. Because of this, the following interpretations are *incorrect*:

- There is a 95% chance that the proportion of volunteers assigned to clean wildlife who will experience adverse symptoms is between 0.167 and 0.407.
- 95% of volunteers assigned to clean wildlife in our sample (or population) had a value between 0.167 and 0.407.

The first statement is incorrect because it treats the parameter as the thing that is moving. Once the data has been collected, the confidence interval is a fixed quantity. At this point, neither the estimate nor the parameter is moving; so, there is no probability left (it either captured the parameter or it did not). Again, think about tossing a ring; once the ring is tossed, you either captured the target or you did not. There is no "I captured the target with 95% probability."

The second statement is absurd in this case. A volunteer either had respiratory symptoms or they did not; so, saying they had a value between 0.167 and 0.407 is ridiculous. However, this is a common misconception with confidence intervals. They are describing reasonable values of the parameter as opposed to values of the variable in the sample or population. We recommend sticking to interpreting a confidence interval as specifying reasonable values for the parameter.

Confidence intervals *do not* provide a probability that the parameter is inside. Nor do they tell you anything about the individual values in a sample or population. They describe reasonable values of the parameter.

Confidence intervals specify *reaonable* values of the parameter based on the data observed.

This is a difficult concept to wrap our heads around; it seems natural to associate the percentage with the values we have obtained. However, our confidence is in the *process*, not the resulting interval itself. That is, 95% confidence intervals work 95% of the time; however, this statement is about the process of constructing confidence intervals. Once we have computed a confidence interval, it has either worked or not; the problem is of course, that since we do not know the parameter, we will never know if it worked or not. For this reason, we prefer the interpretation of a confidence interval which avoids these subtleties: a confidence interval specifies the reasonable values of the parameter. The percentage (95% vs 99% for example) then just specifies what we mean by "reasonable."

It may seem like a good idea to make a 100% confidence interval to be sure we always capture the parameter. But, such intervals are not helpful in practice. For example, a 100% confidence interval for the proportion of volunteers experiencing adverse symptoms would be (0, 1). But, this is useless; it essentially says that the proportion has to be a number between 0 and 1, but we already knew that. Therefore, we must balance the confidence we desire with the amount of information the interval conveys.

If you want both a high level of confidence but also a narrow interval, increase the sample size. As the sample size increases, the variability in the statistic decreases leading to a narrower interval.

95% confidence intervals are the most common in practice; however, 90%, 98%, and 99% intervals are also used. It is extremely rare to use less than a 90% CI.

6.5 Bringing it All Together

Consider the following question:

> Is there evidence that more than 1 in 5 volunteers assigned to clean wildlife will develop adverse respiratory symptoms?

Let's answer this question using a confidence interval. Based on the data obtained, we found that the 95% confidence interval (CI) for the proportion of volunteers experiencing adverse symptoms to be (0.167, 0.407). Is this data consistent with more than 1 in 5 volunteers developing adverse symptoms? Yes, since there are proportions within this interval which are larger than 0.2. But, *consistency* is not the same as *evidence*; remember, evidence is the idea of "beyond a reasonable doubt." After all, is this data *consistent* with less than 1 in 5 volunteers developing adverse symptoms? Yes, since there are proportions within this interval which are less than 0.2.

Confidence intervals specify reasonable values — those values of the parameter which are consistent with the data. This data is then consistent with proportions that are both less than 0.2 and greater than 0.2. So, what can we say then? We can say that there is *not evidence* that more than 1 in 5 volunteers assigned to clean wildlife will develop adverse respiratory symptoms, but the data *is consistent* with this claim.

We can say that there *is evidence* that the proportion of volunteers who develop symptoms is less than 0.5; there is evidence the proportion of volunteers who

develop symptoms is larger than 0.1. That is, the data provides evidence that more than 10% of volunteers develop adverse symptoms and evidence that this percentage is not larger than 50%. How do we know? Because values less than 10% are not reasonable values of the parameter based on the 95% CI. Values like 0.1 are outside of the confidence interval and are therefore not reasonable. Similarly, values above 0.5 are outside the confidence interval and are therefore not reasonable.

The power of a model for the sampling distribution is that it allows us to determine which values of a parameter are reasonable and which values are not.

Chapter 7

Quantifying the Evidence (Rejecting Bad Models)

Again, the goal of statistical inference is to use the sample as a snapshot of the underlying population (Figure 7.1). Recall that there are essentially two categories of questions we ask when trying to perform inference:

- Estimation: for example, what *proportion* of volunteers who clean wildlife following an oil spill experience adverse respiratory symptoms?
- Model Consistency: for example, is it reasonable that no more than 1 in 5 volunteers who clean wildlife following an oil spill experience adverse respiratory symptoms?

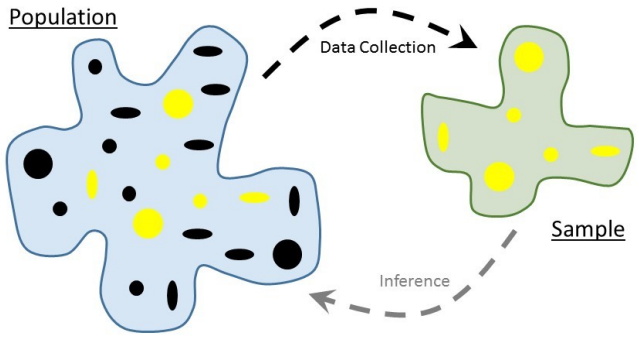


Figure 7.1: Illustration of the statistical process (reprinted from Chapter 1).

In the previous chapter we addressed these questions through the use of confidence intervals — by specifying reasonable values of the parameters through a model of

the sampling distribution. However, when working with questions of the second type (model consistency), there is a second approach; this latter approach is useful when confidence intervals cannot be constructed for the particular question of interest (see Unit 3).

Remember, assessing model consistency is similar to performing a trial in a court of law. After gathering the evidence, the jury is left with the following decision:

- Assuming the defendant is innocent, if the evidence is unlikely to have occurred (so the evidence is not consistent with innocence), then they vote "guilty."
- Assuming the defendant is innocent, if the evidence is reasonably likely to have occurred (so the evidence is consistent with innocence), then they vote "not guilty."

The goal in this section is to somehow quantify the evidence against a particular model to determine if we can say that the data is not consistent with the given model.

7.1 Some Subtleties

In a U.S. trial, there are some subtleties that we should be aware of, as they also creep up in statistical analyses and have implications for how we interpret statistical results. First, the jury weighs the evidence *under the assumption of innocence*. That is, they first develop a working hypothesis (the defendant is innocent). Then, the likelihood of the evidence *under this assumption* is determined. For example, if a defendant were innocent of murder, it is unlikely to have five eye witnesses stating the defendant was seen standing over the victim, holding the murder weapon, and screaming "I killed him!" Since that evidence does not jive with innocence, the jury convicts. If, however, the only evidence is that five eye witnesses place the defendant in the same city as the victim and the defendant matches the description of someone seen fleeing the crime scene, then the jury would not convict. Why? Because the evidence, while pointing toward guilt, is not overwhelming; these things could have happened by chance alone. Therefore, the evidence, while consistent with guilt does not provide evidence for guilt.

As in the previous chapter, we are making a distinction between "evidence for" a hypothesis and the data being "consistent with" a hypothesis. Evidence for a particular claim is only established by providing evidence against the opposite statement. However, consistency can be established without disqualifying any other statement; that is, data can be consistent with two opposing claims, but data cannot provide evidence for two opposing claims.

Also notice that a jury saying "not guilty" is not the same as saying "innocent." That is, a lack of evidence to convict does not imply the defendant is innocent. A lack of evidence is simply a lack of evidence. The defendant may still be guilty,

but the evidence has just not proven it.

Similarly, when assessing model consistency, we will weigh the data *under the null hypothesis* (our working assumption). Then, the likelihood of our data occurring by chance alone *under this hypothesis* is determined. If that likelihood is small (data is not consistent with the null hypothesis), we can conclude the data supports the alternative hypothesis (guilty). If, however, that likelihood is large (data is consistent with the null hypothesis), we can only conclude that the data is consistent with the hypotheses. We are *not* able to say "supports the null" because that would be like saying a defendant is innocent. We can't prove innocence because we started by assuming it!

7.2 Assuming the Null Hypothesis

Consider the question we have been asking regarding the Deepwater Horizon Case Study:

> Is there evidence that more than 1 in 5 volunteers assigned to clean wildlife develop adverse respiratory conditions?

Remember, we framed this question through statements about a parameter in Chapter 3:

> H_0 : the proportion of volunteers assigned to clean wildlife who develop adverse respiratory symptoms is no more than 0.20.
> H_1 : the proportion of volunteers assigned to clean wildlife who develop adverse respiratory symptoms exceeds 0.20.

Within the sample we observed that 27.8% of volunteers experienced adverse symptoms, which is certainly more than the 0.20; therefore, the data is at least trending toward the alternative hypothesis. However, it is also possible that we just have a strange sample; that is, it is possible our data is a fluke, resulting in an estimate larger than 0.2 by chance alone. As we discussed in the previous chapter, we expect our estimate to vary to some degree from one sample to another. Essentially, we need to know if 27.8% of volunteers experiencing symptoms is a strong signal that the rate within the popoulation is larger than 0.2 (1 in 5) or whether 27.8% is simply a fluke that might happen due to sampling variability. While we are going to be attacking the question differently in this chapter than the previous, we see that the key is still variability in the estimate. That is, we are back to the *Fourth Fundamental Idea of Inference*. As stated above, in order to determine evidence for one statement (captured by the alternative hypothesis), we begin by assuming the opposite statement (captured by the null hypothesis) as our working assumption. That is, if we want to know if 27.8% of volunteers experiencing adverse symptoms is "evidence," we need to figure out what we *expect* to happen *if only 1 in 5 volunteers actually develop adverse respiratory symptoms* (the statement represented by the equality portion of the null hypothesis).

Consider this last statement. It is equivalent to saying "what type of evidence would we expect for an innocent person?" Only when we know what to expect can we determine if the evidence in front of us is extreme enough to convict. Only when we know what to expect can we determine if the observed sample provides evidence in favor of the alternative. So, we enter a fake world. . . a world in which exactly 1 in 5 volunteers actually develop respiratory symptoms. That is, we enter a world in which the null hypothesis is true. Now, in this world, how do we know what to expect? We construct the sampling distribution for the proportion under this assumption that the null hypothesis is true; this is known as the **null distribution**.

Definition 7.1 (Null Distribution)**:**
The sampling distribution of a statistic if *the null hypothesis is true.*

The null distribution, the last in our *Distributional Quartet*, is a sampling distribution; it is just a sampling distribution in a world in which the null hypothesis is true. As a result, the process for constructing the null distribution is very similar to the process for constructing the sampling distribution (illustrated in Figure 7.2:

1. Sample randomly from a fake population where the null hypothesis is true.
2. For each sample, compute the statistic of interest.
3. Repeat steps 1 and 2 several thousand times.
4. Plot the statistics retained from each sample.

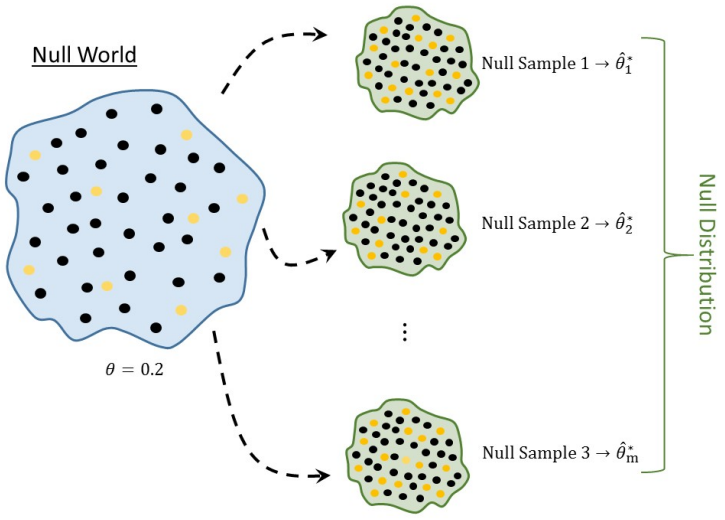


Figure 7.2: Illustration of constructing a null distribution. Notice the similarity to constructing the sampling distributon.

Notice that these are the same steps as in constructing a sampling distribution with the exception that instead of sampling from the population of interest, we sample from a hypothetical population in which the null distribution is true.

Since the null distribution is a sampling distribution when a particular hypothesis is true, we are constrained by the same limitations as before. Namely, we are unable to construct the actual the null distribution; instead, we must construct a model for it. More, since the null distribution is a sampling distribution, the same techniques we use for modeling the sampling distribution can be modified to model the null distribution. The key is to enforce the null hypothesis to be true. As with sampling distributions, we will emphasize the empirical model approach.

Using the computer, we first create a virtual world in which the null hypothesis is true. This often involves adjusting the original sample in order to make it consistent with having been drawn from a population in which the null hypothesis were true. The augmented data becomes the null world. We are then able to bootstrap from the augmented data to simulate what would happen if the null hypothesis were true. The details of this procedure are beyond the scope of our current discussion; it is more important to understand the conceptual idea of a null distribution at this point.

Figure 7.3 represents a model for the null distribution of the proportion of volunteers in a sample of 54 assigned to clean wildlife which would develop adverse symptoms when the null hypothesis is that the proportion is 0.20.

A null distribution is tied to a specific null hypothesis. A sampling distribution does not require a hypothesis to construct. So, while a sampling distribution could be used to address a variety of null hypotheses, a null distribution can only be used to address the corresponding set of hypotheses for which it was developed.

As we are introducing the concept of a null distribution, we will stick to modeling the null distribution of a statistic. Often times in a statistical analysis, the null distribution is computed for a numerical quantity known as a standardized statistic. These will be discussed more in later units of the text.

7.3 Using the Null Distribution

From the figure, we see that *if the null hypothesis were true* — if only 1 in 5 volunteers assigned to clean wildlife experienced symptoms — then in a sample of 54 individuals, we would expect the proportion who experienced symptoms to be somewhere between 0.1 and 0.3. *If the null hypothesis were true*, it would be nearly impossible that half of the individuals experienced symptoms (since 0.5 is

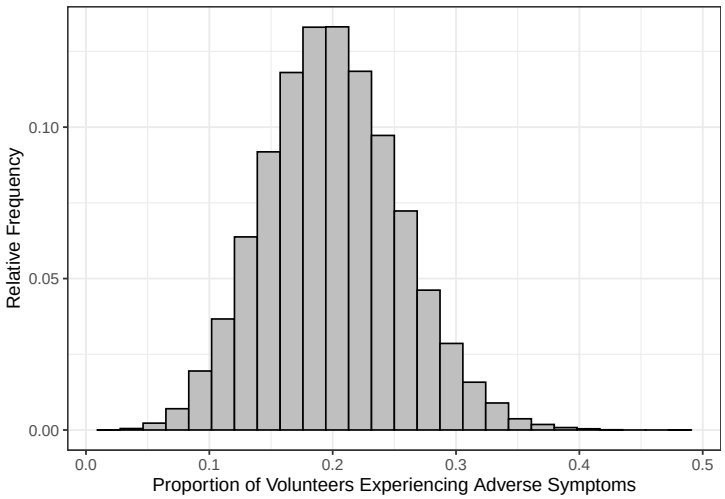


Figure 7.3: Null distribution for the proportion of volunteers assigned to clean wildlife experiencing adverse respiratory symptoms. Null hypothesis is that the proportion is 0.20; this is based on a sample of size 54.

way off in the tail of the distribution). The further in the tail region, the more extreme the sample. The question is then how extreme is our sample? Again, the null distribution is just setting up expectations; now, we have to weigh the data against those expectations.

In our sample, we observed 27.8% of volunteers who experienced symptoms. Since 0.278 is towards the center of the distribution, we would say that it is not an extreme sample. In order to quantify how extreme (or not extreme) it is, we compute the fraction of values which are more extreme (larger in this case) than the value observed; that is, we compute the fraction of values that appear further in the right than 0.278 in the null distribution. Figure 7.4 illustrates this computation. Based on the null distribution, there is a 10.6% chance that *if the null hypothesis were true* — only 1 in 5 volunteers actually experienced symptoms — that in a random sample of 54 volunteers we would obtain data this extreme or more so by chance alone. Essentially, this tail area is quantifying the strength of the evidence. The smaller this area, the further in the tail region our data is; that is, the smaller this area, the more unexpected our data. Therefore, small areas indicate that the data (our evidence) does not jive with our expectations under the null (innocence), forcing us to conclude the data provides evidence *against* the null hypothesis (guilty verdict). In our case, since the area is relatively large, our data is consistent with what we might expect if the null were true. Therefore, in this case, we conclude that there is no evidence that the rate of those experiencing symptoms exceeds 1 in 5. This area is known as the **p-value**.

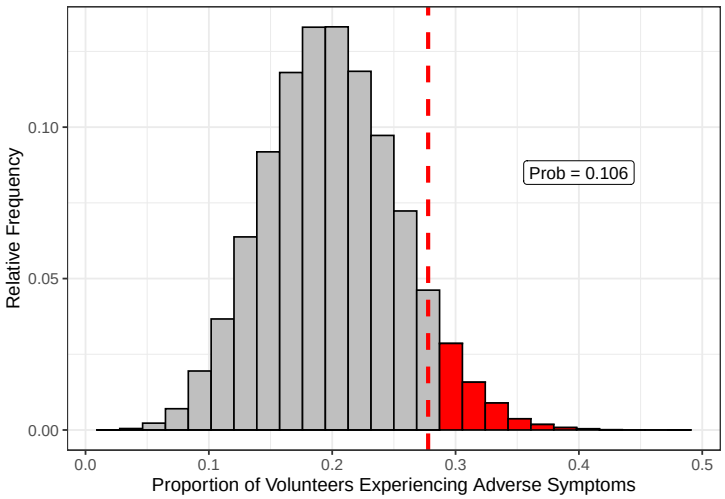


Figure 7.4: Likelihood of obtaining a sample as extreme or more so as that of the original sample when the parameter of interest is the proportion of volunteers assigned to clean wildlife experiencing adverse respiratory symptoms. Null hypothesis is that the proportion is 0.20; this is based on a sample of size 54.

Definition 7.2 (P-Value)**:**
The probability, assuming the null hypothesis is true, that we would observe a statistic, from sampling variability alone, as extreme or more so as that observed in our sample. This quantifies the strength of evidence against the null hypothesis. Smaller values indicate stronger evidence.

It is natural to ask "how small does the p-value need to be to prove a statement?" Like a trial, the weight of the evidence presented depends on the context. In some studies, a p-value less than 0.01 may be strong evidence while in other studies a p-value less than 10^{-6} is required. And, as in a trial, it is not only the strength of the evidence but the type of evidence presented (DNA evidence may be stronger than fingerprint evidence). In statistics, it is important to consider the *effect size* (some measure of the signal in the data) as well as the p-value. That is, consider whether the difference between the estimate and the null value is actually large; this is always based on subject-matter expertise. It is often helpful to report a confidence interval alongside a p-value.

While what constitutes "significant" may vary from discipline to discipline, the list below is a good rule of thumb:

- $p \geq 0.1$: no evidence against the null hypothesis.
- $0.05 \leq p < 0.1$: weak evidence against the null hypothesis.
- $0.01 \leq p < 0.05$: some evidence against the null hypothesis.
- $0.001 \leq p < 0.01$: evidence against the null hypothesis.
- $p < 0.001$: strong evidence against the null hypothesis.

As with any rule of thumb, this should not be considered binding and may vary depending on the application.

A p-value should never be reported in isolation. It should always be accompanied by a confidence interval, a numerical summary of the data, or a graphical summary of the data — something which indicates the effect size and variability in the data.

The following is a general procedure for computing a p-value:

1. Define the null and alternative hypotheses.
2. Construct a model for the null distribution of the desired statistic.
3. Compute the desired statistic for the original sample.
4. Overlay the statistic from step (3) on the model developed in step (2), and then compute the area under the curve for values *more extreme* than that observed in step (3).

Notice that the definition of a p-value, and this general procedure, apply regardless of the technique used for constructing the model of the null distribution.

Like confidence intervals, p-values are often misinterpreted. In fact, they have become so abused that some researchers argue against their use. It is our opinion that the p-value can be a useful tool once it is appropriately understood; so, let's dispell some of the misconceptions. Consider these *incorrect* statements regarding the p-value obtained for the Deewater Horizon Case Study computed above:

- There is a 10.6% chance that only 1 in 5 volunteers assigned to clean wildlife will experience adverse symptoms.
- Since the p-value is large, there is evidence (or the data supports the claim)

that 1 in 5 volunteers assigned to clean wildlife will experience adverse symptoms.

The first statement incorrectly assumes that there is some chance that the null hypothesis is true. Remember, our two hypotheses are statements about the parameter. One is true and other is not. Our ignorance does not change this; therefore, it does not make sense to talk about the probability of the null being true or false. Instead, our job is to quantify the likelihood of the data *assuming the null is true*. The p-value is about the likelihood of the data under a particular model (the null hypothesis).

The second statement makes the common mistake that a lack of evidence for the alternative is evidence in favor of the null. A lack of evidence is like a "not guilty" verdict. It simply means we were not convinced. However, it does not mean that the defendant is innocent. All we are saying with the large p-value in this case is that the data is *consistent* with only 1 in 5 volunteers getting adverse symptoms; unfortunately, it is also *consistent* with more than 1 in 5 volunteers getting adverse symptoms. This may be an unsatisfying conclusion, but it is still a conclusion nonetheless. Our conclusion is based on assessing the variability of a the statistic under a particular model. This is captured in our last of the *Five Fundamental Ideas of Inference*:

Fundamental Idea:

Fundamental Idea V: With a model for the distribution of a statistic under a proposed model, we can quantify the the likelihood of an observed sample under that proposed model. This allows us to draw conclusions about the corresponding parameter, and therefore the population, of interest.

7.4 Sampling Distributions vs. Null Distributions

Clearly the sampling distribution and null distribution of a statistic are closely related. The difference is that the null distribution is created under a proposed model while the sampling distribution lets the data speak for itself. It is worth taking just a moment to highlight the differences in the use of these two components of the *Distributional Quartet*.

The sampling distribution is centered on the true value of the parameter; the null distribution is centered on the null value. Once we assume the null hypothesis is true, we have a value for the parameter; as a result, we expect the sampling distribution under this assumption (that is, the null distribution) to be centered on this hypothesized value. So, null distributions are *always* centered on the null value.

Sampling distributions lead to confidence intervals by specifying reasonable values of the parameter.

Null distributions lead to p-values by quantifying the likelihood of our data under a proposed model.

Model the sampling distribution to construct a confidence interval; to assess a hypothesis the null value is overlayed on the sampling distribution. Extreme values of the distribution are unreasonable values for the parameter.
Model the null distribution to compute a p-value; to assess a hypothesis, the statistic from the sample is overlayed on the null distribution. Extreme values of the distribution are values which provide evidence against the null hypothesis.

Chapter 8

Using the Tools Together

In this unit, we have introduced the key components in both the language and logic of statistical inference. In fact, with a firm grasp of the concepts in this unit, you should be able to read and interpret key statistical findings. All statistical analyses make use of the *Five Fundamental Ideas of Inference* and alternate between the members of the *Distributional Quartet*. The context of each problem differs, but the logic remains the same. In this chapter, we present another analysis based on the Deepwater Horizon Case Study, annotating it along the way to see how these elements work together fluidly to reach a conclusion. Specifically, we are interested in the following question:

> Are volunteers assigned to clean wildlife at higher risk of developing adverse respiratory symptoms compared to those volunteers who do not come into direct contact with oil? If so, estimate the increased risk.

8.1 Framing the Question (Fundamental Idea I)

We are really interested in whether the rate of respiratory symptoms in one group of volunteers is larger than that in a second group. Therefore, our working assumption is that the rate of respiratory symptoms for those assigned to clean wildlife is no more than that for those assigned to tasks which do not involve direct exposure to oil. That is, we have

> H_0 : the rate of adverse respiratory symptoms for volunteers assigned to clean wildlife is no greater than that for those assigned to tasks which do not involve direct exposure to oil.
> H_1 : the rate of adverse respiratory symptoms is greater for volunteers assigned to clean wildlife compared to those assigned to tasks which do not involve direct exposure to oil.

We can also state this more formally with mathematical notation as follows:

> Let θ_1 be the rate of developing adverse respiratory symptoms for volunteers assigned to clean wildlife.
> Let θ_2 be the rate of developing adverse respiratory symptoms for volunteers assigned to tasks without direct exposure to oil.
> $H_0 : \theta_1/\theta_2 \leq 1$
> $H_1 : \theta_1/\theta_2 > 1$

The ratio θ_1/θ_2 is known as the *relative risk* as it captures the increased risk for one group compared to another.

Notice that this is a well-posed question as it centers on parameters which characterize the population. Therefore, it can be answered with appropriate data.

> Distribution of the Population: Our questions of interest are about the population and therefore focus on characterizing this distribution.

8.2 Getting Good Data (Fundamental Idea II)

As we are working with previously collected data, we are unable to design a good sampling scheme. The only thing we can do at this point is critique the sample we have. The key question to ask ourselves is whether there is any reason that this group of volunteers differs systematically from other volunteers working oil spills. For example, this oil spill occurred in the Gulf of Mexico; the majority of volunteers were then naturally residents of Gulf states. It is possible that these residents are somehow fundamentally different with respect to their risk of developing adverse respiratory symptoms compared to the remainder of the United States. If that is the case, the results of this study would not generalize to oil spills occuring in the Atlantic. However, it is probably reasonable to say that these results would apply to future oil spills in the Gulf. If, on the other hand, we believe this group of volunteers is representative of volunteers for other oil spills, regardless of location, our results could generalize more broadly.

Also note that this was not a controlled experiment. Volunteers were not randomly allocated to their assignments that we know of. Therefore, our results could be somewhat limited. The two groups should be compared regarding other attributes (this data is unavailable to us currently) in order to determine if they are similar with respect to other variables which may potentially confound the results.

8.3 Presenting the Data (Fundamental Idea III)

The heart of this question is comparing the rate of adverse events in each group. Figure 8.1 makes this comparison.

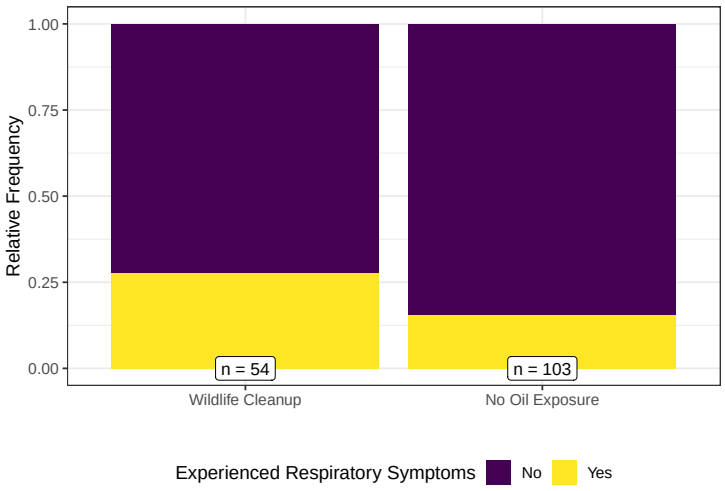


Figure 8.1: The risk of developing adverse respiratory symptoms for volunteers assigned to clean wildlife and those volunteers assigned to tasks which do not have direct exposure to oil.

As seen in the figure, the rate of adverse respiratory symptoms is larger in the group of volunteers assigned to wildlife cleanup. The rate of respiratory symptoms is 1.79 times higher in the volunteers assigned to clean wildlife compared to those assigned to tasks with no direct oil exposure.

Notice that we reported the relative risk comparing the two groups as it is directly tied to how we specified the hypotheses above. That is, the statistic we report is governed by the parameter of interest; we compute a value in the sample to estimate the corresponding value in the population.

> Distribution of the Sample: graphics and numerical summaries characterize this distribution, informing us about the underlying population. This is possible as long as the sample is representative of the population.

8.4 Quantifying the Variability in the Estimate (Fundamental Idea IV)

While we have an estimate for the increased risk of adverse respiratory symptoms for those volunteers assigned to clean wildlife, the estimate has not taken into account the variability in the sample. In order to quantify this variability, we use a bootstrap procedure to model the sampling distribution of the risk ratio. Observe that we focus on the sampling distribution of the statistic that estimates the parameter of interest.

Recall that the bootstrap mimics the process for generating a sampling distribution. In this case, "repeating the study" involves collecting data from not one, but two groups. So, we must resample both from the 54 volunteers who were assigned to clean wildlife and the 103 volunteers assigned to tasks not involving direct oil exposure. Each time we resample, we ensure that we select 54 volunteers who clean wildlife and 103 who do not. We need the process of the original study to be maintained. Each time we resample from these groups, we compute the relative risk and retain this value. Figure 8.2 shows the sampling distribution for the relative risk comparing these two groups. Again, it is important to note that we are not generating *new* data; we are *resampling/reusing* the original sample.

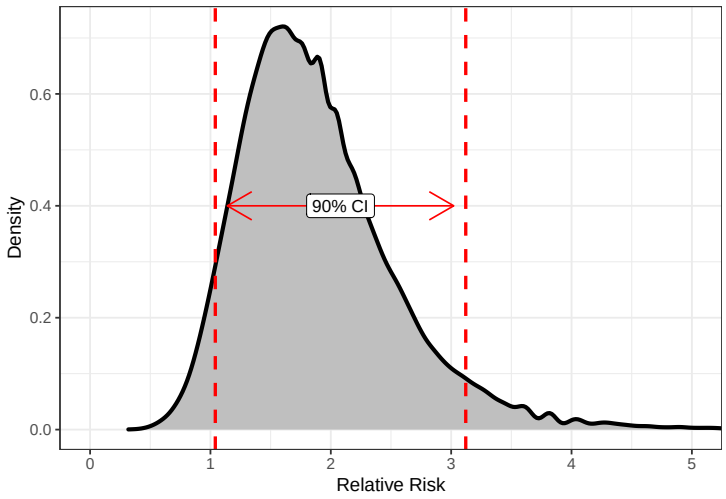


Figure 8.2: Model of the sampling distribution for the relative risk comparing volunteers assigned to clean wildlife to volunteers assigned to tasks not involving oil exposure. The model was developed via bootstrapping using 50000 replications.

Volunteers assigned to clean wildlife are 1.79 times (90% CI = (1.04, 3.12)) more likely to experience adverse respiratory symptoms compared to those volunteers assigned to tasks not requiring direct exposure to oil. Our data is consistent with volunteers assigned to clean wildlife being at increased risk compared to those who do not have direct exposure to oil.

> Sampling Distribution: allows us to quantify the variability in the statistic and provide an interval estimate for the paraemter which incorporates this variability.

8.5 Quantifying the Evidence (Fundamental Idea V)

In order to quantify the departure of the data from our working assumption that the risk is for those assigned to clean wildlife is no more than that for those assigned to tasks without direct oil exposure, we rely on the null distribution and compute a p-value.

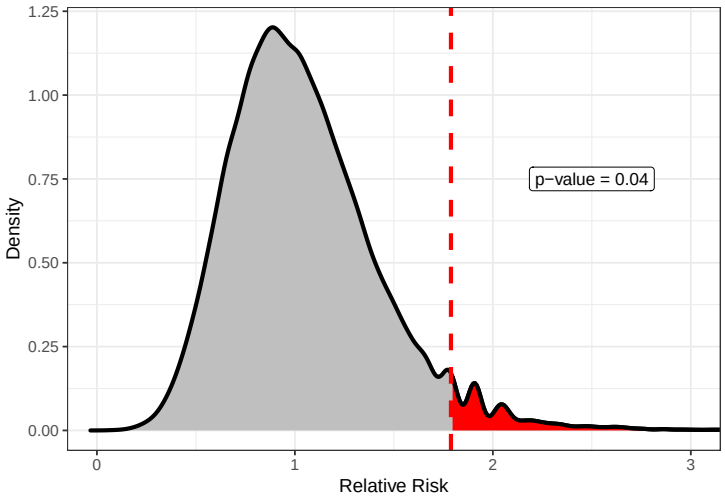


Figure 8.3: Null distribution for the relative risk comparing volunteers assigned to clean wildlife to volunteers assigned to tasks not involving oil exposure. The null hypothesis assumed the two groups of volunteers had the same risk. The null distribution was developed via bootstrapping using 50000 replications.

There is some (borderline weak) evidence (p = 0.04) to suggest that volunteers exposed to oil have an increased risk of developing adverse respiratory symptoms. Given the estimated level of this increased risk, we believe this is something health officials should investigate further. It would be worth investigating what aspects of the oil exposure may have led to the increased risk to determine if it can be avoided in the future.

Note we are careful to not claim that the assignments have caused an increase in the risk as this data is not from a controlled experiment. This is one of the limitations of this analysis. However, if we are able to assume the two groups are fairly similar with respect to other attributes — that is, there is no reason why people prone to respiratory symptoms would become assigned to wildlife cleaning — then we may have some reason to believe the results are causal. We will wrestle more with these types of conclusions in future units.

> Null Distribution: allows us to quantify the level of evidence against a particular claim; how strongly do the data disagree with the working

assumption.

8.6 Summary

Notice that our analysis moved through the *Five Fundamental Ideas*, and in doing so made use or referenced each of the four components of the *Distributional Quartet*. As we move through the remainder of the text, we will explore how these frameworks are used in various other analysis scanarios. As we do, we reveal additional concepts that underly statistical modeling.

We admit that there are several other questions that may be raised by the above analysis. This unit is meant to introduce the big concepts of inference. We will concern ourselves more with the details as we progress through the text.

Part II

Unit II: Implementing the Logic of Inference for a Single Mean

Chapter 9

Case Study: Birth Weights of Babies

The Centers for Disease Control and Prevention (CDC) — using data provided by the U.S. Department of Health and Human Services, National Center for Health Statistics, the Division of Vital Statistics and the CDC — maintains a database on all babies born in a given year[1]. This database contains key metrics on each child born, including the weight of the infant. Low birthweight can be indicative of poor health or illness in children. High birthweight can be indicative of obesity later in life. One use of this database is for researchers to examine links between lifestyle choices of the parents (such as whether the mother consumed alcohol during pregnancy) and birthweight of the infant.

Chihara and Hesterberg (2011) describe a random sample from this database; specifically, the sample consists of 1009 babies born in North Carolina during 2004. The babies each had a gestation period of at least 37 weeks (full term) and were single births (no twins, triplets, etc.). For each birth in the sample, we have the following information:

- Age: Age of the mother (in years).
- Tobacco: An indicator of whether the mother used tobacco during the pregnancy.
- Alcohol: An indicator of whether the mother used alcohol during the pregnancy.
- Sex: Sex of the child.
- Weight: Weight of the child at birth (grams).
- Gestation: Gestation time (length of pregnancy, weeks).
- Smoker: An indicator of whether the mother is a current smoker.

A subset of the collected data is shown in Table 9.1.

[1] http://wonder.cdc.gov/natality-current.html

Table 9.1: Subset of a sample of 1009 babies born in North Carlina during 2004.

Subject ID	Age Range (years)	Sex of Baby	Weight of Baby (g)	Gestation (weeks)
1	30-34	Male	3827	40
2	30-34	Male	3629	38
3	35-39	Female	3062	37
4	20-24	Female	3430	39
5	25-29	Male	3827	38
6	35-39	Female	3119	39
7	20-24	Female	3260	40
8	20-24	Male	3969	40
9	20-24	Male	3175	39
10	25-29	Female	3005	39

Chapter 10

Model for the Data Generating Process

The numerical summaries of any study are subject to sampling variability. That is, if we were to repeat the study with new subjects, the statistics we compute would almost certainly change to some degree. The key to feeling confident in our results is to quantify the variability in our estimates; this was the argument made in Chapters 6 and 7. The goal of any statistical analysis is then to develop a model for the sampling (or null) distribution of a statistic. Often times, this requires modeling the data-generating process as a precursor. As in any other discipline, statistical models simplify the actual process being modeled by making certain assumptions. In this chapter, we develop a model that will help us make inference about the mean of a single population.

10.1 General Formulation

Consider dropping a tennis ball from the top of a 50-meter building and recording the time required before the ball hits the ground. Applying the principles learned in a first course in physics, we would be able to compute the time precisely using the formula

$$\text{time} = \sqrt{\frac{2(\text{distance})}{9.8}}$$

where $9.8 m/s^2$ is the acceleration due to gravity; further, this formula works regardless of the mass of the object. Plugging 50 meters into the equation yields a time of 10.2 seconds. If we were to drop a second tennis ball from the same building, the formula tells us that it will also take 10.2 seconds to hit the ground

below. This is known as a **deterministic** system since entering a constant input always results in the same output.

Definition 10.1 (Deterministic Process)**:**
One which is completely determined by the inputs. That is, entering the same input twice will always result in the same output with certainty.

This is a model; it simplifies extremely complex processes involving the gravitational pull between objects and works reasonably well. However, it does not always match reality. If we were to repeatedly drop tennis balls from the same 50-meter building and record the time before hitting the ground, we might find that the time differs slightly from one ball to the next (it is true that these differences may be negligible, but they would exist nonetheless). There are several reasons why our observed responses do not line up directly with those predicted by the above equation; for example, our device for measuring time may be subject to some measurement error, a strong gust of wind could alter the results (while the above equation assumes no air resistance), or the person dropping the ball may have inadvertantly increased the initial velocity of the ball. These reasons, and others, contribute to the observations not lining up with the model. That is, there is associated noise in the resulting measurements. A model which incorporates this noise might be written as

$$\text{time} = \sqrt{\frac{2(\text{distance})}{9.8}} + \text{noise}$$

where the noise is not a known quantity. As a result, this is a **stochastic** model as the same value for distance may result in different outputs even if the same input is used.

Definition 10.2 (Stochastic Process)**:**
One which has an element of randomness. That is, the resulting output of the system cannot be predicted with certainty.

This leads us to our general formulation for a statistical model:

$$\text{Response} = f(\text{predictor variables, parameters}) + \text{noise} \tag{10.1}$$

The response we observe is the result of two components:

- A deterministic component which takes the form of a function of predictor variables and unknown parameters. It is often this component on which we would like to make inference.
- A stochastic component which captures the unexplained variability in the data generating process.

Since the noise is a random element, it has a distribution. We often place conditions on the structure of this distribution to enable inference on the deterministic component of the model. We discuss this later in the chapter.

This general model adheres to the idea of partitioning the variability in the response. It says that a part of the reason the responses differ between subjects is because they have different predictor variables (remember, parameters are fixed for all subjects in a population), and part of the reason is unexplained noise. The overall goal of a statistical model is to give an explanation for why the value of the response is what it is. How did it come to be? What process generated the values I have observed? Our statistical model says that these values have some deterministic component plus some additional noise we cannot explain.

We now simplify this general formulation for the specific case of making inference on the population mean.

10.2 Statistical Model for a Quantitative Response with No Predictors

Consider the Birth Weights Case Study. Suppose we are interested in estimating the average birth weight of infants born in North Carolina, the population from which our sample was taken. Our response variable is the birth weight of the infant. Our question of interest is not about the relationship of the birth weight to any other variable; that is, there are no predictor variables being considered. But, that does not mean the deterministic portion of our model is empty. We have a parameter of interest: the average birth weight. This parameter lives in the deterministic portion of the model. In particular, consider the following data generating process:

$$(\text{Birth Weight})_i = \mu + \epsilon_i$$

where μ represents the average birth weight of infants born in North Carolina. In this model, the function $f(\cdot)$ takes the value μ, a constant. The term ϵ_i is used to capture the noise in the i-th measurement (the subscript indexes the individual subjects in the sample) — the shift the response for the i-th individual is from the overall mean response. This model says that the birth weight for the i-th infant is shifted (as a result of the noise term) from the overall average birth weight μ. Notice that if there were no noise in the system, the data generating process would say that all infants have the same birth weight μ. However, due to genetic variability, differences in the lifestyle of each mother, and measurement error, ϵ_i is not a constant (noise does exist) resulting in each subject having a different response.

Notice that the deterministic portion of the model describes the *mean response* through the parameter. We will see this throughout the text.

The deterministic portion of the data generating process encodes the parameters which specify the mean response.

So, when the model for the data generating process does not contain a predictor variable, we are saying that the only source of variability in the response is due to noise. In reality, we are not claiming that there do not exist any other sources of variability, we are simply not taking them into account at this point.

The stochastic component of a statistical model captures the unexplained variability due to natural variability in the population or measurement error in the response.

In general, given a quantitative response variable and no predictors, our model for the data generating process is

$$(\text{Response})_i = \mu + \epsilon_i$$

where μ represents the average response in the population, and the parameter of interest.

It is worth pointing out that we have two "models" at this point: a model for the data generating process and a model for the sampling distribution of a statistic. The model for the data generating process is used to develop a model for the sampling distribution (or null distribution) of a statistic. It is the second model that is actually necessary in order to conduct inference; the model for the data-generating process is simply a stepping stone to the model of interest.

The function $f(\cdot)$ is often referred to as the model for the *mean response*, for obvious reasons. So, for the model of a quantitative response variable with no predictors, our model for the mean response is simply μ.

10.3 Conditions on the Error Distribution

In our model for the data-generating process we incorporated a component ϵ to capture the noise observed in the response. Since the error is a random variable (stochastic element), we know it has a distribution. We typically impose a certain structure to this distribution through the assumption of specific conditions. The

more conditions we impose, the easier it is to construct an analytical model for the sampling distribution of the corresponding statistic. However, the more conditions we impose, the less applicable our model is in a general setting. More importantly for our discussion, the conditions we make dictate how we conduct inference (the computation of a confidence interval or p-value).

Why we need conditions on the stochastic portion of a model can be confusing at first. Think of it this way. . . saying a term is "random" is just too broad. It is like saying "I am thinking of a number. What number?" There are too many choices to even have a hope of getting it correct. We need structure (boundaries, conditions) on the problem. By placing conditions on what we mean by "random" it is like saying "I am thinking of a whole number between 1 and 10." Now, we have a problem we can at least attack with some confidence.

The first condition we consider is that the noise attributed to one observed individual is **independent** of the noise attributed to any other individual observed. That is, the amount of error ϵ in any one individual's response is unrelated to the error in any other response observed. It is easiest to understand this condition by examining a case when the condition would not hold.

Definition 10.3 (Independence)**:**
Two variables are said to be independent when the likelihood that one variable takes on a particular value does not depend on the value of the other variable.

Example 10.1: "Puzzle Speed"
Suppose we are conducting a study to estimate the amount of time, on average, required for a student to complete a small puzzle. We obtain a random sample of 25 students. We have student 1 complete the puzzle, allowing the other students to watch, and we record the time required for him to complete the puzzle. Then, we have student 2 complete the same puzzle, again allowing the other students to watch, and we record her time. We continue in this way until we have recorded the time for each of the 25 students.

The model for the data generating process would be

$$(\text{Time})_i = \mu + \epsilon_i$$

where μ is the average time required to complete a puzzle by a student. We might estimate μ with $\bar{x} = \frac{1}{25}\sum_{i=1}^{25}(\text{Time})_i\$$, the sample mean time for the 25 students observed.

Given the method in which the data as collected, it would *not* be reasonable to assume the error are independent of one another. Since later students observed the puzzle being put together more times prior to completing the task themselves, we might expect their time to get faster. So, the noise in one student's time would be related to the noise in the next student's time. This violates the independence condition.

A second condition we might consider is that the error for each subject is **identically distributed**. This ensures that every student essentially belongs to the same population.

Definition 10.4 (Identically Distributed)**:**
A set of variables is said to be identically distributed if they are from the same population.

Practically, this means that we do not have a systematic component which is causing our population to be different from what we expected. As an example, consider Example **??** again. Suppose that 5 of the students in the sample belonged to the puzzle club. Clearly we would expect these 5 individuals to perform differently than students in general. If students belonging to a puzzle club were not a part of our target population, this would result in our sample reflecting two distinct populations: those in a puzzle club and those not in a puzzle club. Therefore, the data would not satisfy the identically distributed condition.

These two conditions alone are sufficient for modeling the sampling distribution of the sample mean, our estimate for the mean response, using the bootstrap process we described in Chapter 6. It is worth noting that the *identically distributed* condition could be relaxed, or we could actually impose further conditions on the model. These alterations to our model for the data generating process will be discussed later in the text. For now, we will assume that the data is consistent with both the independence and identically distributed conditions.

We distinguish between a "condition" and an "assumption" (not all authors make such a distinction). A *condition* is a requirement for the statistical theory on which we are relying to be justified. In practice, we can never guarantee a condition is satisfied; as a result, we *assume* the data is consistent with the condition. This will become clearer as we assess conditions in later units.

Before leaving this chapter, it is worth noting that what we have discussed in this chapter does not change any of the fundamentals we discussed in previous

chapters. This chapter will serve as a way of uniting all the methods we discuss in this text under a single framework. We still summarize the data in the same way as before; we now simply have an additional tool for developing our inferential methods.

Chapter 11

Estimating with Confidence

Let's consider the following research goal related to the Birth Weight Case Study:

> On average, what is the birth weight of an infant born in North Carolina?

If we are willing to assume the data is a representative sample of all infants born in North Carolina and the birth weight of one infant is independent of any other, then we have the following model for the data generating process:

$$(\text{Birth Weight})_i = \mu + \epsilon_i$$

where μ represents the average birth weight of infants born in North Carolina and the errors are independent of one another and identically distributed.

We can estimate the parameter μ with the average birth weight of babies in our sample: 3448.26 g. The data graphically shown in Figure 11.1.

In order to construct an estimate of μ which incorporates the variability in the sample mean, we must model the sampling distribution of our estimate. The bootstrap procedure for this case would be

1. Randomly sample, with replacement, 1009 records from the original sample.
2. For this bootstrap resample, compute the mean birth weight and retain this value.
3. Repeat steps 1 and 2 many (say 5000) times.

This process is illustrated in Table 11.1. Each row represents the birth weights for a single resample taken with replacement from the original data. The final column is the computed (and retained), sample mean from each resample. This is the bootstrap statistic.

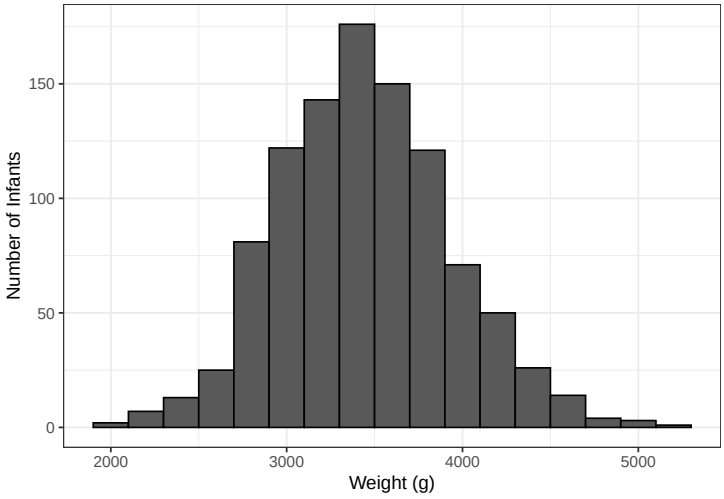


Figure 11.1: Weight of infants born in North Carolina.

Table 11.1: Partial printout of first 10 bootstrap resamples and the resulting bootstrap statistic.

Value 1	Value 2	Value 3		Value 1007	Value 1008	Value 1009	Boostrap Mean
3345	3572	3572	...	3827	3827	3119	3461.89
3629	2892	3827	...	4111	3374	2948	3476.69
2495	3686	3827	...	3289	3544	3487	3428.90
3856	3430	3771	...	3487	3742	2665	3436.20
3430	3119	4479	...	3686	3090	3005	3451.09
3289	3459	3827	...	3600	3856	3260	3473.89
2863	3345	3232	...	3345	3544	2948	3427.89
3289	4026	3856	...	4338	3771	3714	3435.78
3175	3544	3771	...	3572	3515	3005	3419.37
3260	3771	3742	...	3572	4054	3033	3447.77

A plot of the resulting bootstrap sample means is shown in Figure 11.2. Notice that the x-axis is different from that of Figure 11.1. While a graphical summary of the raw data is summarizing the weight of individual infants, the sampling distribution is summarizing the statistic we compute in various samples of the same size. We are not keeping track of individual infant weights but average weights for collections of 1009 infants.

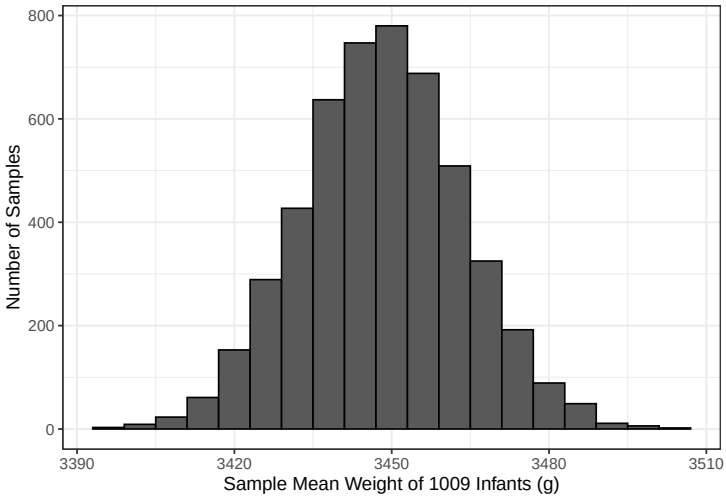


Figure 11.2: Bootstrap model for the sampling distribution of the average birth weight for a sample of 1009 infants born in North Carolina.

Using this model, we can then grab the middle 95% of values in order to construct a confidence interval for the parameter of interest. This results in a 95% confidence interval of (3418.73, 3479). Therefore, the data is consistent with the average birth weight of infants in North Carolina being between 3418.73 and 3479; that is, these are the reasonable values of the mean birth weight.

Notice that we are able to narrow down the reasonable values of the parameter to a relatively small interval (a difference of about 60 grams). This is not because all babies in North Carolina have an extremely similar birth weight. It is because we have a relatively large sample, allowing us to have high confidence in our estimate.

Also, notice how much narrower the model for the sampling distribution is compared to the raw data. Remember, statistics have less variability than individual values. This also illustrates why a confidence interval could never describe the fraction of values in the population which fall within a certain range — the variability is not comparable because a sampling distribution has a different x-axis than the distribution of the population or sample.

Chapter 12

Quantifying the Evidence

In the previous chapter, we estimated the mean response for a single quantitative variable. In this chapter, we consider hypothesis testing when the parameter of interest is the mean response for a single quantitative variable.

Let's consider the Birth Weight Case Study. In 2004, when the data was collected, an infant was considered "full term" if it was born anytime between 37 and 42 weeks. However, in 2013 the American College of Obstetricians and Gynecologists redefined "full term" to mean an infant born anytime between 39 and 40 weeks. We will consider the following research question:

> Is there evidence that the gestation time for infants born in North Carolina exceeds 38 weeks (so that the baby is at least full term on average)?

This question is captured by the following set of hypotheses:

$$H_0 : \theta \leq 38 \qquad \text{vs.} \qquad H_1 : \theta > 38$$

where θ is the average gestation period (weeks) of an infant born in North Carolina. This parameter is also present in the data generating process:

$$(\text{Gestation Period})_i = \theta + \epsilon_i$$

We will assume that the gestation period for one infant is independent of the gestation period for any other infant and that this data is representative of all infants born in North Carolina; this implies we can assume the errors are independent and identically distributed.

We can estimate the parameter θ with the average gestation period for the babies in our sample: 39.11 weeks. We seek to quantify the evidence against the null hypothesis summarized by this data.

In Chapter 7, we developed the null distribution of the statistic used to estimate the parameter. Following that chapter, we would model the null distribution of the sample mean gestation for a sample of 1009 infants. This null distribution, modeled via bootstrapping assuming the data is consistent with the above conditions on the error term, is shown in Figure 12.1.

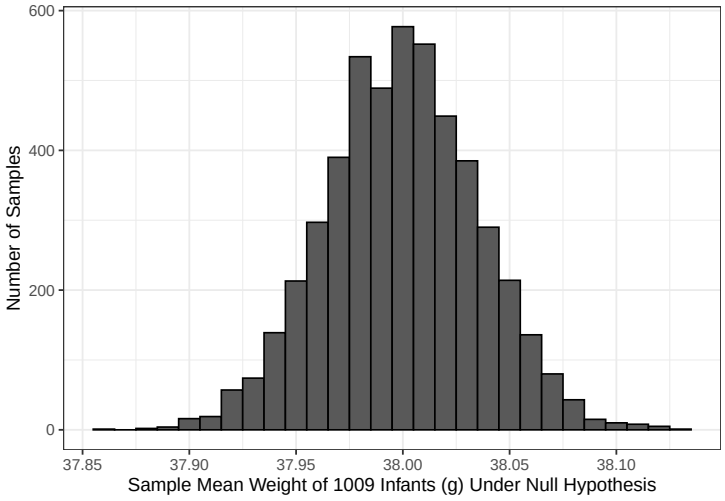


Figure 12.1: Model of the null distribution of the sample mean gestation period for a sample of 1009 infants. The model is based on 5000 bootstrap replications under the null hypothesis that the average gestation period is 38 weeks.

This figure was constructed using the following procedure:

1. Alter the sample to be representative of having come from a population in which the null hypothesis is true; the data was recentered to have a sample mean of 38.
2. Randomly sample, with replacement, 1009 records from the altered original sample.
3. For this bootstrap resample, compute the mean gestation period and retain this value.
4. Repeat steps 2 and 3 many (say 5000) times.

The resulting simulated data is illustrated in Table 12.1. Each row represents the gestation periods for a single resample taken with replacement from the altered original data. The final column is the computed (and retained), sample mean from each resample. This is the bootstrap statistic *under the null hypothesis*.

Notice that the null distribution is centered on 38; this is not an accident. Recall that sampling distributions are centered on the true value of the parameter; since a null distribution is just the sampling distribution when the parameter is equal to the null value (in this case 38), it should be centered on the null

Table 12.1: Partial printout of first 10 bootstrap resamples under the null hypothesis and the resulting bootstrap statistic.

Value 1	Value 2	Value 3		Value 1007	Value 1008	Value 1009	Boostrap Mean
36.89	36.89	39.89	...	36.89	36.89	37.89	37.96
36.89	37.89	37.89	...	39.89	36.89	35.89	37.91
37.89	37.89	37.89	...	38.89	37.89	39.89	37.95
36.89	37.89	35.89	...	36.89	38.89	37.89	38.03
36.89	36.89	37.89	...	38.89	37.89	40.89	38.00
39.89	38.89	36.89	...	36.89	37.89	37.89	38.03
38.89	38.89	36.89	...	37.89	36.89	38.89	38.07
36.89	35.89	39.89	...	36.89	38.89	37.89	38.00
37.89	36.89	37.89	...	37.89	35.89	35.89	37.96
39.89	37.89	35.89	...	36.89	35.89	36.89	38.00

value. That is, the null distribution is designed to be centered on the null value in the hypotheses. In order to determine if our sample is consistent with our expectations, we overlay our observed sample mean ($\widehat{\theta} = 39.11$) on the null distribution. Since this value is in the far right tail of the null distribution (off the edge of the graph in this case), our sample is *inconsistent* with the null distribution. That is, we have evidence that the population from which our sample was drawn has an average gestation period larger than 38 weeks.

12.1 Standardized Statistics

In the above discussion, we compared the observed sample mean to our distribution of expectations if the null hypothesis were true. We were essentially comparing $\widehat{\theta}$ to 38 while accounting for the sampling variability of our estimate $\widehat{\theta}$, the sample mean. This is a completely valid approach to inference. In this section, we consider an equivalent (conceptually), though alternative, approach which will provide a more general framework for inference.

At its heart, hypothesis testing is about comparing two models for the data generating process. So far, we have stated one of those models:

$$\text{Model 1}: \quad (\text{Gestation Period})_i = \theta + \epsilon_i$$

This is the data generating process under the alternative hypothesis in which no restrictions are placed on the value of θ. However, *if* the null hypothesis is true, then the model for the data generating process simplifies to

$$\text{Model 0}: \quad (\text{Gestation Period})_i = 38 + \epsilon_i$$

This may not seem like a simpler model, but it is because there are less (in this case none) unknown parameters. A null hypothesis essentially places further restrictions on the data generating process. A hypothesis test is then about comparing these two models.

Hypothesis testing is about comparing two models for the data generating process.

The hypotheses we have been considering in this chapter could be rewritten as:

$$H_0 : \text{Model 0 is sufficient for explaining the data observed.}$$
$$H_1 : \text{Model 0 is not sufficient for explaining the data observed.}$$

That is, when conducting a hypothesis test, we are really determining whether the data provides evidence that the model for the data generating process under the null hypothesis is sufficient for explaining the observed data. This is why we refer to hypothesis testing as assessing model consistency. We are determining if there is evidence that the data is inconsistent with a proposed model for the data generating process.

Intuitively, the two proposed models would be equivalent (Model 0 would be sufficient for explaining the data) if they both performed similarly in predicting a response. Model 1 would be preferred (Model 0 would not be sufficient for explaining the data) if it performs better in predicting the response. We can assess "prediction" by the amount of variability in the data. For Model 0, the amount of variability can be quantified by

$$SS_0 = \sum_{i=1}^{n} \left[(\text{Gestation Period})_i - 38\right]^2$$

For Model 1, the amount of variability can be quantified by

$$SS_1 = \sum_{i=1}^{n} \left[(\text{Gestation Period})_i - \widehat{\theta}\right]^2$$

where $\widehat{\theta} = 39.11$, the observed sample mean. Notice that these sums of squared (SS) terms are similar to the definition of sample variance discussed in Chapter 5, without the scaling factor. The rationale for using these to assess predictive ability of the model will be further discussed in a later chapter. Here, we simply note that they are measuring a distance the observed data is from a mean; the difference is whether that mean is unrestricted (and therefore estimated from the data, Model 1) or restricted under the null hypothesis (Model 0). If SS_0 and SS_1 were similar, then it would suggest that $\widehat{\theta}$ differs from the null value only due

to sampling variability, which would be in line with the null hypothesis. If, on the other hand, SS_0 and SS_1 differ substantially from one another, it suggests $\widehat{\theta}$ differs from the null value more than we would expect due to variability alone. Therefore, the difference in these two sums of squares gives us a measure of the signal in the data against the null hypothesis. The larger this difference, the stronger the signal.

Unfortunately, the difference between these two values alone is not sufficient. That is, a signal is not enough without knowing the background noise. Think about having a radio on in the background of a party, and suppose the radio is set to a specific volume. If there are not many people talking at the party, it is easy to hear the radio; the signal is strong relative to the background noise. However, if there are a lot of people talking at the party, the radio is difficult to hear even though its volume hasn't changed; the signal is weak *relative* to the background noise. A signal is more difficult to locate if the background noise is elevated. The same principle holds in data analysis.

Consider Figure 12.2. Suppose we want to use each of these datasets (both containing a sample of size $n = 20$) to test the hypotheses:

$$H_0 : \mu = 0 \qquad \text{vs.} \qquad H_1 : \mu \neq 0$$

where μ is the population mean. Both datasets have *exactly* the same observed sample mean response (the black diamond in the figure). Therefore, it can be shown that the difference between SS_0 and SS_1 is exactly the same for both datasets. However, just visually, it should be clear that Dataset A provides stronger evidence against the null hypothesis than Dataset B; that is, Dataset A is more inconsistent with a mean of 0. What is the difference? The variability; the background noise.

Therefore, when quantifying the strength of a signal in a statistical analysis, it is common to measure the signal relative to the background noise. Returning to our example for the Birth Weight Case Study, we have that $SS_0 - SS_1$ is our signal. The noise is the variability in the sample

$$s^2 = \frac{1}{n-1} \sum_{i=1}^{n} \left[(\text{Gestation Period})_i - \widehat{\theta} \right]^2$$

as measured by the sample variance. Our signal-to-noise ratio is then

$$T^* = \frac{SS_0 - SS_1}{s^2} = 963.2$$

for our example. Such signal to noise ratios are known as **standardized statistics**.

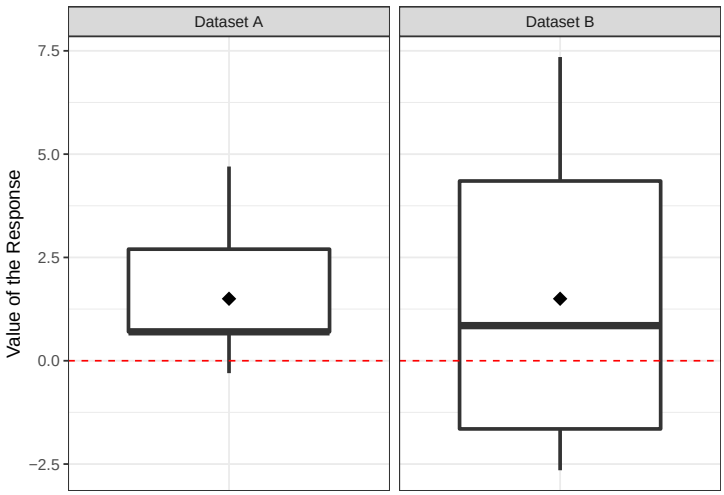


Figure 12.2: Illustration of the need to compare a signal to the noise in the data to assess its true strength.

Definition 12.1 (Standardized Statistic)**:**
A ratio of the signal of the sample and the noise in the sample. The larger the test statistic, the stronger the evidence of a signal; said another way, the larger the test statistic, the stronger the evidence against the null hypothesis.

A standardized statistic is often refered to as a "standardized test statistic" because they are heavily used in hypothesis testing.

Just as we constructed the null distribution for the observed sample mean in order to construct a distribution of our expectations under the null hypothesis, we can construct a null distribution of the standardized statistic to determine our expectations of this ratio under the null hypothesis. Figure 12.3 provides a model for this distribution. This is constructed in the same way as we did the null distribution for the sample mean except that instead of retaining the sample mean from each resample, we compute and retain the standardized statistic from each resample.

Notice that we reach the same conclusions. Our data is inconsistent with null hypothesis because our observed test statistic of 963.2 is in the far right tail of the null distribution. That is, if the null distribution were true, it would be very unlikely to obtain a sample which was this extreme due to sampling variability alone.

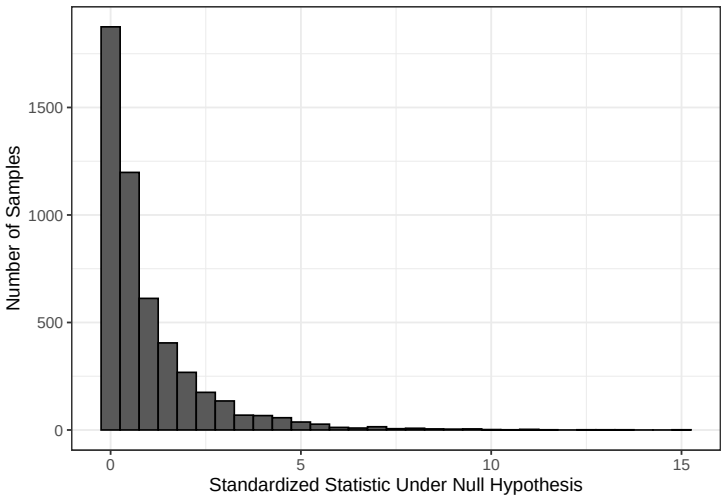


Figure 12.3: Model of the null distribution of the standardized statistic for a sample of 1009 infants. The model is based on 5000 bootstrap replications under the null hypothesis that the average gestation period is 38 weeks.

So, if our conclusions do not change, why the two different approaches? It turns out there is some theory that says bootstrapping standardized statistics tends to behave computationally a bit better, and these standardized statistics are a bit easier to model analytically using probability theory. We prefer talking about them because it again provides a nice overarching framework.

Quantifying evidence compares the signal in the data to the noise.

Before moving on, we should note that there is not a unique standardized statistic. Other standardized statistics are often quoted, such as

$$\frac{\sqrt{n}\left(\widehat{\theta}-38\right)}{s}$$

It can be shown that many such standardized statistics are related to the one we have described above (this one is the square root of that described above, for example). When the same conditions are applied, various standardized statistics yield the same results. Again, we opt for the one described earlier because it will provide continuity in the text.

12.2 Computing the P-value

Now that we have a model for the null distribution of the standardized statistic, we can compute a p-value. The p-value is the probability of observing a sample more extreme due only to sampling variability. Our standardized statistic has the form

$$T^* = \frac{SS_0 - SS_1}{s^2}$$

If the sample were more extreme — that is, if it produced a larger signal — then we would expect the difference between SS_0 and SS_1 to be even larger. Therefore, larger values of the standardized statistic present stronger evidence of the data. So, when looking at the null distribution of the standardized statistic, computing the p-value corresponds to computing the area to the right of the observed standardized statistic.

Looking back at Figure 12.3, our observed standardized statistic is not even on the graphic, meaning the p-value would be essentially 0. The data therefore provides strong evidence that the average gestation period of infants born in North Carolina exceeds 38 weeks.

Part III

Unit III: Modeling the Average Response as a Function of a Continuous Predictor

Chapter 13

Case Study: Seismic Activity in Greece

At the intersection of the African plate, the Eurasia plate, and the smaller Aegean plate, Greece is one of the most earthquake-prone regions in the world. Between July 2016 and July 2017, Greece experienced 179 earthquakes; by contrast, the state of Texas experienced 28 over the same span of time. In a region with such seismic activity, careful consideration must be given to municipal construction. Further, understanding how the motion experienced in a location is related to the soil properties in the area or the magnitude and distance of an earthquake is important.

An article in the *Journal of Earthquake Engineering* (Koutrakis et al. 2002) examined seismic events in Greece occurring between 1978 and 1997. Of interest for construction is characterizing the "strong ground motion," when the earth shakes with enough force to cause damage to infrastructure, with respect to the properties of a location. The study recorded several measurements from 121 stations (representing 93 distinct seismic events)[1]. The primary variable of interest is the *bracketed duration*, "the time interval [in seconds] between the first and last excursion of the peak ground acceleration beyond a certain predefined level." For our purposes, we only consider the data corresponding to a threshold of 2% of the acceleration due to gravity. In addition, the following measurements were available for each observation:

- Moment Magnitude: a measure of the size of the earthquake; larger values

[1]The original article presented repeated measurements at each location. We present here only the first measurement from each location to simplify any analyses. Repeated measurements are discussed briefly later in the text; for a more thorough treatment of the subject, we recommend a course in Designed Experiments or Biostatistics. The dataset presented here corresponds to that presented in Navidi's "Statistics for Engineers and Scientists" (Chapter 8, Supplementary Exercise 22).

Table 13.1: Data for first 5 observations from study characterizing seismic activity in Greece.

Magnitude	Distance from Epicenter (km)	Bracketed Duration (s)	Soil Conditions
6.4	30	8.82	Soft
5.3	6	4.31	Intermediate
5.6	15	5.74	Intermediate
5.2	7	4.08	Intermediate
6.6	31	28.27	Soft

indicate more severe earthquakes.

- Epicentral Distance: distance (kilometers) from the epicenter of the earthquake to the location at which the measurement was taken.
- Soil Condition: indicator of the type of soil present at the measurement site. Soil was categorized as one of three types - alluvium (soft, fine particles of clay, silt, sand, and gravel), intermediate soil conditions, or tertiary or older rock (those older than 2.58 million years).

The first 5 observations in the dataset are shown in Table 13.1. We are interested in characterizing the relationship between bracketed duration and the magnitude of the earthquake.

Chapter 14

Myriad of Potential Questions

For the Seismic Activity Case Study, we are primarily interested in characterizing the relationship between bracketed duration and the magnitude of the earthquake. First, note that this question is about the relationship between a quantitative response (bracketed duration; see Definition 3.2) and a quantitative predictor (magnitude). Also note that the question is quite broad. We might actually have one of the following more specific ideas in mind:

- In general, does the bracketed duration increase as the magnitude increases?
- If two earthquakes with different magnitudes occur in the same location, would we expect the same bracketed duration regardless of their magnitudes?
- Is the relationship between the bracketed distance and the magnitude different depending on the soil condition of where the measurement is taken?

These illustrate an array of potential questions we could address with the data. Each represents a different emphasis that we might have in a research question:

- Marginal Relationship: overall, do two variables tend to move together (are they correlated)?
- Isolation of Effect: does a relationship exist after accounting for the effect of additional variables? Or, what is the effect "above and beyond" the effect of additional variables?
- Interplay: how does the relationship between two variables change as a result of a third?

There is no right question to ask; each question examines a different facet of the relationship between two quantitative variables. In this unit, we will focus on questions of the first type. However, the framework we introduce is broad

enough to be extended to address each of these types of questions. This may sound daunting, but keep in mind that the fundamental ideas we discussed in Unit I and applied in Unit II will continue to form the foundation of the analyses discussed in this unit; namely,

- We are using a sample to say something about the underlying population.
- In order to make inference, we will need a model for the sampling (or null) distribution of our statistic.
- In order to form a standardized statistic of interest which measures the strength of the signal in the dataset, we think about variability.

The ideas remain the same; the context has changed. Stating these questions mathematically will require us to extend the model for the data-generating process we developed in Unit 2.

There is one more thing we want to point out before moving on: any relationships we observe are overall trends, not guaranteed to hold for any single individual. Recall that in Unit II we emphasized that our conclusions were about the mean response (the parameter of interest). Specifically, even if we know the average response within the population, due to variability, we do not expect every individual to have that specific value for the response. This will continue in this unit. If we observe, for example, that an increase in the magnitude is associated with an increase in the bracketed duration, we are describing an overall trend. It is highly likely there is some location for which this trend does not hold, simply due to variability.

Chapter 15

Nature of Collecting Multivariable Data

For the Seismic Activity Case Study, we are primarily interested in characterizing the relationship between bracketed duration and the magnitude of the earthquake. As we discussed in the previous chapter, this general goal might be refined into one of many specific questions:

- In general, does the bracketed duration increase as the magnitude increases?
- If two earthquakes with different magnitudes occur in the same location, would we expect the same bracketed duration regardless of their magnitudes?
- Is the relationship between the bracketed distance and the magnitude different depending on the soil condition of where the measurement is taken?

Notice that these last two questions actually require knowledge of more than just the braketed duration and the magnitude of each seismic event. In order to address the second question, we would also need the distance from the center of the earthquake; in order to address the third question, we also need the soil conditions of where the measurement is taken. Often, research questions require knowledge of more than just a single variable; such questions are **multivariable**.

Definition 15.1 (Multivariable)**:**
Refers to questions of interest which involve more than a single variable. Often, these questions involve many variables.

Consider going to the doctor because you are feeling ill. The doctor does not have you simply enter your most prominent symptom (fever, for example) into a computer and then prescribe a medication based solely on that single symptom.

Instead, a good physician will review all symptoms you are experiencing, as well as your medical history, other medications, allergies, etc. The physician operates in a multivariable world in which there are many contributing factors to a response. Therefore, when you arrive for this hypothetical visit, they record several variables which may be of interest.

Studies which collect several variables can be observational studies or controlled experiments. If an observational study, we want to ensure the sample of subjects is representative of the target population. Then, for each individual, we simply record several variables. If a controlled experiment, we randomly assign subjects to a particular treatment group; afterwards, we would measure the response in addition to other variables. Notice that with the latter, subjects are randomly assigned to only one of the variables; the remaining variables are simply observed.

When a study is primarily interested in characterizing the relationship between two or more quantitative variables, the data is typically from an observational study.

What we want to emphasize here is that how we collect the data has not really changed from what we have discussed in previous units. The primary difference is that we are very aware that we are collecting several measurements on each subject. The critical element is that our sample be representative of the target population if we want to apply any findings to that population.

Chapter 16

Summarizing Multivariable Data

For the Seismic Activity Case Study, we are primarily interested in characterizing the relationship between bracketed duration and the magnitude of the earthquake. As we discussed in the previous chapters, this broad question could be refined into a question falling into one of three categories:

- Marginal Relationship: overall, do two variables tend to move together (are they correlated)?
- Isolation of Effect: does a relationship exist after accounting for the effect of additional variables? Or, what is the effect "above and beyond" the effect of additional variables?
- Interplay: how does the relationship between two variables change as a result of a third?

As always, the key is developing summaries which help to address the question of interest.

16.1 Characterizing the Marginal Relationship of Two Quantitative Variables

Suppose we are interested in the following question:

> In general, does the bracketed duration increase as the magnitude increases?

This question is about the overall relationship between these two quantitative variables. Graphically, we can examine the relationship between these two variables using a *scatter plot*. The response is placed on the y-axis and the

predictor along the x-axis. Figure 16.1 illustrates the relationship between the bracketed duration and the magnitude.

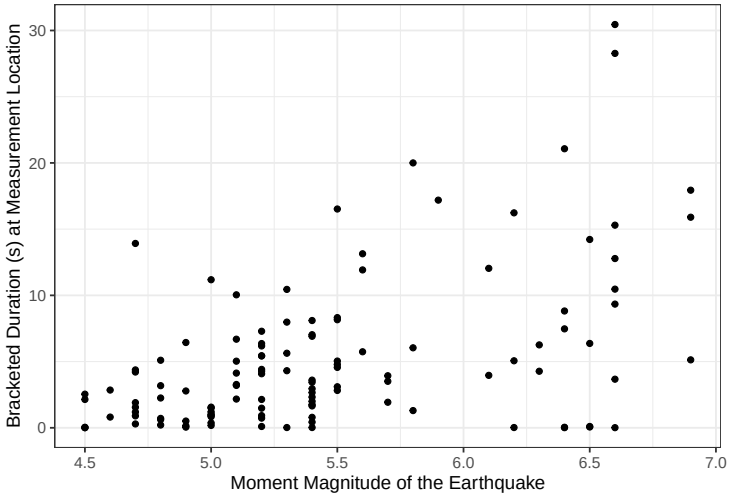


Figure 16.1: Relationship between the bracketed duration and the magnitude of an earthquake for locations Greece.

The graphic highlights several components of the relationship. First, we note that as the magnitude of the event increases, the bracketed duration also tends to increase. This is intuitive — as the size of the earthquake increases, the length of time the ground shakes with extreme force increases. This is a *trend*; it is not a universal truth. There are cases for which the magnitude was high, but the bracketed duration was lower. Our goal is to characterize the overall trend. We also notice that as the magnitude increases, the variability in the bracketed duration also tends to increase. That is, for earthquakes of small magnitudes, it seems fairly easy to anticipate the bracketed duration; however, the bracketed duration is much more difficult to anticipate for larger magnitudes.

A nice visual tool when exploring the relationship between two quantitative variables is a *smoothing spline*. The details of its construction are beyond the scope of this text, but we can think of it as representing where the response tends to be located for a particular value of the predictor and then smoothing that relationship out (hence the name). We do want to point out that this is an exploratory device; we should be cautious about over-emphasizing relationships we observe from the spline. Figure 16.2 illustrates a spline for the Seismic Events Case Study. The addition of the spline confirms what we had previously stated about the relationship appearing fairly linear (as the magnitude of the earthquake increases so does the bracketed duration at a location). In addition to the spline, there is a confidence band (generalization of a confidence interval) around the line in order to convey the variability in the estimated smoothing

spline.

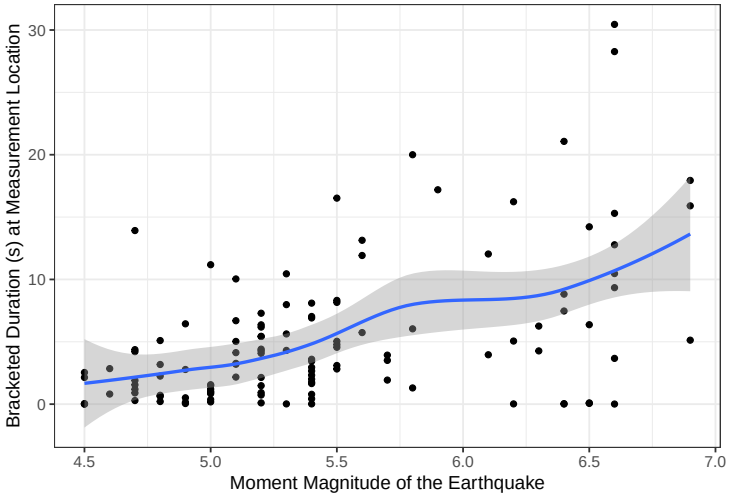


Figure 16.2: Illustrating the use of a smoothing spline to explore the relationship between the bracketed duration and the magnitude of an earthquake for locations Greece.

As we have seen, supplementing graphical summaries with numerical summaries can help convey our message. As an example, there is a positive linear relationship between the response and predictor in each of the cases illustrated in Figure 16.3. However, that relationship is much stronger or more apparent for Dataset A compared to Dataset B, for example. It would be nice to have a numeric summary which captured this; such a metric is known as the **correlation coefficient**.

Definition 16.1 (Correlation Coefficient)**:**
A numerical measure of the strength *and* direction *of the* linear *relationship between two quantitative variables.*

The classical Pearson Correlation Coefficient r is given by the following formula:

$$r = \frac{\sum_{i=1}^{n} (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n} (x_i - \bar{x})^2 \sum_{i=1}^{n} (y_i - \bar{y})^2}}$$

where $\bar{x}$ and $\bar{y}$ represent the sample means of the predictor and response, respectively.

The correlation between the bracketed duration and the magnitude of an earthquake is 0.497, indicating the two variables are positively linearly related, though perhaps the relationship is not strong.

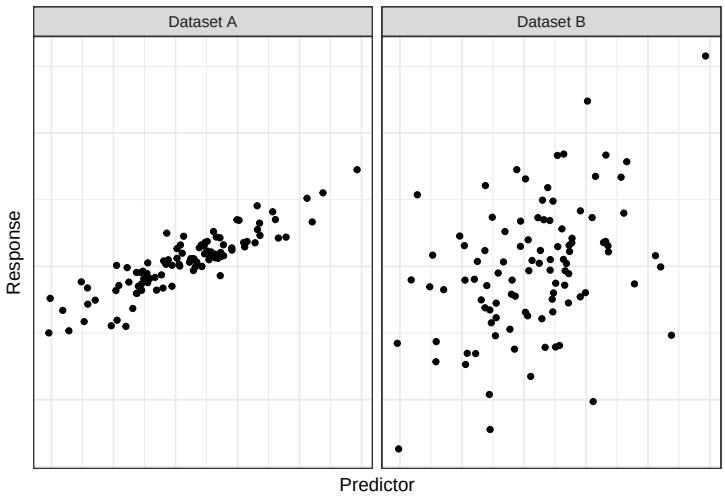


Figure 16.3: Pairs of hypothetical variables which exhibit different correlations; that is, the relationship between each pair exhibit different strengths.

Correlation coefficients measure both the strength and direction of linear relationships. Here are a few of their key properties:

- Takes a value between -1 and 1.
- Negative values mean that the variables tend to move in opposite directions.
- Positive values mean that the variables tend to move in the same direction.
- Unitless and therefore unaffected by unit changes in the variables.

The biggest thing to remember is that a correlation coefficient measures the strength of a *linear* relationship. A correlation of 0 does not mean that two variables are unrelated. It simply means they are not linearly related.

16.2 Visualizing the Impact of a Third Variable on the Marginal Relationship

In the previous section, we stated that the bracketed duration tended to increase as the magnitude increased. It is reasonable to ask the following question:

Is the relationship between the bracketed distance and the magnitude

different depending on the soil condition of where the measurement is taken?

That is, we want to determine the impact that a third variable (soil condition) has on the relationship we have observed. While the bulk of this unit will focus on inferential methods for the marginal relationship, graphically assessing questions isolating a single predictor or about the interplay of two predictors is fairly intuitive. In order to add more depth to our graphical representations, we make use of various attributes of the graphic: color of the points used in plotting, shape of the points used in plotting, size of the points used in plotting, facets (multiple graphics each with a different subset of the data). Figure 16.4 uses color to distinguish between the three possible types of soil conditions of the measurement locations. Notice the graphic allows us to both visualize the relationship for each soil condition but also facilitates our comparing these relationships.

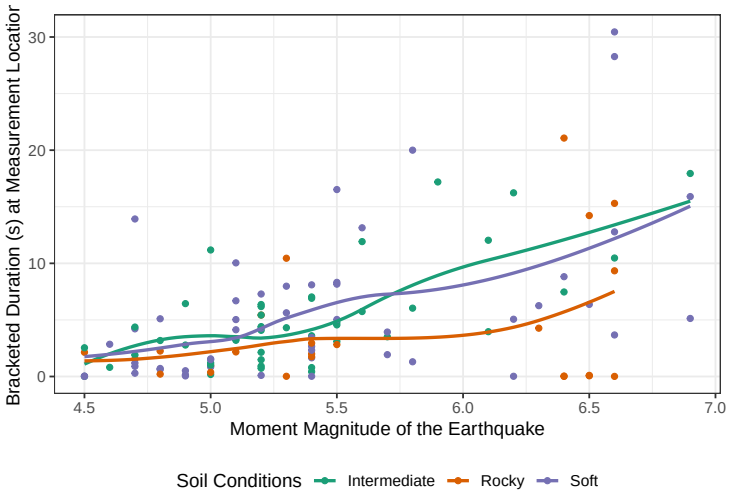


Figure 16.4: Relationship of the bracketed duration and the magnitude of an earthquake with various soil conditions.

The figure illustrates that the relationship between magnitude and bracketed duration is similar for both locations which have soft or intermediate soil conditions. However, for rocky conditions, the magnitude of the earthquake has a smaller impact on the resulting bracketed duration. This suggests, possibly, that foundations on rocky soils are less subject to the effects of an earthquake.

While our focus in this chapter has been on the scatter plot, our emphasis remains the same as when we used simpler graphics in the first unit — summaries need to be constructed to address the question of interest.

Chapter 17

Building our Statistical Model

In Chapter 10 we introduced the statistical modeling framework. In particular, our general model (see Equation (10.1)) was given as

$$\text{Response} = f(\text{variables, parameters}) + \text{noise}$$

As before, this model has two components:

- A deterministic component which takes the form of a function of variables and unknown parameters. It is often this component on which we would like to make inference.
- A stochastic component which captures the unexplained variability in the data generating process.

In the previous unit, we made use of this model, but we only scratched the surface of its potential applications. In this unit, we begin to explore the full capabilities of such a model. In particular, we will consider a model in which the deterministic component is a smooth function (specifically, a line) of potentially several variables. In general, this model building process is known as **regression**.

Definition 17.1 (Regression)**:**
Used broadly, this refers to the process of fitting a statistical model to data. More specifically, it is a process of estimating the parameters in a data generating process.

17.1 Statistical Model for A Quantitative Response and Quantitative Predictor

Recall that in Chapter 10, we described a general model for the data generating process of a quantitative response:

$$\text{Response} = f(\text{predictor variables, parameters}) + \text{noise}$$

While Chapter 10 focused on the function $f(\cdot)$ being a constant, this chapter considers alternative formulations. We believe these models are best discussed in the context of the graphics used to visualize them. Consider the Seismic Activity Case Study. Let's begin with a broad question:

> In general, does the bracketed duration increase as the magnitude increases?

As we are interested in predicting the bracketed duration, we will treat it as the response. In order to imagine what an appropriate model might look like, consider the graphical summary of this relationship. As we have discussed, we can use a scatter plot to visualize the relationship between the bracketed duration and the magnitude of the corresponding earthquake. Figure 17.1 gives the scatterplot but also overlays a straight line relationship on top of the data.

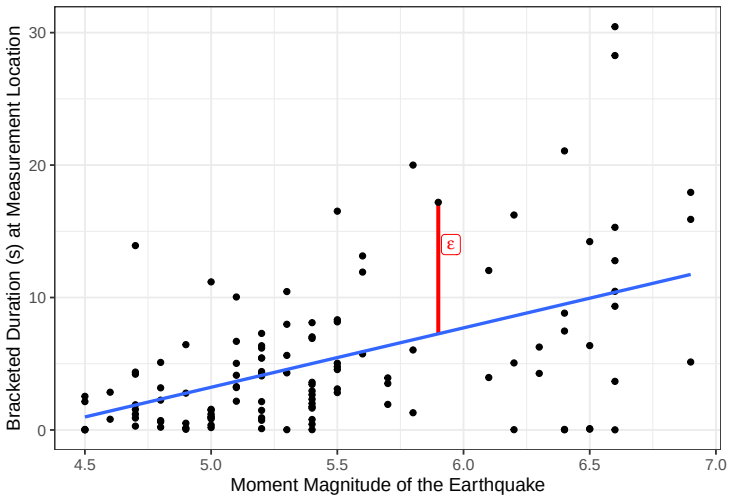


Figure 17.1: Relationship between bracketed duration and the magnitude of an earthquake with a line overlayed on the graphic as a potential explanation of the data generating process.

Suppose we feel that this line is a good model for the data generating process. Before proceeding, consider what this statement says. We are not trying to say

that the relationship explains every response we observe. Instead, the relationship explains the underlying trend — what happens on average. While not perfect, this linear relationship at least appears plausible. Therefore, we replace $f(\cdot)$ in the general form of a data generating process with a simple line, which we express as

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Magnitude})_i + \epsilon_i \tag{17.1}$$

where β_0 represents the intercept of the line and β_1 the slope. Now, observe that very few points in Figure 17.1 actually fall on the line, which is to be expected. This emphasizes the idea that the deterministic portion of the model is not meant to fully capture a data generating process since variability is inherent in any process. This is why statistical models embed a deterministic component alongside a stochastic component — to capture the variability due to error or noise in the data generating process.

The model suggests that the bracketed duration at a location is primarily determined by the magnitude of the correpsonding event; however, there is a component we cannot explain. That is, the model does not explain why, for example, when an earthquake with a magnitude of 5.5 hits, all locations do not have the same bracketed duration. This noise is picked up by the ϵ_i term in the model (as illustrated in red on Figure 17.1). The model essentially says that the bracketed duration for a specific magnitude are simply scattered vertically about the line. As we saw in Chapter 10, we refine this model further by placing additional conditions on the noise term in order to aid in conducting inference.

For a quantitative response and quantitative predictor, the general form of a simple linear regression model is then

$$(\text{Response})_i = \beta_0 + \beta_1(\text{Predictor})_i + \epsilon_i$$

17.2 Using a Categorical Predictor

We have described the simple linear model in this chapter as one which relates two quantitative variables. However, this framework can be extended to make use of a categorical predictor. For example, we saw in Chapter 16 that the bracketed duration for locations with rocky soils could differ from that of locations with other types of soil. How do we include whether a location has rocky soil or not when this is a categorical variable? The key is to construct an **indicator variable**.

Definition 17.2 (Indicator Variable)**:**
A binary variable (one which takes on a value of 0 or 1) used to represent

whether the value for a categorical variable for an observation takes a particular value.

Indicator variables essentially create a numeric variable which represents a yes/no decision regarding a categorical variable. For example, consider the following variable definition:

$$(\text{Rocky Soil})_i = \begin{cases} 1 & \text{if } i\text{-th location has rocky soil} \\ 0 & \text{if } i\text{-th location has a different soil type} \end{cases}$$

We can then use this variable in our model for the data generating process. Specifically, consider the following model

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Rocky Soil})_i + \epsilon_i \tag{17.2}$$

You may at first feel the need to have another indicator that takes the value 1 when the soil is not rocky. But, this is not necessary. Think of an indicator variable like a "light switch." The indicator variable turns on when an observation falls into a particular group and turns off otherwise. So, if you have a location which has "Intermediate" soil conditions, then that location cannot have "Rocky" soil, turning the indicator off. Setting the indicator to 0 (turning it "off") then leaves only the intercept in the model. So, the group which has a 0 for the indicator is encoded in the intercept; this is known as the **reference group**.

Definition 17.3 (Reference Group)**:**
The group defined by setting all indicator variables in a model to 0.

The indicator variable essentially creates two mean responses, one for each value of the indicator.For the model in Equation (17.2), we have the following:

$$\begin{aligned} \text{Rocky Soil:} \quad & (\text{Bracketed Duration})_i = \beta_0 + \beta_1 + \epsilon_i \\ \text{Intermediate/Soft Soil:} \quad & (\text{Bracketed Duration})_i = \beta_0 + \epsilon_i \end{aligned}$$

So, the "slope" β_1 is really capturing the shift in the deterministic portion of the model from one group to the other. This is illustrated in Figure 17.2. The "line" is really connecting the location of the two groups.

17.3 Estimating the Parameters

Recall the goal of statistics — to use a sample to say something about the underlying population. There is something intuitive about using the sample mean as an estimate of the population mean; however, now we have a model

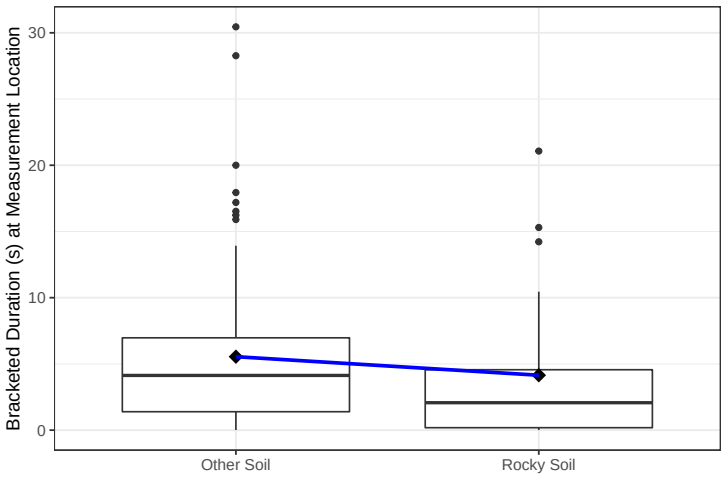


Figure 17.2: Comparison of the bracketed duration between locations with rocky soil and those with other soil types.

with both a slope and an intercept and we want to use the data to say something about these parameters. That process begins by computing an estimate for each of those parameters.

Before describing how such estimates are constructed, let us revisit the model in Equation (17.1). In this equation, both β_0 and β_1 are parameters and are therefore unknown values, and they will always be unknown. We can use available data to estimate these parameters with confidence (confidence intervals) or determine if there is evidence they are outside of a specific region (hypothesis testing), but we will never be able to definitively state the value of these parameters. As scientists and engineers, many are undoubtedly familiar with a line of "best fit." We need to keep in mind that any such line is simply an *estimate*; no analysis can actually provide the exact values of β_0 and β_1. But, how are such estimates constructed?

Think about what we would like to do. We believe there is a linear relationship which generated the data, and we want to use the data to estimate what that relationship looks like. We want to draw a line through the points that gives the "best fit." Figure 17.3 illustrates this for a hypothetical dataset; it compares two *estimated relationships*. We note that these are just estimates; neither represents the actual line from which the data was generated. Something inside us knows that the blue line is preferred to the orange line. The orange line does not seem to represent the pattern in the data because it leaves the cloud of points. We want a line that goes through the points. Trying to formalize this, we are saying we want a line that is somehow simultaneously as close to all the data as possible.

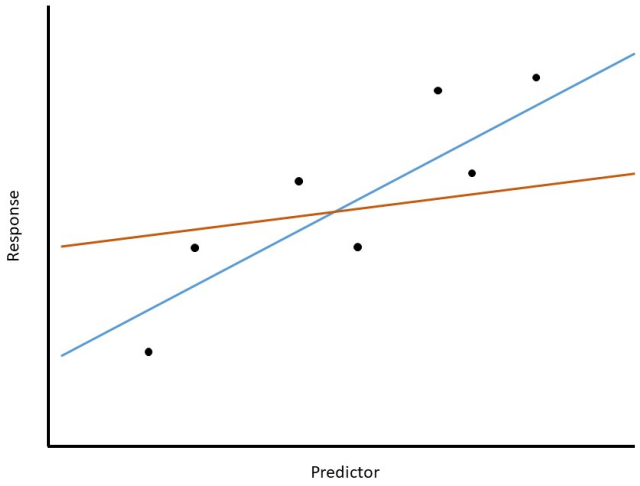


Figure 17.3: Illustration of two competing estimates of a line which runs through the data.

The most widely used method for estimating the parameters is known as "the method of least squares." For this reason, the estimates are often referred to as the **least squares estimates**. This method essentially minimizes the amount of error (as measured by the vertical distance a point is from the line) within the dataset.

Definition 17.4 (Least Squares Estimates)**:**
Often called the "best fit line," these are the estimates of the parameters in a regression model chosen to minimize the sum of squared errors. Formally, they are the values of β_0 *and* β_1 *which minimize the quantity*

$$\sum_{i=1}^{n} \left((Response)_i - \beta_0 - \beta_1 (Predictor)_i \right)^2$$

These estimates are often denoted $\widehat{\beta}_0, \widehat{\beta}_1$.

This estimation is carried out using statistical software.

Estimation is often associated with statistics. However, the least squares estimates are actually the result of a mathematical minimization process. The real statistical aspect comes in when we move back into one of our components of the *Distributional Quartet*. In particular, the estimates are only useful if we can

quantify the variability in those estimates. In order to construct a model for the sampling distribution of these statistics, we place additional conditions on the stochastic portion of the model. That is the focus of the next chapter.

Chapter 18

Conditions on the Error Term of a Regression Model

In the previous chapter we developed a general model for generating a quantitative response as a linear function of a quantitative predictor:

$$(\text{Response})_i = \beta_0 + \beta_1(\text{Predictor})_i + \epsilon_i$$

We also discussed a common method for estimating the parameters of this model from a sample — the least squares method. However, if we are to construct a model for the sampling distribution of these estimates we must add some structure to the stochastic component ϵ in the model. We will find that the more assumptions we are willing to make, the easier the analysis, but the less likely our model is to be applicable to the actual data-generating process we have observed. The conditions we make dictate how we conduct inference (the computation of a p-value or confidence interval).

18.1 Correctly Specified Model

The first condition we consider is the most important. It states that for every value of the predictor, the average error is 0. This condition implies that the model we have posited for the data generating process is accurate; that is, it implies that the form of the model is appropriate — that the response is linearly related to the predictor. There are two reasons we say that this is the most important condition:

1. If this condition is violated, it says your model for the data generating process is incorrect. Generally this is the result of ignoring some curvature or additional feature.

2. This condition allows us to interpret the parameters of the model.

18.1.1 Interpreting the Parameters

In the second unit, we were were focused on the mean response. Now, instead of considering the average response overall, we are asking what the average response is for subjects in the population with a specific value of the predictor(s). When we impose the "mean 0 condition," we are saying the errors are not biasing the average response (since on average, they have a value of 0); therefore, we are able to say that the determinisic portion of our model is giving the *average* response for a specified value of the predictor(s).

The deterministic portion of a regression model specifies the *average* value of the response given the value(s) of the predictor(s).

As an example, consider our model for the Seismic Activity Case Study which predicted the bracketed duration as a function of the magnitude of the earthquake:

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Magnitude})_i + \epsilon_i$$

When the errors have mean 0 for all magnitudes (our first condition), then earthquakes with a 5.0 magnitude have an *average* bracketed duration of

$$\beta_0 + \beta_1(5)$$

Similarly, earthquakes with a 6.0 magnitude have an *average* bracketed duration of

$$\beta_0 + \beta_1(6)$$

As we have mentioned, the deterministic portion of the model does not specify the exact response for any individual but the trend. We are now able to say that the "trend" we are modeling is the average response. Further, we can estimate this average response by plugging in the least squares estimates $\widehat{\beta}_0$ and $\widehat{\beta}_1$. Specifically, using the method of least squares, the line of best fit was estimated as

$$(\text{Bracketed Duration}) = -19.19 + 4.48(\text{Magnitude})$$

Therefore, we estimate the average bracketed duration for locations with 5.0 magnitude earthquakes to be 3.22 seconds (7.71 seconds for locations with 6.0

magnitude earthquakes). While we do not expect every location which has a 5.0 magnitude earthquake to have a bracketed duration of this length, we expect the bracketed duration to vary about this length of time. This is huge; it says that when we use a regression model to predict a response, we are actually predicting the *average* response. More, we can interpret the parameters themselves.

Let's begin with the intercept term, β_0. Notice that in our model above, if we try to predict the bracketed duration for a location with an earthquake which has a magnitude of 0, then our model returns β_0. In fact, for any regression model, the intercept β_0 is the value of the deterministic portion of the model whenever all predictors in the model are set to 0. And, that deterministic portion is the average response.

The intercept in a regression model β_0 represents the *average* response when all predictors in the model are set equal to 0. Note that this may not be practically meaningful in all contexts.

For our particular example, the estimate of the intercept does not make sense — what does it mean to have a duration of -19.19 seconds? More, it does not make sense to estimate the average bracketed duration for an earthquake which had a magnitude of 0 (not even an earthquake). This can often be the case when trying to interpret the intercept term due to what we call **extrapolation**. We do not have any data on the bracketed duration for locations which experienced an earthquake with a magnitude less than 4.5. Therefore, we are using a model to predict for a region over which the model was not constructed to operate. This is a lot like using a screw driver to hammer a nail — we are using a tool to accomplish a task for which it was not designed. We should not be surprised when it fails. The primary reason extrapolation is dangerous is that without data in a particular region, we have nothing supporting that the model will continue to hold in that region. We have illustrated this when discussing the intercept, but extrapolation can occur in any region for which there is no data. For this reason, unless you have strong scientific justification for why a model will hold over all values of the predictor, extrapolation should be avoided

Definition 18.1 (Extrapolation)**:**
Using a model to predict outside of a region for which data is available.

We have seen that the intercept is the average value of the response when the predictor has the value of 0. How then do we interpret the coefficient associated with the predictor (the slope). We again use an example. Notice that based on our estimates, the average bracketed duration is 4.48 seconds longer for those locations which experience a 6.0 magnitude earthquake compared to those which experience a 5.0 magnitude earthquake, and this difference is the value of the

estimated slope. This leads us to observing that 4.48 seconds is the change in the average bracketed duration that is associated with a 1-unit increase in the magnitude of an earthquake.

The coefficient (or slope) β_1 in a regression model represents the *average* change in the response associated with a 1 unit *increase* in the predictor.

18.1.2 Embedding our Question in a Statistical Framework

Our first fundamental idea centers on the idea that the majority of research questions can be framed in terms of a parameter within the population. This seemed somewhat intuitive when the parameter was simply the mean response. With parameters which are the slope and intercept of a line, this seems less clear. However, this condition that the errors have mean 0 for all values of the predictor (because of its implications on the interpretation of the parameters) ensures that our questions of interest can be framed in terms of the parameters. Consider the following question:

> On average, is the bracketed duration related to the magnitude of an earthquake?

Let's consider how we might write this in terms of a null and alternative hypotheses.

> H_0 : the bracketed duration does not change, on average, as the magnitude changes.
> H_1 : the bracketed duration is linearly related, on average, with the magnitude; that is, as the magnitude increases, the bracketed duration changes, on average.

In order to address this question, we considered the following model for the data generating process:

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Magnitude})_i + \epsilon_i$$

If the null hypothesis above is true, then that suggests that the bracketed duration is flat on average, regardless of the value of the magnitude. What would be true about the parameters if that were true? Remember that β_1 captures the change in the average bracketed duration as the magnitude increases by 1 unit; and, the null hypothesis says that there is no change in the average bracketed duration as the magnitude changes. That is, if the null hypothesis is true, $\beta_1 = 0$. Said another way, we need a model for which changing the value

of the magnitude does not affect the resulting bracketed duration — a flat line. Therefore, our null and alternative hypotheses can be written as

$$H_0 : \beta_1 = 0$$
$$H_1 : \beta_1 \neq 0$$

where β_1 is the parameter linearly relating the bracketed duration to the magnitude. That is, if the paramter associated with magnitude is 0, then it is plays no role in the data generating process; if it is anything other than 0, then magnitude has a role within the data generating process.

Setting a slope parameter to 0 in the model for a data generating process is associated with saying that the corresponding predictor is not associated with the response in a linear fashion — that it does not belong in the model.

The interpretation of our parameters allows us to see that our research questions are characterizing the relationship between the response and the predictor, *on average*. As in the previous unit, our questions are about the average response; instead of looking at the overall average, however, we are allowing it to depend upon a predictor.

This first condition on the error term — holding the average error to be 0 for all values of the predictor — is only one condition typically placed on the stochastic portion. We now desribe others.

18.2 Additional Conditions

The second condition we consider is that the noise attributed to one observed individual is independent of the noise attributed to any other individual observed. That is, the amount of error in any one individual's response is unrelated to the error in any other response observed. This is the same condition we introduced in Chapter 10. We still want each observation in our data to be independent of one another.

With just these first two conditions (that the average error is 0 for all values of the predictors and the errors are independent of one another), we can use a bootstrap algorithm in order to model the sampling distribution of the least squares estimate for the slope (as well as the intercept). However, additional conditions are often placed on the error term.

The third condition that is typically placed on the distribution of the errors is that the errors are identically distributed. Again, we introduced this condition in Chapter 10. However, in the context of regression, this is often described a bit differently. In particular, if the errors are not identically distributed, it is typically because the variability of the error differs for one value of the

predictor compared to another. Practically, this reveals itself as our response being more precise in one region than in another. As a result of focusing on the variability of the response for each predictor, this condition is often referred to as *homoskedasticity* instead of the errors being identically distributed.

With this additional condition imposed, we are able to modify our bootstrap algorithm when constructing a model for the sampling distribution of the least squares estimates. Because we are relying on a bootstrap procedure, our model for the sampling distribution or null distribution, depending on whether we are interested in computing a confidence interval or p-value) is empirical. As a result, our model for the sampling distribution can be unstable in small sample sizes; this can be avoided by building an analytical model for the sampling distribution. This requires us to impose a fourth condition (common in the engineering and science disciplines) on the distribution of the errors and then rely on some probability theory.

18.2.1 Modeling the Population

Before we delve into more detail, let's set the stage for the bigger story being told. Recall that our goal is to say something about the population using a sample. We have developed a process to address this goal:

1. Frame our question through a parameter of interest.
2. Collect data that allows us to estimate the parameter using the analogous statistic within the sample.
3. Summarize the variability in the data graphically.
4. Quantify the variability in the statistic through modeling the sampling distribution (or null distribution, whichever is appropriate).
5. Using the sampling distribution , quantify the evidence in the sample.

This process is presented through our *Five Fundamental Ideas of Inference* and the *Distributional Quartet*. The key step in this process is quantifying the variability by modeling the *sampling distribution* (or *null distribution*, whichever is appropriate for our research goal). We have described the construction of these models empirically, through repeating the study by appropriately resampling the data available and performing the analysis on each resample.

Our goal is still to model the sampling distribution; that is the key inferential step. Instead of building an empirical model, we can construct an exact analytical model through an additional step: modeling the population directly.

A model for the sampling distribution of a statistic can often be obtained by placing a model on the distribution of the population.

So, we have two distributional models; the model for the distribution of the

population is simply a stepping stone to a model for the sampling distribution of the statistic, which is what we really need. It is important to separate these steps. We are not interested in directly modeling the population; we do it in order to construct a model for the sampling distribution.

There is one other distinction to make: a model for the population is *always* an assumption. We hope that the data is consistent with this assumption in order to apply the resulting model for the sampling distribution. In later chapters, we will discuss how we assess whether our data is consistent with these conditions; for now, we simiply want to understand we are making an assumption when we place such a condition on the stochastic portion of data generating process.

18.3 Adding the Assumption of Normality

Probability, a sub-field of mathematics which is used heavily in statistics, is the discipline of modeling randomness. In particular, we make use of probability to model a distribution. In order to get a feel for probability models, consider the following example.

Example 18.1: "Iris Characteristics"
The discipline of statistics began in the early 1900's primarily within the context of agricultural research. Edgar Anderson was a researcher investigating the characteristics of the iris. He had collected measurements on over one hundred iris flowers, including their petal length and width and their sepal length and width. The sepal is the area (typically green) beneath the petal of a flower. It offers protection while the flower is budding and then support for the petals after the flower blooms.

Figure 18.1 is a histogram of the sepal width for the iris plants observed by Edgar Anderson; overlayed is the density plot for the same dataset, which we have described as a smoothed histogram. Both the histogram and the density plot are empirical models of the distribution of the sepal width.

Probability models are analytical models for the distribution of a variable. Instead of constructing a density using data, probability theory posits a functional form for the density. For example, Figure 18.2 overlays the following function on top of the the iris data:

$$f(x) = \frac{1}{\sqrt{0.380\pi}} e^{-\frac{1}{0.380}(x-3.057)^2}$$

A density (whether constructed empirically or posited analytically) is just a model for the distribution of a variable. Further, all density functions share a few basic properties:

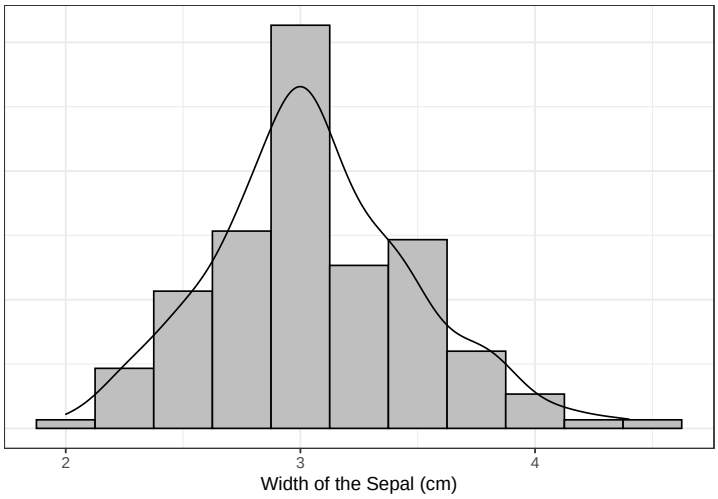


Figure 18.1: Summary of the distribution of sepal widths for a sample of irises.

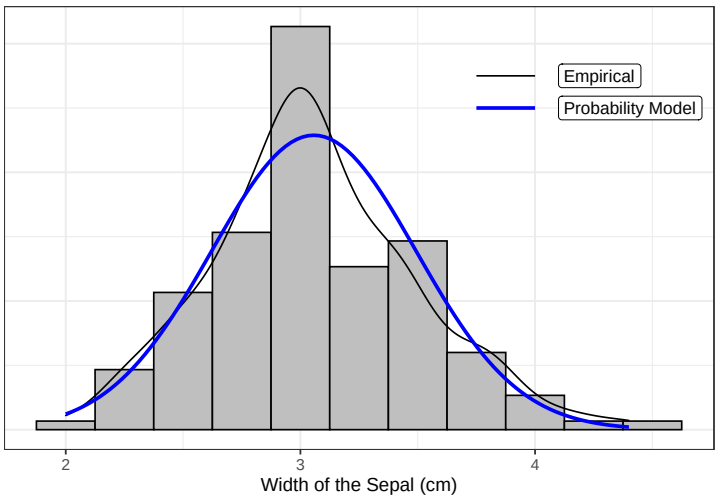


Figure 18.2: Summary of the distribution of the sepal widths for a sample of irises with a probability model overlayed.

1. The density is non-negative for all values of the variable.
2. The area under the density function must equal 1.

While the value on the y-axis is not directly meaningful, density functions provide a link between the value of the variable and the likelihood of it occuring. Specifically, the probability that a variable falls in a specific range corresponds to the area under the curve in that region. For example, based on the analytical model described above (the blue curve in the figure), the probability that an iris has a sepal width between 3.5 and 4 centimeters is 0.14, illustrated in Figure 18.3. That is, there is a 14% chance we find an irish with a sepal width between 3.5 and 4 centimeters.

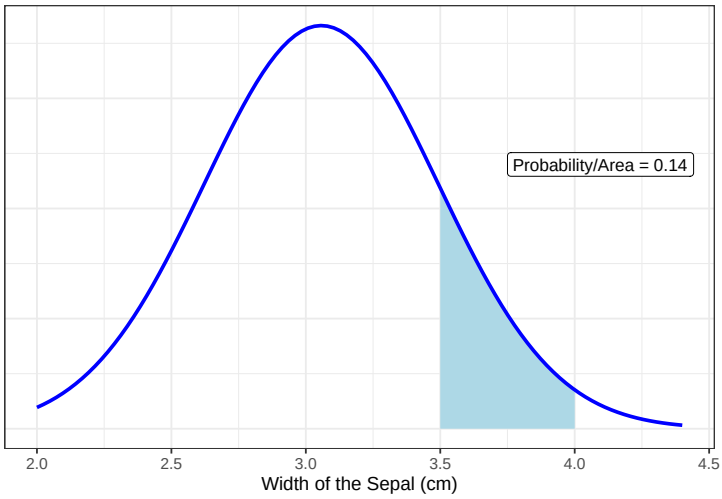


Figure 18.3: Using the model for a density function to compute a probability.

While the above model for the density is not perfect, it does capture many of the characteristics present in the data. Similar to empirical models, analytical models for distributions are just that — *models*. This particular model, characterized by the bell-shape density, is known as the **Normal Distribution**.

Definition 18.2 (Normal Distribution)**:**
Also called the Gaussian Distribution, this probability model is popular for modeling noise within a data-generating process. It has the following characteristics:

- *It is bell-shaped.*
- *It is symmetric, meaning the mean is directly at its center, and the lower half of the distribution looks like a mirror image of the upper half of the distribution.*
- *Often useful for modeling natural phenomena or sums of measurements.*

The functional form of the Normal distribution is

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2\sigma^2}(x-\mu)^2}$$

where μ is the mean of the distribution and σ^2 is the variance of the distribution.

While there are several nice properties of the Normal Distribution, we are primarily interested in the fact that if the error in a data generating process follows a Normal Distribution (in addition to the other three conditions described above placed on the error term), then the form of the sampling distribution for the least squares estimates of the slope and intercept is known. That is, with all four conditions in place, we have an analytical model for the sampling distribution. This means we avoid simulating in order to build a model for the sampling distribution; so, computationally it is faster. If the errors really are from a Normal Distribution, then we also gain power in our study by imposing this condition. Finally, such a model does not rely on sufficient data to construct; it is valid for any sample size (of course, large samples will always decrease variability in the estimates, which is a plus).

Let's think about what this condition means for the responses. Given the shape of the Normal distribution, imposing this condition (in addition to the other conditions) implies that some errors are positive and some are negative. This in turn implies that some responses will tend to fall above the line (we will underpredict for these observations), and some response will tend to fall below the line (we will overpredict for these observations).

18.4 Classical Regression Model

We have discussed four conditions we could place on the stochastic portion of the data generating process. Placing all four conditions on the error term is what we refer to as the "Classical Regression Model."

Definition 18.3 (Classical Regression Model)**:**
For a quantitative response and single predictor, the classical regression model assumes the following data-generating process:

$$(Response)_i = \beta_0 + \beta_1(Predictor)_i + \epsilon_i$$

where

1. *The error in the response has a mean of 0 for all values of the predictor.*
2. *The error in the response for one subject is independent of the error in the response for all other subjects.*

3. *The errors are identically distributed for all values of the predictor. This is often stated as the variability in the error of the response is the same for all values of the predictor.*
4. *The errors follow a Normal Distribution.*

This is the default "regression" analysis implemented in the majority of statistical packages.

We note that regression need not require these conditions. Placing all four conditions on the error term results in a specific analytical model for the sampling distribution of the least squares estimates. Changing the conditions changes the way we model the sampling distribution.

The model for the sampling distribution of a statistic is determined by the conditions you place on the data generating process.

We have stressed the implications of each condition individually. Figure 18.4 illustrates these conditions working together. The condition that the errors have mean 0 implies that for a given value of the predictor, the average response is given by the line (shown as the green dot in the figure). The condition of Normality implies that for a given value of the predictor, the response is distributed evenly about the regression line, with some above and some below. Further, the shape of the Normal distribution implies that these responses will cluster about the line. The identically distributed condition (specifically homoskedasticity) implies that while the responses vary around the line, they do so the same degree, regardless of the value of the predictor. Therefore, the model is just as precise for all values of the predictor. Finally, any two responses must be unrelated.

18.5 Imposing the Conditions

Let's return to our model for the bracketed duration as a function of the magnitude of the corresponding earthquake:

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Magnitude})_i + \epsilon_i$$

Our hypotheses of interest which captures the question of interest was

$H_0 : \beta_1 = 0$
$H_1 : \beta_1 \neq 0$

which corresponds to testing whether there is evidence of a linear relationship between the two variables. Using the method of least squares, we estimated the

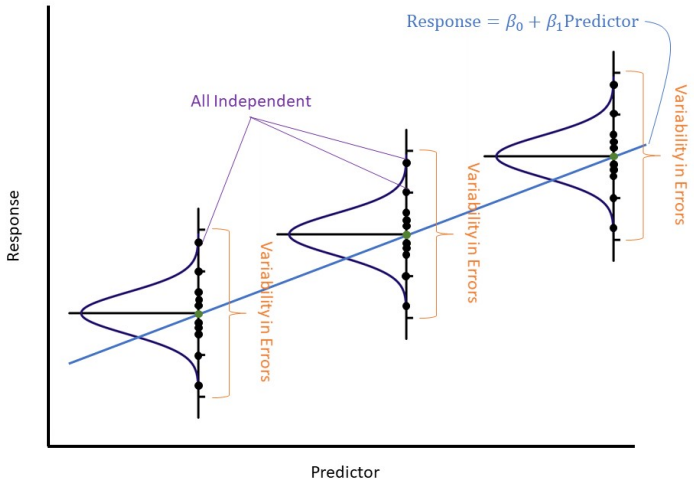


Figure 18.4: Illustration of the conditions on the error term for the classical regression model.

parameters in the model; this leads to the following equation for estimating the average bracketed duration given the magnitude:

$$(\text{Brackted Duration}) = -19.19 + 4.48(\text{Magnitude})$$

If we are willing to assume the data is consistent with the conditions for the classical regression model, we are able to model the sampling distribution of these estimates and therefore construct confidence intervals. Table 18.1 summarizes the fit for the above model. In addition to the least squares estimates, it also contains the **standard error** of the statistic, quantifying the variability in the estimates.

Definition 18.4 (Standard Error)**:**
The estimated standard deviation of a statistic, computed from the model for the statistic's sampling distribution. It quantifies the variability in the sampling distribution of the statistic.

Finally, there is a 95% confidence interval estimating each parameter. Notice that based on the confidence interval for the slope, 0 is not a reasonable value for this parameter. Therefore, we have evidence that the slope coefficient associated with the magnitude differs from 0; that is, we have evidence of a linear relationship between the bracketed duration and the magnitude of the earthquake.

Table 18.1: Summary of the linear model fit relating the bracketed duration at locations in Greece following an earthquake with the magnitude of the event.

Term	Estimate	Standard Error	Lower 95% CI	Upper 95% CI
(Intercept)	-19.194	3.975	-27.066	-11.323
Magnitude	4.484	0.724	3.050	5.917

We have described in general how confidence intervals are constructed. Under the classical regression model, there is an analytical model for the sampling distribution, and it is known. As a result, the confidence interval can be computed from a formula.

If the classical regression model is assumed, the 95% confidence interval for the parameter β_j can be approximated by

$$\widehat{\beta}_j \pm (1.96)\left(\text{standard error of } \widehat{\beta}_j\right)$$

The confidence interval for the change in the average bracketed duration for each 1-unit increase in the magnitude of an earthquake (the slope β_1) was constructed assuming the classical regression model. Suppose, however, that we are only willing to impose the following conditions:

- The error in the bracketed duration is 0 on average for earthquakes of any magnitude.
- The error in the bracketed duration for one earthquake is independent of the error in the bracketed duration for any other earthquake.

Since the conditions have been altered, the model for the sampling distribution of the estimates will change and therefore the corresponding confidence intervals. Under these conditions, we can appeal to a bootstrapping algorithm. Specifically, we could resample (with replacement) 119 earthquakes from the original data; for each resample, we compute the least squares fit (see Figure 18.5). Since the observations selected change with each resample, the least squares estimates will also change. By repeating this process over and over again, we can obtain a model for how the estimates would change in repeated sampling.

Using the empirical model of the sampling distribution for each estimate, we can construct confidence intervals. These updated confidence intervals are shown in Table 18.2

While the exact interval differs from what we computed previously, our overall conclusion remains the same (there is evidence of a relationship). It is reasonable to ask, which confidence interval should we use? That depends on the conditions you are willing to assume, which is an issue we will tackle soon.

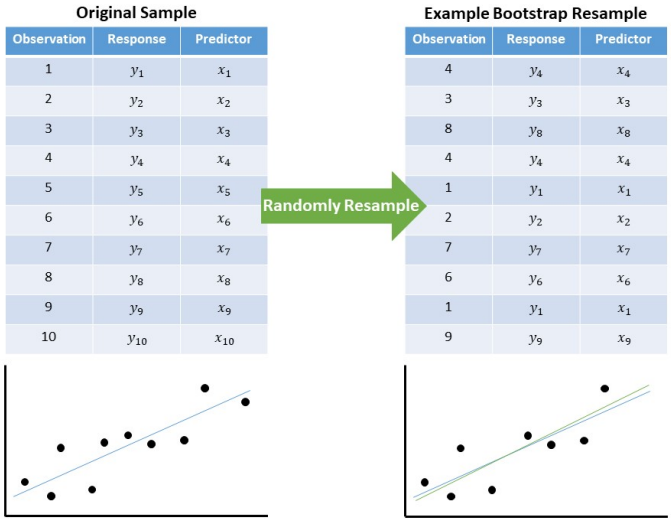


Figure 18.5: Illustration of a single iteration of a bootstrap procedure to construct an empirical estimate of the sampling distribution for the estimates of the coefficients in a regression model.

Table 18.2: Summary of the linear model fit relating the bracketed duration at locations in Greece following an earthquake with the magnitude of the event. Only assumes errors are independent and have mean 0.

Term	Estimate	Standard Error	Lower 95% CI	Upper 95% CI
(Intercept)	-19.194	4.960	-29.258	-9.545
Magnitude	4.484	0.965	2.593	6.437

18.6 Recap

We have covered a lot of ground in this chapter, and it is worth taking a moment to summarize the big ideas. In order to construct a model for the sampling distribution for the estimates of the parameters in the regression model, we took a step back and modeled the data generating process. Such a model consists of two components: a deterministic component explaining the differences in the response as a function of the predictor and a stochastic component capturing the noise in the system.

Certain conditions are placed on the distribution of the noise in our model. With a full set of conditions (classical regression model), we are able to model the sampling distribution analytically. We can also construct an empirical model for the sampling distribution assuming the data is consistent with fewer conditions.

Chapter 19

Quantifying the Quality of a Model Fit

In the previous two chapters, we described a model for describing the data generating process for a quantitative response as a function of a single quantitative predictor:

$$(\text{Response})_i = \beta_0 + \beta_1(\text{Predictor})_i + \epsilon_i$$

We can obtain estimates of the unknown parameters in this model using least squares. Further, under certain conditions on the error term, we are able to construct valid confidence intervals for the parameters. We have not yet discussed how to compute p-values to test hypotheses about the parameters, nor have we discussed how to determine if our model is useful for making predictions. It turns out these two tasks are very much related and are accomplished through partitioning variability. Much of statistics is about accounting for various sources of variability; and, this process allows us to compare models for the data generating process. In this chapter, we will describe what we mean by partitioning variability and how it is used to derive a measure for the overall performance of a model and to develop a standardized statistic for comparing two models.

19.1 Partitioning Variability

Consider modeling the bracketed duration as a function of the distance the location is from the center of the earthquake:

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Epicentral Distance})_i + \epsilon_i$$

Table 19.1: Summary of the model fit explaining the bracketed duration as a function of epicentral distance.

Term	Estimate	Standard Error	Lower 95% CI	Upper 95% CI
(Intercept)	4.462	0.726	3.024	5.899
Epicentral Distance	0.029	0.018	-0.007	0.064

Using least squares to estimate the parameters, and assuming the data is consistent with the conditions for the classical regression model, the resulting model fit is summarized below in Table 19.1.

Remember, the goal of the model for the data generating process is to explain why the response is the value we see — we are essentially explaining why the values of the response differ from one individual to another (its variability). Consider the model for the data generating process summarized above; it posits two reasons why the bracketed duration is not the same value at each measured location:

- The locations are located different distances from the epicenter of each earthquake.
- Additional noise due to measurement error in the bracketed duration or additional natural sources we are unable to explain.

Looking at the form of the model for the data generating process, it may seem obvious that there are these two sources of variability — two sources for why the bracketed duration differs from one individual to another. However, it is not yet clear how we quantify the amount of variability in each. We want to quantify the amount of variability in the response that can be attributed to each of these components. That is, we move forward with a goal of trying to say something like

$$\begin{aligned}(\text{Total Variability in Bracketed Duration}) = &(\text{Variability due to Distance}) \\ &+ (\text{Variability due to Noise})\end{aligned}$$

As we have seen in both Chapters 5 and 12, variability can be quantified through considering the "total" distance (squared) the observations are from a common target (the mean response). That is, the total variability in bracketed duration can be measured by

$$\sum_{i=1}^{n} \left((\text{Bracketed Duration})_i - (\text{Mean Bracketed Duration})\right)^2$$

Notice this quantity is similar to, but not exactly the sample variance. It measures the distance each response is from the sample mean and then adds

these distances up. This is known as the **Total Sum of Squares** since it captures the total variability in the response.

Definition 19.1 (Total Sum of Squares)**:**
Let y_i denote the response for the i-th observation and $\bar{y}$ denote the sample mean response. Then, the Total Sum of Squares (abbreviated SST) is given by

$$SST = \sum_{i=1}^{n} (y_i - \bar{y})^2$$

We now have a way of quantifying the total variability in bracketed duration; we now want to quantify its two components specified by the model (variability due to epicentral distance and variability due to noise). In order to capture the variability due epicentral distance, we consider how epicentral distance plays a role in the model for the data generating process: it forms the line which dictates the mean response. That is, the linear portion in the model $\beta_0 + \beta_1$(Epicentral Distance) is the model's attempt to explain how epicentral distance explains the bracketed duration; further, this explanation comes in the form of the average response. Plugging into this equation then provides a predicted mean response (where we substitute in the least squares estimates for the unknown parameters). Finding the variability in the bracketed duration due to the epicentral distance is then equivalent to finding the variability in these predicted mean responses:

$$\sum_{i=1}^{n} ((\text{Predicted Bracketed Duration})_i - (\text{Mean Bracketed Duration}))^2$$

This is known as the **Regression Sum of Squares** as it captures the variability explained by the regression line.

Definition 19.2 (Regression Sum of Squares)**:**
Let $\widehat{y}_i$ denote the predicted response for the i-th observation and $\bar{y}$ denote the sample mean response. Then, the Regression Sum of Squares (abbreviated SSR) is given by

$$SSR = \sum_{i=1}^{n} (\widehat{y}_i - \bar{y})^2$$

Finally, the unexplained noise, ϵ in our model, is the difference between the response and the regression line. This essentially considers the variability in the bracketed duration where the average is conditional on the epicentral distance

(we use the regression model) instead of computing the average of just the bracketed duration values:

$$\sum_{i=1}^{n} ((\text{Bracketed Duration})_i - (\text{Predicted Bracketed Duration})_i)^2$$

This is known as the **Error Sum of Squares** as it captures the variability not explained by the model but represented by the error term in the model.

Definition 19.3 (Error Sum of Squares)**:**
Let y_i denote the response for the i-th observation and $\widehat{y}_i$ denote the predicted response for the i-th observation. Then, the Error Sum of Squares (abbreviated SSE, and sometimes referred to as the Residual Sum of Squares) is given by

$$SSE = \sum_{i=1}^{n} (y_i - \widehat{y}_i)^2$$

With some clever algebra, it can be easily seen that the variability does in fact partition into these two components. This discussion is represented in Figure 19.1.

The total variability in a response can be partitioned into two components: the variability explained by the predictor and the unexplained variability captured by the error term. This is represented in the formula

$$SST = SSR + SSE$$

19.2 Hypothesis Testing

Partitioning the variability in a response into two components allows us to conduct hypothesis tests to compare two models. We will be expanding upon the ideas initially presented in Chapter 12. Recall that hypothesis testing is really about comparing two models for the data generating process: a more complex model in which the parameters are free to take on any value, and a restricted model in which the parameters are constrained in some way. We "fail to reject" the null hypothesis when there is not enough evidence to suggest that the more complex model is needed to explain the variability in the response. We "reject" the null hypothesis when the data is inconsistent with our expectations under the null hypothesis, suggesting that the more complex model is needed to explain the variability in the response.

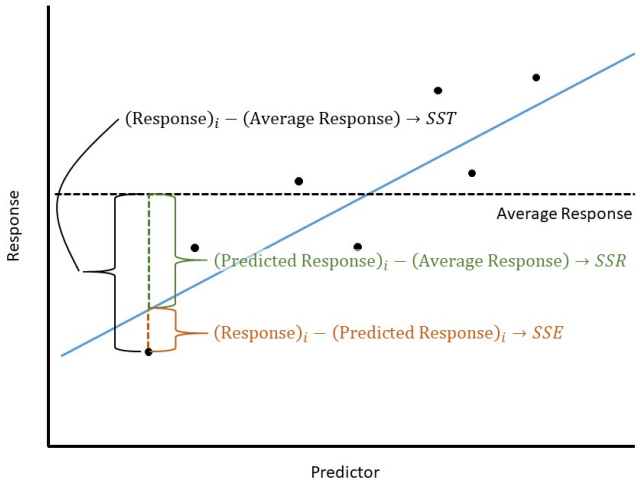


Figure 19.1: Illustration of partitioning the variability of a response using a regression model.

Consider the following research question:

> Is there evidence that the average bracketed duration for a location following an earthquake is linearly related to the distance the location is from the center of the earthquake?

If we consider the simple linear model for the data generating process described above, this question can be captured using the following set of hypotheses:

$$H_0 : \beta_1 = 0 \qquad \text{vs.} \qquad H_1 : \beta_1 \neq 0$$

Again, these hypotheses are really suggesting two separate models for the data generating process:

$$\begin{aligned} \text{Model 1}: &\quad (\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Epicentral Distance})_i + \epsilon_i \\ \text{Model 0}: &\quad (\text{Bracketed Duration})_i = \beta_0 + \epsilon_i \end{aligned}$$

The model under the null hypothesis (Model 0) is simpler because it has less parameters; in fact, while Model 1 says that there are two components (the epicentral distance and noise) contributing to the variability observed in the response, Model 0 says that there is only a single component (noise). So, we can think of our hypotheses as

H_0 : Model 0 is sufficient for explaining the variability in the response.
H_1 : Model 0 is not sufficient for explaining the variability in the response.

Regardless of which model we choose, the total variability in the response remains the same. We are simply asking whether the variability explained by the predictor is sufficiently large for us to say it has an impact. In particular, if the null hypothesis were true, we would expect all the variability in the response to be channeled into the noise ($SST \approx SSE$). If, however, the alternative hypothesis is true, then some of the variability in the response is explained by the predictor beyond just noise ($SSR > SSE$). Further, since we have a partition, as we increase the regression sum of squares, the error sum of squares must go down (that variability we are putting into the predictor must come out of the noise). So, the regression sum of squares is equivalent to the shift in the error sum of squares as we move from the null model to the more complex model.

For a particular dataset, the larger the regression sum of squares, the higher the variability in the response being explained by the predictor in the model for the data generating process.

The regression sum of squares represents our signal. The larger the value, the more evidence we have that the data is not consistent with the null hypothesis. However, as we saw in Chapter 12, we should always examine our signal relative to the noise in the data. But, we have quantified the noise in the data through the error sum of squares! It then seems reasonable to consider the standardized statistic

$$\frac{SSR}{SSE}.$$

While this is a reasonable statistic, it is not standardized. Remember that sums of squares capture variability but are themselves not variances. If we take a sum of squares and divide by an appropriate term, known as the **degrees of freedom**, we get a true variance term, which turns out to be easier to model analytically.

Definition 19.4 (Degrees of Freedom)**:**
A measure of the flexibility in a sum of squares term; a variance is computed by taking the sum of squares and dividing by the corresponding degrees of freedom.

Degrees of freedom are a very difficult concept to grasp, even for those who have been studying statistics for a while. Here is my way of thinking about them — they are the difference of available terms to work with. For example, think about the total sum of squares:

$$SST = \sum_{i=1}^{n} (y_i - \bar{y})^2$$

The first term of the difference has n different values (one response for each observation). However, the sample mean $\bar{y}$ is just one value. Therefore, there are $n - 1$ degrees of freedom associated with the total sum of squares. This is often described as starting out with n estimates (the data), but needing to estimate one parameter (the mean) along the way, leading to $n - 1$.
Similarly, consider the regression sum of squares:

$$SSR = \sum_{i=1}^{n} (\widehat{y}_i - \bar{y})^2$$

While there are n predicted values, they are all generated from the same least squares fit $\widehat{\beta}_0 + \widehat{\beta}_1(\text{Predictor})_i$ which can be computed from two estimates (that for the intercept and slope). Therefore, we begin with only 2 unique values. Again, the sample mean has just one value, leading to $2-1 = 1$ degree of freedom associated with the regression sum of squares.
Finally, consider the error sum of squares:

$$SSE = \sum_{i=1}^{n} (y_i - \widehat{y}_i)^2$$

We have n initial values (one for each observation). However, as described above, we only need 2 terms to estimate the predicted values. So, we have $n - 2$ degrees of freedom associated with the error sum of squares.
Note that $(n - 1) = (2 - 1) + (n - 2)$ in the same way that $SST = SSR + SSE$.

The measure of variability determined by taking the ratio of a sum of squares and its associated degrees of freedom is known as a **mean square**.

Definition 19.5 (Mean Square)**:**
The ratio of a sum of squares and its corresponding degrees of freedom.

Specifically:

- ***Mean Square Total (MST)**: estimated variance of the responses; this is the same as the sample variance of the response.*
- ***Mean Square for Regression (MSR)**: estimated variance of the predicted responses.*
- ***Mean Square Error (MSE)**: estimated variance of the responses about the regression line; this is the same as the estimate of the variability of the errors.*

Since mean squares are proportional to their corresponding sum of squares, an increase in one is associated with an increase in the other. We are now ready to define our standardized statistic as the ratio of the mean square for regression with the mean square error.

Consider the simple linear model

$$(\text{Response})_i = \beta_0 + \beta_1(\text{Predictor})_i + \epsilon_i$$

A standardized statistic for testing the hypotheses

$$H_0 : \beta_1 = 0 \qquad \text{vs.} \qquad H_1 : \beta_1 \neq 0$$

is given by

$$T^* = \frac{MSR}{MSE} = \frac{SSR}{SSE/(n-2)}$$

We should not lose sight of the fact that our standardized statistic is really a result of partitioning the variability and considering the variability explained by the predictor relative to the noise in the response. Our analysis of these sources of variability is often summarized in a table similar to that represented in Figure 19.2.

The last entry in the table is the p-value. As with any p-value, it is computed by finding the likelihood of getting a standardized statistic as extreme or more than that observed when the null hypothesis is true. "More extreme" values of the statistic would be larger values; so, the area to the right in the null distribution is needed. The key step is modeling that null distribution. This is where the conditions we place on the error term come into play. Under the classical regression conditions, we can model the null distribution analytically; otherwise, we can rely on bootstrapping to model the null distribution.

Let's return to our question of whether the bracketed duration, on average, is linearly related to the distance a location is from the corresponding earthquake. From Table 19.2, we have a larger p-value (computed assuming the data is

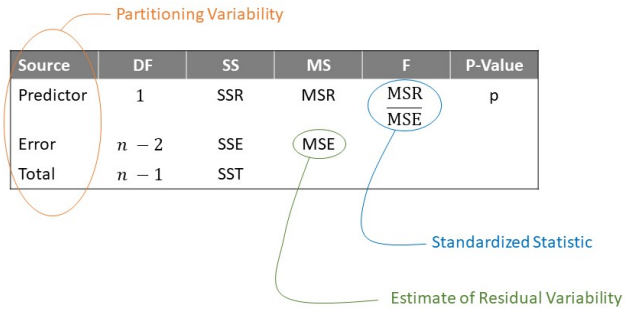


Figure 19.2: Table for summarizing the partitioning of variability in a regression model.

Table 19.2: Analysis of the sources of variability in the bracketed duration as a function of epicentral distance.

Term	DF	Sum of Squares	Mean Square	Standardized Statistic	P-Value
Epicentral Distance	1	85.733	85.733	2.583	0.111
Residuals	117	3883.708	33.194		

consistent with the classical regression model). That is, we have no evidence to suggest that locations further from the center of the earthquake experience bracketed durations which differ from those closer to the center of the earthquake, on average.

Determining if a response is linearly related to a predictor is done by determining if the predictor explains a significant portion of the variability in the response.

In this section, we partitioned variability as a way of evaluating the strength of evidence the predictor plays in determining the response. This begs the question; can we quantify the predictive ability of the model for the data generating process using this same partition?

19.3 R-squared

The key to quantifying the quality of a model for the data generating process is to understand that a partition breaks a whole into smaller, distinct components. This means that if you put the components back together, you have the whole. The sums of squares are a method of measuring the variability directly with respect to our partition. That is, the total variability in the bracketed duration is given by

$$\begin{aligned} SST &= SSR + SSE \\ &= 85.733 + 3883.708 \\ &= 3969.44 \end{aligned}$$

The benefit partitioning variability is that it makes clear the breakdown between the variability in the response that the model is explaining (SSR) versus the variability in the response that cannot be explained (SSE). We are now in a position to quantify the amount of variability the model is explaining:

$$\text{Proportion of Variability Explained} = \frac{85.733}{85.733 + 3883.708} = 0.0216$$

This is known as the **R-squared** for the model. The R-squared value has a very nice interpretation; in this case, it says that only 2.16% of the variability in the bracketed duration at a location is explained by its distance from the center of the corresponding earthquake.

Definition 19.6 (R Squared)**:**
Sometimes reported as a percentage, this measures the proportion of the variability in the response explained by a model.

As R-squared is a proportion, it must take a value between 0 and 1. If 0, that means our model has no predictive ability within our sample. That is, knowing the predictor does not add to our ability to predict the response any more than guessing. A value of 1 indicates that our model has predicted all the variability in the response; that is, given the predictor, we can perfectly predict the value of the response.

It may appear that obtaining an R-squared value of 1 should be our goal. And, in one sense, it is. We want a model that has strong predictive ability. However, there is a danger in obtaining an R-squared of 1 as well. We must remember that variability is inherent in any process. Therefore, we should never expect to fully explain all of the variability in a response. George Box (a renowned statistician) once made the following statement (Box 1979):

> "Now it would be very remarkable if any system existing in the real world could be exactly represented by any simple model. However, cunningly chosen parsimonious models often do provide remarkably useful approximations. For example, the law $PV = RT$ relating pressure P, volume V and temperature T of an 'ideal' gas via a constant R is not exactly true for any real gas, but it frequently provides a useful approximation and furthermore its structure is informative since it springs from a physical view of the behavior of gas molecules.
>
> For such a model there is no need to ask the question 'Is the model true?' If 'truth' is to be the 'whole truth' the answer must be 'No.' The only question of interest is 'Is the model illuminating and useful?'

The idea here is that we know the model will not capture the data generating process precisely. Therefore, we should be skeptical of models which claim to be perfect. For example, consider the two models illustrated in Figure 19.3. The black line has a perfect fit, but we argue the blue line is better. While the black line captures all the variability in the response for this sample, it is certainly trying to do too much. In reality, the blue line captures the underlying relationship while not overcomplicating that relationship. We sacrifice a little quality in the fit for this sample in order to better represent the underlying structure. The black line suffers from what is known as *overfitting*; the blue line is a more *parsimonious* model, balancing complexity with model fit.

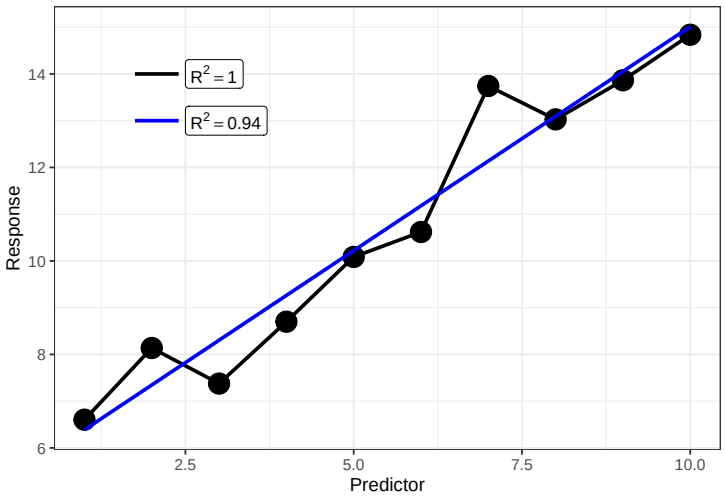


Figure 19.3: Illustration of a parsimonious model compared to one which overfits the data.

Students often ask, "if not 1, how high of an R-squared represents a *good* model?" The answer depends a lot on the discipline. In many engineering

applications within a lab setting, we can control much of the external variability leading to extremely high R-squared values (0.95 to 0.99). However, in biological applications, the variability among the population can be quite large, leading to much smaller R-squared values (0.3 to 0.6). What is considered "good" can depend on the specific application.

While R-squared is useful for quantifying the quality of a model on a set of data, it should not be used to compare two different models as R-squared always favors more complex models. There are better methods which adjust for the complexity of the model fit.

In addition to the discipline, how you view the R-squared of a model may depend on the goal of the model. There are generally two broad reasons for developing a statistical model:

- Explain the relationship between a response and one or more predictors. This can involve examining the marginal relationship, isolating the effect, or examining the interplay between predictors.
- Predict a future response given a specific value for the predictors.

If all we are interested in doing is explaining the relationship, we may not be concerned about the predictive ability of the model. That is, since our goal is not to accurately predict a future response, we are primary concerned with whether we have evidence of a relationship. But, if our goal is prediction, we would like that estimate to be precise. In such cases, a high R-squared is required before really relying on the model we have.

Regardless of our goal, conducting inference or predicting a future response, partitioning the variability is a key step. If inference is our primary aim, this partitioning allows us to determine if a predictor adds to the model above and beyond the error alone. If prediction is our primary aim, the partitioning allows us to quantify the quality of the model.

Chapter 20

Assessing Modeling Conditions

We have been considering the simple linear model

$$(\text{Response})_i = \beta_0 + \beta_1(\text{Predictor})_i + \epsilon_i$$

for the data-generating process of a quantitative response. For example, for the Seismic Activity Case Study, we considered a model that explained the bracketed duration at a location as a function of the magnitude of the earthquake:

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Magnitude})_i + \epsilon_i$$

Estimates for the unknown parameters in this model were obtained via least squares estimation. In order to obtain a model for the sampling distribution of these estimates (or the null distribution as appropriate), and thereby conduct inference, we added conditions to the distribution of the error term. For example, under the "classical regression model" we require the following four conditions:

1. The error in the bracketed duration has an average of 0 regardless of the magnitude of the earthquake.
2. The error in the bracketed duration for one location is independent of the error in the bracketed duration for any other location.
3. The variability of the error in the bracketed duration is the same regardless of the magnitude of the earthquake.
4. The errors in the bracketed duration follow a Normal distribution.

We are also able to develop an empirical model for the sampling distribution only enforcing the first two of these conditions on the distribution of the error. Which of the models for the sampling distribution should be used? Unfortunately, we

cannot simply state conditions and then proceed blindly. In order to rely on the p-values and confidence intervals produced from any modeling procedure, the data must be consistent with these conditions.

In this section, we discuss how we assess these conditions qualitatively.

20.1 Residuals

One of the complications we face is that we are imposing conditions on the error term, but we do not observe the error (since the parameters are unknown). However, we are able to determine the "error" in each observation with respect to the estimated model for the data generating process. That is, we consider the difference between each observed response and what we would have predicted for this observation using the least squares estimates; this difference is called a **residual**.

Definition 20.1 (Residual)**:**
The difference between the observed response and the predicted response (estimated deterministic portion of the model). Specifically, the residual for the i-th observation is given by

$$(Residual)_i = (Response)_i - \widehat{\beta}_0 - \widehat{\beta}_1(Predictor)_i$$

Residuals approximate the noise in the data-generating process.

We can use the residuals to qualitatively assess if the observed data is consistent with each of the four potential conditions we might place on the distribution of the error term.

Residuals, since they are estimates of the noise in the data-generating process, provide a way of assessing the modeling conditions placed on the distribution of the error term.

20.2 Assessing Mean 0

> The error in the bracketed duration has an average of 0 regardless of the magnitude of the earthquake.

It is tempting to read this condition and believe that a rational way to assess this assumption is determine if the average of the residuals is 0. However, while the difference is subtle, the condition is *not* that the average error is 0. The condition is that the average error is 0 for *all values of the predictor*. It would seem we need

to determine if, for each value of the predictor possible, if the residuals average to 0. This is infeasible because we do not generally have multiple responses for each value of the predictor. We can, however, assess whether the data is consistent with this condition graphically. That is, in order to assess this assumption, we need to graphically assess how the average behaves over a range of predictor values. We capture this by looking at the *predicted values*. Figure 20.1 shows the relationship between the residuals and the associated predicted (or fitted) values for the observations in the data set.

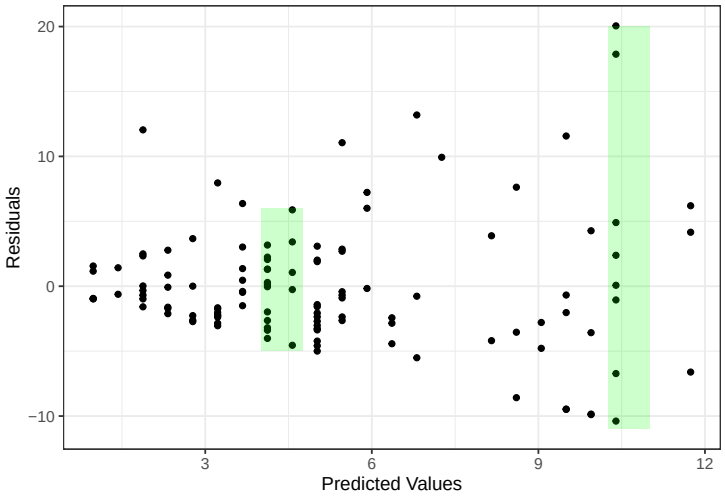


Figure 20.1: Plot of the residuals vs. the predicted values for a model predicting bracketed duration as a function of the magnitude of an earthquake.

If the data is consistent with the condition, then as you move left to right across the plot, the residuals should tend to balance out at 0. Imagine a window around the residuals (shown in the figure as green rectangles), and imagine moving that window from left to right. If that window has to shift up or down to contain the cloud of residuals (so that the window is no longer centered around 0), that signals a problem. Any trends in the location of this graphic would indicate the data is *not* consistent with the condition.

There does not appear to be strong evidence of curvature in this plot. It is reasonable to say this dataset is consistent with these conditions.

20.3 Assessing Independence

> The error in the bracketed duration for one location is independent of the error in the bracketed duration for any other location.

Generally, independence is assessed through the context of the data collection

scheme. By carefully considering the manner in which the data was collected, we can typically determine whether it is reasonable that the errors in the response are independent of one another. Some key things to consider when examining the data collection process:

- Are there repeated observations made on the same subject? This often suggests some type of relationship between the responses and therefore would not be consistent with errors being independent.
- Is the response measured over time (time-series) such as daily temperature over the course of a month? Time-series data often exhibits strong period-to-period relationships suggesting the errors are not independent. For example, if it is hot today, it will probably be hot tomorrow as well.
- Is there a learning curve in how the data was collected? Learning curves again suggest some dependence from one observation to the next. For example, a new nurse may become better at collecting pulse readings with more practice over time.
- Measurement devices which are failing over time will introduce a dependence from one observation to the next. Imagine a bathroom scale that begins to add an additional pound each day. Then, being above average weight one day will most likely lead to an above average weight the next, due primarily to the measurement device.

These last three points illustrate a particular deviation from our condition of independence in which two observations collected close together in time are related. When we know the order in which the data was collected, we can assess whether the data tends to deviate from the condition of independence in this manner. This is done graphically through a **time-series plot** of the *residuals*. If two errors were unrelated, then the value of one residual should tell us nothing about the value of the next residual. Therefore, a plot of the residuals over time should look like noise (since residuals are supposed to be estimates of noise). If there are any trends, then it suggests the data is not consistent with independence.

Definition 20.2 (Time Series Plot)**:**
Plot of a variable over time. This plot allows us to assess some deviations from independence. A trend in the location *or* spread *of the points over time suggests a deviation from independence.*

As an example, consider the time-series plots shown in Figure 20.2, both representing hypothetical datasets. In Panel A, the residuals display a trend in the location over time. Knowing that a response was below average suggests the next response will also be below average. In Panel B, the results deplay a trend in the spread over time. This suggests that measurements taken later in the study were less precise. Both panels are then examples of patterns which would suggest the data is not consistent with the condition of independence.

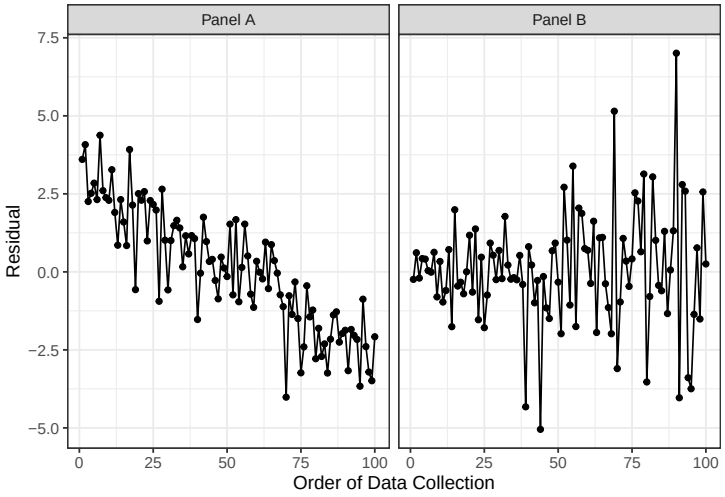


Figure 20.2: Examples of trends in a time-series plot of the residuals. Such trends indicate the data is not consistent with the condition that the errors are independent of one another.

Instead, if the data were consistent with the condition of independence on the error terms, we would expect to see a plot as in Figure **??**. Notice there are no trends in the location or spread of the residuals.

For the Seismic Activity Case Study, the data was actually collected over time as earthquakes occurred. More, as technology has changed over time, it is reasonable to fear that the errors in our observations are related over time. In order to assess this, consider the plot of the residuals from fitting the above model against the order in which they were collected; this is shown in Figure 20.4. Based on the figure, there is no clear trend in either the *location* or *spread* of the residuals over time (the figure resembles noise with no patterns). As a result, it is reasonable to assume that the data is consistent with the errors being independent of one another.

The condition of independence is another reason we consider randomization when collecting data. Both random sampling and random assignment reduces the likelihood of the errors in two observations being related.

20.4 Assessing Homoskedasticity

> The variability of the error in the bracketed duration is the same regardless of the magnitude of the earthquake.

Similar to assessing whether the data is consistent with the condition of the errors being 0 on average for all values of the predictor, homoskedasticity suggests the

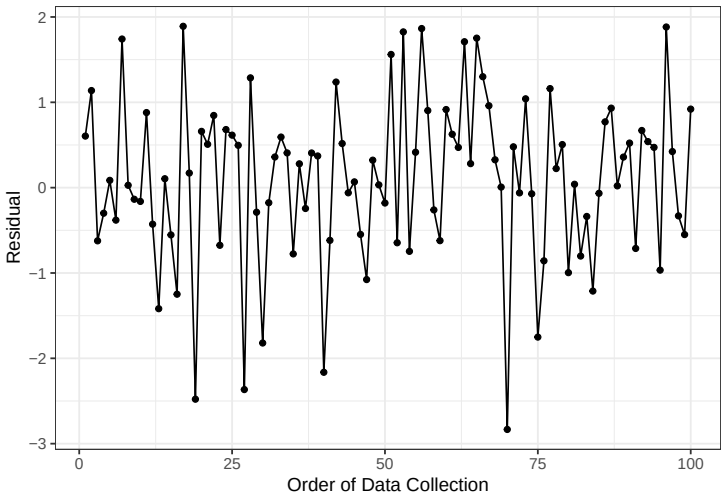


Figure 20.3: Example of a time-series plot of residuals which shows no trends in location or spread. This is consistent with what we would expect if the condition of independence among errors were satisfied.

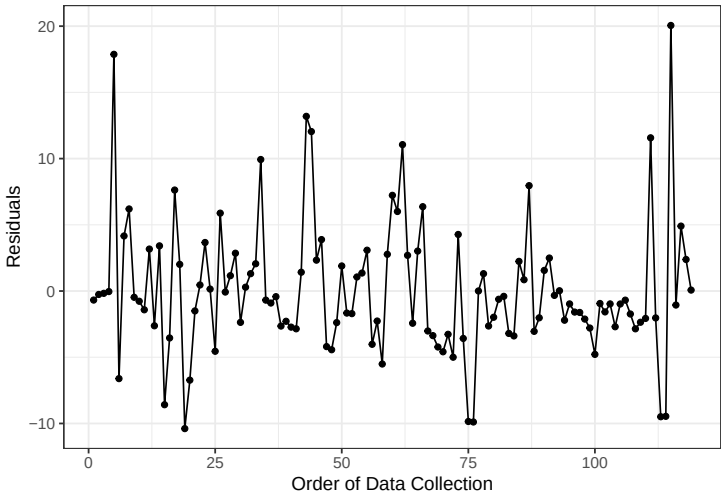


Figure 20.4: Time series plot of the residuals for a model predicting bracketed duration as a function of the magnitude of an earthquake.

variability in the errors is consistent for all values of the predictor. Therefore, we rely on the same graphical assessment: Figure 20.1. However, instead of focusing on a trend in the location of the residuals, we are focused on a trend in the variability. Again, imagine a window (illustrated as green rectangles) around the residuals. As you move left to right, if the size of the window has to change in order to keep the residuals inside (the window stretches or compresses vertically), then that is an indication that the variability is changing. For our example, there is a clear "fan shape" to the residuals as you move left to right suggesting the precision of the model decreases when making larger predictions. This goes back to something we observed in Chapter 16 when examining a plot of the raw data. Figure 16.1 illustrates that for large earthquakes (high magnitudes), the bracketed duration was much more variable than for smaller earthquakes. So, our model is not as precise for some values of the predictor. This is evidence that our data is *not* consistent with the condition that the errors have the same variability for all values of the predictor.

This partially explains the differences in the confidence intervals reported in Tables 18.1 and 18.2. Since there is clear evidence that the data is not consistent with the condition that the variability of the errors is constant for all levels of the predictor, then it is not safe to assume the classical regression model. That is, the confidence intervals and p-values, as well as the underlying models for the sampling distribution and null distribution that generated them, constructed assuming the data is consistent with all four conditions, are suspect. We should instead rely on an empirical model for the sampling distribution of the estimates when constructing confidence intervals or an empirical model for the null distribution if computing a p-value.

20.5 Assessing Normality

The errors in the bracketed duration follow a Normal distribution.

Assessing whether observations adhere to a particular distribution is a large area in statistical research. Many methods have been developed for this purpose. We emphasize a single graphical summary known as a **probability plot**. The construction of the plot is beyond the scope of this text, but the concepts underlying its construction actually tie in nicely to the big themes of the course. Recall that if a sample is representative, then it should be a snapshot of the underlying population. Therefore, if we believe the underlying population has some particular distribution, we would expect the properties of this distribution to be apparent in the sample as well.

If we believe the errors follow a Normal distribution, then it is reasonable that the residuals should maintain some of those properties. For example, the 10-th percentile of the residuals should roughly equate to the 10-th percentile expected from a Normal distribution. Mapping the percentiles that we observe to those that we expect is the essence of a probability plot.

Definition 20.3 (Probability Plot)**:**
Sometimes called a "Quantile-Quantile Plot," a graphic for comparing a theoretical probability model for the distribution of an underlying population with the distribution of the sample. The resulting plot should exhibit a straight line. If points deviate from this linear trend, that suggests the sample does not align with the proposed model for the distribution.

While a probability plot can be used for a host of probability distributions, the most common is the Normal probability plot. The plot compares the percentiles observed residuals with those we would expect if the sample were from a Normal distribution. Trends away from a linear relationship suggest the proposed Normal distribution is not a reasonable model for the distribution of the errors.

Figure 20.5 shows the probability plot for the residuals.

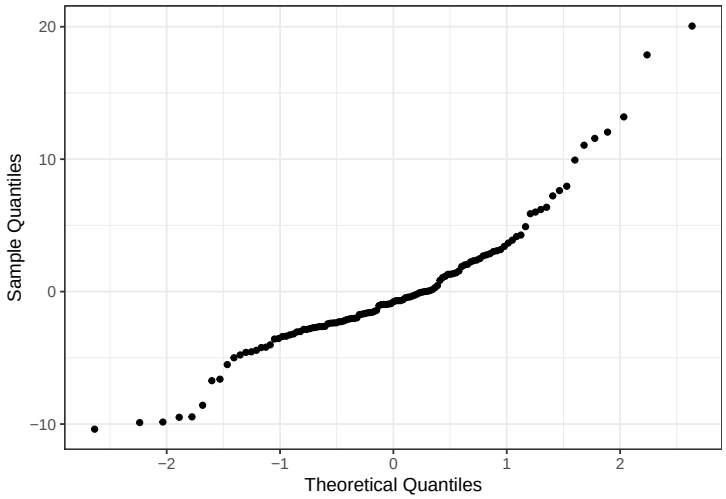


Figure 20.5: Probability plot of the residuals for a model predicting bracketed duration as a function of the magnitude of an earthquake.

There is some evidence that the residuals are moving away from a linear relationship. This is because we note some curvature in the plot, particularly toward the bottom left portion of the graphic. While we want to avoid over-interpreting small deviations from the linear trend, we should pay attention to clear departures.

We note that of the conditions considered, Normality is probably the least important as the analytic models for the sampling distribution are generally fairly robust to this condition. That is, those models for the sampling distribution, as well as the confidence intervals and p-values they produce, tend to be accurate even if the data is not consistent with this condition. This is especially true in

large samples. However, we can always relax this condition by building an empirical model for the sampling distribution. Given the curvature observed in this graphic, we would consider an empirical model, especially given we have already established the data is not consistent with the condition of homoskedasticity.

For comparison, Figure 20.6 illustrates a hypothetical dataset for which the residuals suggest the condition of the errors following a Normal distribution is violated.

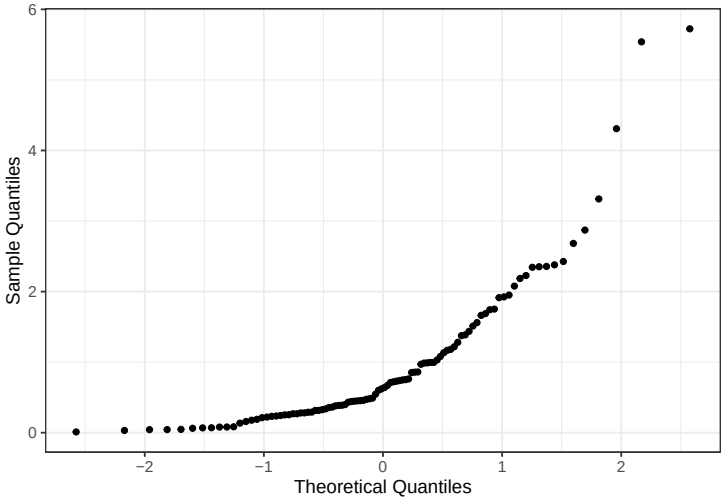


Figure 20.6: Probability plot of residuals for a hypothetical dataset. The trend away from a straight line suggests assuming the errors follow a Normal distribution would be unreasonable.

20.6 General Tips for Assessing Assumptions

Each of the methods presented here are qualitative assessements, which means they are subjective. That is okay. As the analyst, it is up to you to determine which conditions you are willing to assume are reasonable to impose. That is, with which conditions do you believe the data is consistent? Here are three overall things to keep in mind.

First, do not spend an extraordinary amount of time examining any one residual plot. If you stare at a plot too long, you can convince yourself there is pattern in anything. We are looking for glaring evidence that the data is not consistent with the conditions we have imposed on our model. This is especially true when we have only a few observations. In these settings, reading plots can be very difficult. Again, it is about what you are comfortable assuming; how much faith do you want to place in the results?

Second, we have chosen the language carefully throughout this chapter. We have never once stated that a condition "was satisfied." When we perform an analysis, we are making an *assumption* that the conditions are satisfied. We can never prove that they are; we can only show that the data is consistent with a particular condition. We can, however, provide evidence that a condition is violated. When that is the case, we should be wary of trusting the resulting p-values and confidence intervals. This is not unlike hypothesis testing; just as we can never prove the null hypothesis is true, we cannot prove that a condition is satisfied.

Finally, any conditions required for a particular analysis should be assessed. If your sample is not consistent with the necessary conditions, you should choose a different analysis. The inference you obtain from an analysis is only reliable of the data is consistent with any necessary conditions.

The conditions for a model are placed on the error, but the residuals are used to assess whether a dataset is consistent with these conditions, allowing us to determine if assuming the conditions are satisfied is reasonable.

1. We can never prove a condition is satisfied.
2. The assumptions are not on the residuals, but the errors.
3. A sample should be consistent with any conditions you impose on your model.

If a sample is not consistent with the conditions you impose, you should consider revising your analysis.

Chapter 21

Extending the Regression Model

The last several chapters have developed an approach for modeling a quantitative response as a function of a single quantitative predictor:

$$(\text{Response})_i = \beta_0 + \beta_1(\text{Predictor})_i + \epsilon_i$$

This model is well suited for addressing questions about the marginal relationship between two variables. However, as we saw in Chapter 14, not all our questions are about the marginal relationship. The real power of the model in Equation (10.1) is our ability to generalize it to encompass multiple predictors and various types of relationships. In this chapter, we briefly describe how to extend the regression model to address some additional questions of interest.

21.1 Including Multiple Precitors

The real power of the model in Equation (10.1) is our ability to generalize it to encompass multiple predictors and various types of relationships. That is, suppose we consider not the marginal relationship between the bracketed duration and the magnitude of the corresponding earthquake but to one *isolating* the effect of the magnitude on the bracketed duration:

> If two earthquakes with different magnitudes occur in the same location, would we expect the same bracketed duration regardless of their magnitudes?

This particular question requires a model which has multiple predictors. What bracketed duration would we expect given the magnitude and epicentral distance

(to capture earthquakes occurring in the same location)? We extend the simple linear model to include an additional predictor:

$$(\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Magnitude})_i + \beta_2(\text{Epicentral Distance})_i + \epsilon_i \tag{21.1}$$

This more complex model is more difficult to visualize, but conceptually is similar to the simple linear model. Given a value for the magnitude and epicentral distance, we can predict the bracketed duration; our model accounts for the fact that these two variables together will not explain the entire data generating process. There will still be unexplained variability. One way of envisioning what this model does is to think about taking the linear relationship we previously had and observing that we are now saying that the *model* differs for each group of observations which have a different epicentral distance. For example, consider all locations which were located 10 km away from the center of an earthquake; we would have that Equation (21.1) becomes

$$\begin{aligned}(\text{Bracketed Duration})_i &= \beta_0 + \beta_1(\text{Magnitude})_i + \beta_2(10) + \epsilon_i \\ &= (\beta_0 + 10\beta_2) + \beta_1(\text{Magnitude})_i + \epsilon_i\end{aligned}$$

Similarly, if we only consider locations which were located 32 km away from the center of an earthquake, then Equation (21.1) becomes

$$\begin{aligned}(\text{Bracketed Duration})_i &= \beta_0 + \beta_1(\text{Magnitude})_i + \beta_2(32) + \epsilon_i \\ &= (\beta_0 + 32\beta_2) + \beta_1(\text{Magnitude})_i + \epsilon_i\end{aligned}$$

Figure 21.1 represents this graphically for a range of potential epicentral distances. Essentially, the relationship between the bracketed duration and the magnitude shifts depending on the epicentral distance. The overall trend is similar (the lines are parallel), but where the line is located is really dependent upon the distance of the location from the earthquake.

This model has what may appear as an obvious requirement; you cannot use this model to predict the bracketed duration without specifying *both* the magnitude of the earthquake and the epicentral distance of the location. However, it also isolates the effect of the magnitude above and beyond the epicentral distance.

21.1.1 General Model Formulation

Nothing limits us from the inclusion of several predictors. Each predictor is simply added to the model. That is, a model which predicts a quantitative response as a function of p predictors has the mathematical form

$$(\text{Response})_i = \beta_0 + \sum_{j=1}^{p} \beta_j(\text{Predictor})_{j,i} + \epsilon_i$$

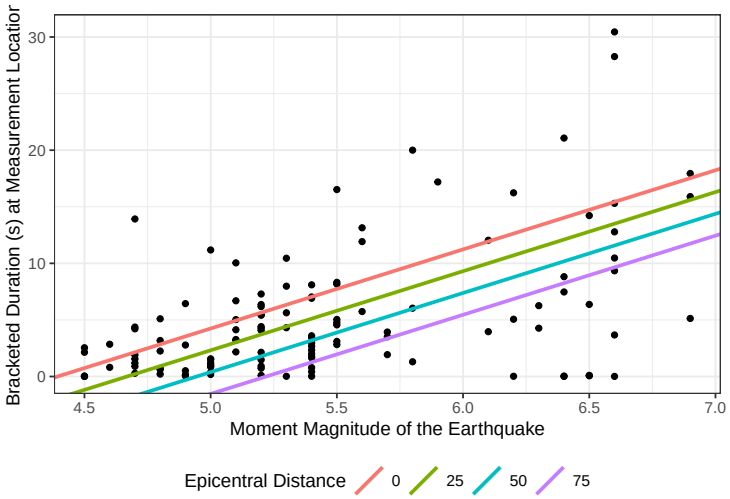


Figure 21.1: Relationship between bracketed duration and the magnitude of an earthquake after also considering the epicentral distance from an earthquake. Lines estimating this relationship for various values of the epicentral distance are overlayed.

where some of the predictors may be indicator variables used to capture a categorical variable. The problem, of course, is that the parameters (the β's in the model) are unknown. However, we can use the method of leasst squares to estimate each of the parameters simultaneously.

Definition 21.1 (General Least Squares Estimates)**:**
The least squares estimates for a general linear model are the values of $\beta_0, \beta_1, \beta_2, \ldots, \beta_p$ *which minimize the quantity*

$$\sum_{i=1}^{n} \left((Response)_i - \beta_0 - \sum_{j=1}^{p} \beta_j (Predictor)_{j,i} \right)^2$$

where the residual variance is estimated by

$$\frac{1}{n-p} \sum_{i=1}^{n} \left((Response)_i - \widehat{\beta}_0 - \sum_{j=1}^{p} \widehat{\beta}_j (Predictor)_{j,i} \right)^2$$

21.1.2 Interpretation of Parameters

The same conditions described in Chapter 18 can be placed on the stochastic portion of the model. Just as with the simple linear model, assuming the model is correctly specified provides us with an interpretation of each of the parameters.

Consider the model defined in Equation (21.1). If we assume that the error in the bracketed duration has an average of 0 regardless of the magnitude of the corresponding earthquake and distance of the location to the center of the earthquake, then notice that we are saying that the formula

$$\beta_0 + \beta_1(\text{Magnitude}) + \beta_2(\text{Epicentral Distance})$$

defines the average bracketed duration (given the magnitude of the earthquake and epicentral distance of the location). Therefore, we can interpet the value of β_2 as the change in the average bracketed duration given a 1-kilometer increase in the distance a location is from the center of the earthquake *for all locations which experience an earthquake of the same magnitude*. This last part is important. In order to interpret one coefficient, we must hold the value of all other predictors fixed.

For the general linear model, the intercept β_0 is the average response when *all* predictors are set equal to 0. The j-th slope β_j represents the average change in the response associated with a 1-unit increase in the j-th predictor holding the value of all other predictors constant.

This phrase "holding the value of all other predictors constant" has extreme power. It is this understanding of how the parameters are interpreted that we are able to take our first steps toward addressing confounding. For example, consider the model in Equation (21.1).

Using least squares, we estimate that for every kilometer further the epicenter of the earthquake is, we can expect the brackted duration to decrease by 0.08 seconds, on average. Someone might argue as follows: "This is not a controlled experiment; therefore, while there is a relationship here, it is possible that what is really happening is that earthquakes which were further away tended to also be smaller in magnitude. Therefore, it is not the distance that is driving this relationship but the magnitude of the earthquake." Here, this individual is saying that magnitude is a confounder — related to both the bracketed duration (response) and the variable of interest (distance from the epicenter). If we had fit a marginal model, this would be a valid concern. However, remember our interpretation of β_2 (and our estimate of it). Our fit suggests that for every kilometer further the epicenter of the earthquake is, we can expect the bracketed duration to decrease by 0.08 seconds, on average, *holding the magnitude of the*

earthquake constant. Therefore, since this estimate is comparing two earthquakes of the same magnitude, magnitude cannot be confounding the relationship observed. We have isolated the effect of the epicentral distance.

Our solution to confounding is to incorporate the relationship between the confounder and the response into our model. Then, any remaining variables cannot be affected by the confounder. Of course this has one major limitation — we cannot account for any variables which are not recorded.

There are entire texts devoted to this topic. Here, we simply emphasize that regression models allow us to control for the confounders we have observed. The relationships are "adjusted for" these confounders due to the interpretation that a coefficient is the effect "holding all other predictors constant." Regression models allow us to compare similar groups, which are balanced on these confounders, after the fact (instead of having addressed confounding through the design of the study).

21.2 Modifying an Effect

We now have a flexible strategy for modeling a quantitative response:

$$(\text{Response})_i = \beta_0 + \sum_{j=1}^{p} \beta_j (\text{Predictor})_{j,i} + \epsilon_i$$

However, there is one type of question we have not yet addressed — assessing the interplay between two variables on the response.

Consider the following question from the Seismic Activity Case Study:

> Is the relationship between the bracketed distance and the magnitude different depending on whether the soil is rocky where the measurement is taken?

This question explains the bracketed duration in terms of both the magnitude as well as whether the soil is rocky. A first pass at such a model might be

$$\begin{aligned}(\text{Bracketed Duration})_i = \beta_0 &+ \beta_1 (\text{Magnitude})_i \\ &+ \beta_2 \mathbb{I}(\text{i-th observation has a Rocky soil}) + \epsilon_i\end{aligned}$$

where we use an indicator variable to capture whether the soil is rocky. Exploring this model further, it suggests there are actually two equations combined into a single formula, depending on the soil type:

$$\begin{aligned}\text{Rocky Soil:} \quad & (\text{Bracketed Duration})_i = \beta_0 + \beta_2 + \beta_1 (\text{Magnitude})_i + \epsilon_i \\ \text{Other Soil:} \quad & (\text{Bracketed Duration})_i = \beta_0 + \beta_1 (\text{Magnitude})_i + \epsilon_i\end{aligned}$$

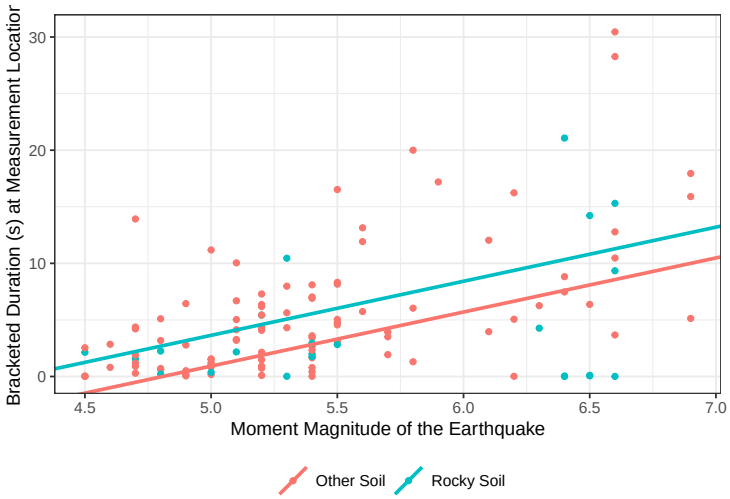


Figure 21.2: Relationship between the bracketed duration and magnitude for locations with rocky soil and those with other soil types.

Graphically, this is represented by two parallel lines (see Figure 21.2).

The lines are parallel because the coefficient associated with Magnitude is the same in each case: β_1. That is, regardless of whether the soil is rocky, the change in the bracketed duration, on average, for each 1-unit increase in the magnitude of an earthquake is the same. Our question of interest is essentially, is there evidence that this is not the case? So, the above model actually represents the model under the null hypothesis of our current question. Under the null hypothesis, the effect of the magnitude on the bracketed duration (which captures the relationship between these two variables) is the same for regardless of soil condition. The question is, how do we form the alternative model, which allows the slope to look differently depending on soil type?

Consider adding an additional term to our model above, yielding the following model:

$$\begin{aligned}(\text{Bracketed Duration})_i = \beta_0 &+ \beta_1(\text{Magnitude})_i \\ &+ \beta_2 \mathbb{I}(\text{i-th observation has a Rocky soil}) \\ &+ \beta_3 \mathbb{I}(\text{i-th observation has a Rocky soil})(\text{Magnitude})_i + \epsilon_i\end{aligned}$$

This additional term is formed by taking the product of the indicator variable with the variable magnitude; such a product is known as an **interaction term**.

Definition 21.2 (Interaction Term)**:**
The product of two variables in a regression model. The product allows

the effect of one variable on the response to depend on another, essentially modifying the effect.

In order to see the impact of adding the interaction term, let's consider the model for each soil type:

$$\begin{aligned} \text{Rocky Soil:} \quad & (\text{Bracketed Duration})_i = (\beta_0 + \beta_2) + (\beta_1 + \beta_3)\,(\text{Magnitude})_i + \epsilon_i \\ \text{Other Soil:} \quad & (\text{Bracketed Duration})_i = \beta_0 + \beta_1(\text{Magnitude})_i + \epsilon_i \end{aligned}$$

Notice that in this revised model, not only is the intercept term different in each case, the slope term in front of the magnitude differs also. The model with the interaction term allows the effect of the magnitude on the bracketed duration to be modified by the soil type. That is, the effect differs across the soil type.

It is common to believe that the interaction term measures the effect between the two variables in the product. However, this is incorrect. The interaction term allows the effect of one variable in the product on the response to differ across the levels of the other variable in the product.

Visually, this revised model allows two completely different relationships — depending on the soil type. This is shown in Figure 21.3. The question of course is which of the two models is more appropriate. Is there actually evidence that the more complex model, which allows the relationship to differ for locations with different soil types, is required? Or, is the more simplistic model, which says the relationship is the same across all locations of different soil types, sufficient?

21.2.1 Inference for Effect Modifications

We can capture our question of interest in the following hypotheses:

$$\begin{aligned} H_0 &: \beta_3 = 0 \\ H_1 &: \beta_3 \neq 0 \end{aligned}$$

Notice that if the null hypothesis were true, then the slope would be the same regardless of whether the soil was rocky because we resort to the earlier model which only allows the intercept to vary. However, if β_3 is nonzero, then the slope will differ for the rocky soil. So, under the null hypothesis, the lines are parallel; under the alternative hypothesis, the lines are not parallel.

Conceptually, testing this model is just like testing any other. We can generate samples under the null hypothesis using our reduced model. For each sample, we can compute the standardized test statistic — a signal to noise ratio — measuring the signal in the data (in this case, the evidence for non-parallel lines). Doing this repeatedly gives us a null distribution allowing us to compute a p-value.

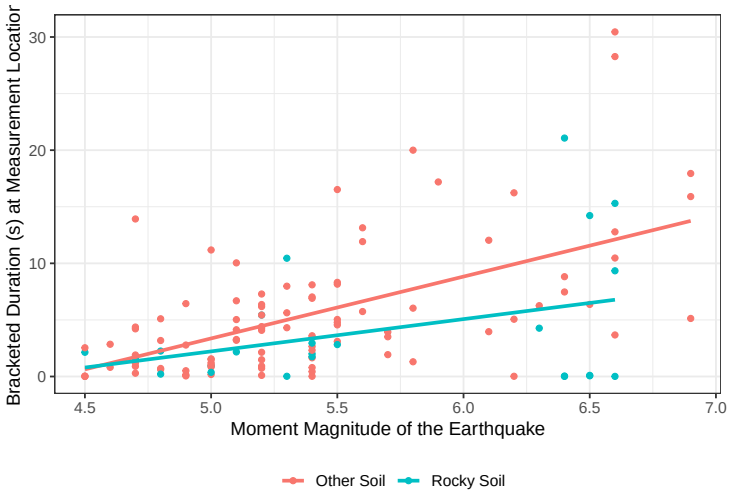


Figure 21.3: Relationship between bracketed duration and the magnitude of an earthquake after also considering the soil conditions of the measurement location. The relationship between the bracketed duration and the magnitude is allowed to differ within each type of soil condition.

Just as before, if the conditions of the classical regression model hold, then we can model the null distribution analytically using a probability model.

This process relies on our ability to partition the variability. Remember that a model for the data-generating process simply specifies the various sources of variability. In this case, we have partitioned the variability into the following components:

- Magnitude: one reason the bracketed duration differs between two locations is the magnitude of the corresponding earthquake.
- Soil Conditions: another reason for a difference in the bracketed duration is due to the soil conditions at the measurement site.
- Interplay between Magnitude and Soil Conditions: in addition, we believe that the effect of the magnitude may differ for various soil conditions.
- Noise: even for two locations which have the same magnitude and soil conditions, there may be a difference in the bracketed duration. These differences we cannot resolve and attribute them simply to error.

By partitioning the variability, we are able to compute a signal-to-noise ratio. For each component, we can essentially determine how much variability is explained relative to the noise in the process. So, despite talking about "regression models," we are still just comparing variabilities; that is, we are still doing an analysis of variance.

Specifically, Table 21.1 gives the estimates associated with each parameter, and

Table 21.1: Summary of the model fit explaining the bracketed duration as a function of both magnitude and soil condition at the measurement location. The effect of the magnitude was allowed to differ across soil conditions.

Term	Estimate	Standard Error	P-Value
(Intercept)	-23.966	4.531	< 0.001
Magnitude	5.466	0.834	< 0.001
Soil Conditions (Rocky)	11.925	9.181	0.197
Interaction: Magnitude & Rocky Soil	-2.614	1.626	0.111

Table 21.2: ANOVA table corresponding to the model fit explaining the bracketed durationa s a function of both magnitude and soil condition at the measurement location. The effect of the magnitude was allowed to differ across soil conditions.

Source	DF	SS	MS	F	P-Value
(Intercept)	1	678.562	678.562	27.980	< 0.001
Magnitude	1	1041.776	1041.776	42.957	< 0.001
Soil Conditions	1	40.913	40.913	1.687	0.197
Interaction: Magnitude & Soil Conditions	1	62.663	62.663	2.584	0.111
Residuals	115	2788.908	24.251		

Table 21.2 presents the corresponding ANOVA table. The ANOVA table shows how the variability is partitioned.

In both tables, the p-values are computed assuming the conditions of the classical regression model are appropriate. In Table 21.1, the p-value corresponds to testing if the corresponding parameter is 0, *holding all other parameters fixed*. Assuming the conditions for the classical regression model are appropriate, we have no evidence ($p = 0.111$) that the effect of the magnitude differs across the various soil conditions. That is, it is reasonable that the effect of the magnitude is similar for locations with and without rocky soil.

Chapter 22

Putting it All Together

For the Seismic Activity Case Study, consider the following question:

> After accounting for the various soil conditions, is there evidence that the protective effect of a location being further away from the epicenter with regard to the bracketed duration depends upon the magnitude of the earthquake?

22.1 Graphical Summary

Before developing a statistical model to address our question, we summarize the data graphically. The question involves three different predictors: magnitude, epicentral distance, and soil conditions. As a result, we must carefully consider how we visualize the data. The primary emphasis in the question is on the impact the magnitude has on the *effect* of the epicentral distance. That is, is the relationship of the epicentral distance and bracketed duration similar regardless of the magnitude of the earthquake?

Figure 22.1 illustrates the relationship between the bracketed duration and the epicentral distance. We note that the axis for the epicentral distance takes logarithmic steps to better illustrate the relationship. That is, moving from 1 to 10 kilometers has roughly the same effect as moving from 10 to 100 kilometers from the earthquake. Also note that we have displayed the relationship within each of the three soil conditions for the measurement location. The pattern within each of the soil conditions appears to differ. Finally, the color of the point indicates the magnitude of the earthquake. It can be difficult to isolate points of a similar color, but there does appear to be some evidence that the relationship between the bracketed duration and the epicentral distance depends on the magnitude.

In order to visualize complex multivariable relationships, we need to make use

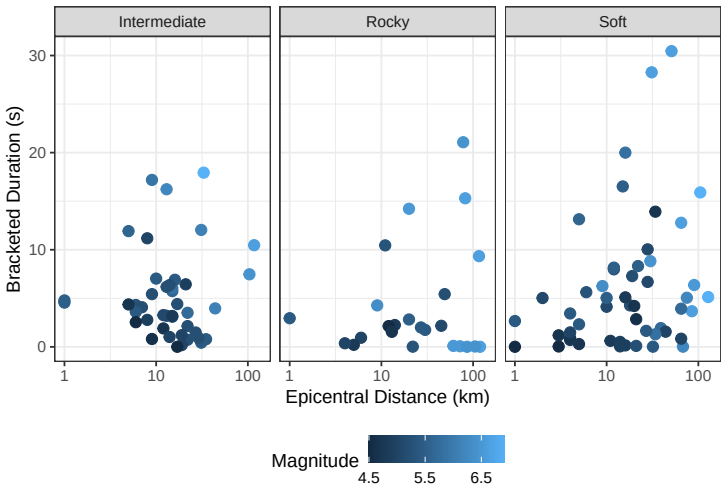


Figure 22.1: Relationship between the bracketed duration and the distance from the epicenter of an earthquake for locations measuring seismic activity in Greece. The relationship is presented for various soil types.

of multiple graphical elements.

22.2 Development of Statistical Model

In order to address our primary question of interest, we must develop a statistical model which explains the data generating process and embeds our question of interest in terms of the parameters of the model. Based on the question of interest, our model should incorporate the following elements:

- Soil condition of the location should be included to account for this effect.
- Magntidue of the earthquake should be included.
- Distance the location is from the epicenter of the earthquake should be included.
- Interaction of the epicentral distance and magnitude should be included; the associated parameters are the key to address our question of interest.

In addition, based on the graphical exploration of the data in Figure 22.1, we should also include the following elements:

- The relationship between the bracketed duration and the epicentral distance should be on a logarithmic scale. This accounts for the "stretched" scale in the above graphic.
- The relationship between the epicentral distance and bracketed duration appears to differ for each of the three soil conditions; therefore, an interaction term between these variables should be included.

Putting these together, we have the following model:

$$\begin{aligned}(\text{Bracketed Duration})_i = \beta_0 &+ \beta_1 \log_{10}(\text{Epicentral Distance})_i + \beta_2(\text{Magnitude})_i \\ &+ \beta_3 \mathbb{I}(\text{i-th location has Rocky soil}) + \beta_4 \mathbb{I}(\text{i-th location has Soft soil}) \\ &+ \beta_5 \log_{10}(\text{Epicentral Distance})_i \mathbb{I}(\text{i-th location has Rocky soil}) \\ &+ \beta_6 \log_{10}(\text{Epicentral Distance})_i \mathbb{I}(\text{i-th location has Soft soil}) \\ &+ \beta_7 \log_{10}(\text{Epicentral Distance})_i (\text{Magnitude})_i + \epsilon_i \end{aligned} \tag{22.1}$$

This model is complex, but it captures each of the elements that we described above. Indicator variables are used to capture the various soil conditions; this includes when constructing interaction terms. In addition to modeling the deterministic portion of the data generating process, we must also place conditions on the stochastic portion in order to make inference. We consider the conditions of the classical regression model:

- The error in the bracketed duration for one location is independent of the error in the bracketed duration for any other location.
- The error in the bracketed duration is 0, on average; that is, the model above for the mean response is correctly specified.
- The variability of the error in the bracketed duration is the same for all locations with a similar epicentral distance, magnitude and soil condition.
- The error in the bracketed duration follows a Normal distribution.

22.3 Assessment of Conditions

Before making inference regarding our question of interest, we should determine if our data is consistent with the conditions on the error term we have specified. Figure 22.2 is a probability plot of the residuals used to assess whether the data is consistent with the assumption of normality. The plot reveals some departure from the linear relationship we would expect if the residuals were a sample from a Normal distribution. That is, there is some evidence to suggest that the data is not consistent with the condition of Normality.

Figure 22.3 is a plot of the residuals for the observations in the order in which they were collected. Since the data was collected over time, this plot could reveal potential patterns among the residuals which suggest a departure from independence among the errors. As there are no trends in either the location or spread of the residuals, the data is consistent with the condition of independence.

Figure 22.4 is a plot of the residuals against the predicted values from the model. While there are some signs of curvature in these residuals, we do not feel the deviation is sufficient enough to warrant believing the model is misspecified. That is, we are willing to assume the data is consistent with the condition that the mean of the errors is 0 for each combination of the predictors. However, we

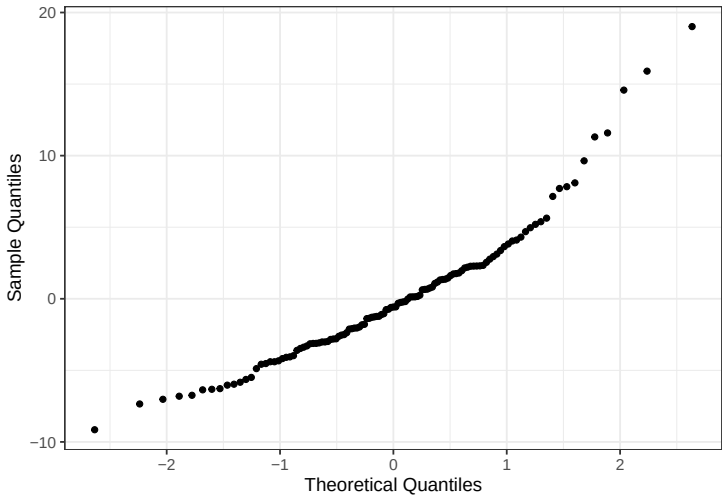


Figure 22.2: Probability plot of the residuals corresponding to a model for the bracketed duration of seismic events in Greece. The model is described by Equation (22.1).

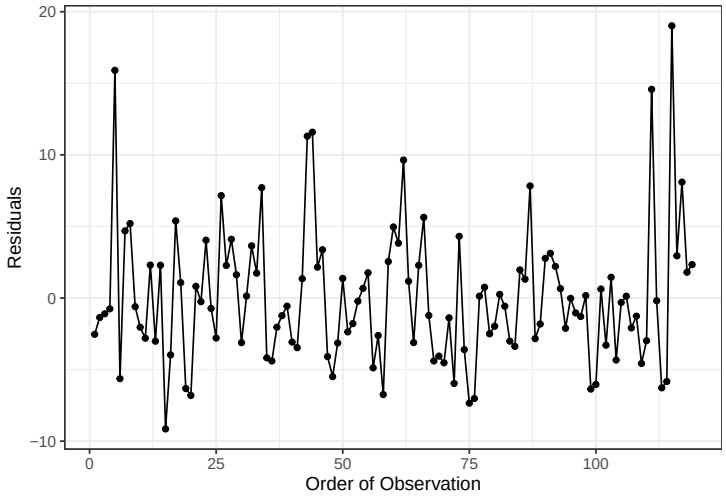


Figure 22.3: Time-series plot of the residuals corresponding to a model for the bracketed duration of seismic events in Greece. The model is described by Equation (22.1).

cannot ignore the change in the spread as the predicted values increase. This suggests that for larger bracketed durations, the model is not as precise.

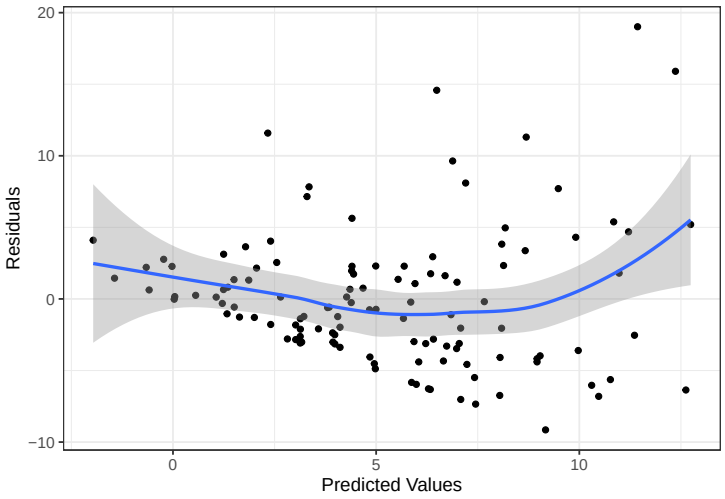


Figure 22.4: Plot of the residuals against the predicted values corresponding to a model for the bracketed duration of seismic events in Greece. The model is described by Equation (22.1).

Examining the residuals, we determined that the data is consistent with the following two conditions:

- The error in the bracketed duration for one location is independent of the error in the bracketed duration for any other location.
- The error in the bracketed duration is 0, on average; that is, the model above is correctly specified.

There is evidence that the data obtained is not consistent with the remaining two conditions enforced in a classical regression model. As a result, we choose to model the sampling distribution of our estimates empirically, via bootstrapping.

22.4 Summary of Model Fit

The parameters in our model are estimated via least squares. The variability in these estimates is quantified using an empirical model of the sampling distribution based on 5000 bootstrap replications. Table 22.1 summarizes the estimates for the parameters in Equation (22.1).

The results suggests that for each 1-unit increase in the magnitude of an earthquake, the reduction in the bracketed duration for each 10-fold increase in the number of kilometers a location is from the epicenter of an earthquake is reduced a further 2.9 seconds, on average (95% CI: (0.14, 5.90)). That is, we have

Table 22.1: Summary of the model fit to characterize the bracketed duration of seismic events in Greece. The model is described by Equation (22.1).

Term	Estimate	Standard Error	95% lower	95% upper
Intercept	-44.038	12.572	-69.205	-19.607
Log of Epicentral Distance	13.642	8.404	-2.491	30.378
Magnitude	9.636	2.353	5.083	14.309
Indicator: Rocky Soil	-2.065	2.836	-7.699	3.532
Indicator: Soft Soil	-0.762	2.322	-5.284	3.884
Interaction: Distance and Rocky Soil	0.146	2.410	-4.533	4.937
Interaction: Distance and Soft Soil	1.211	1.980	-2.713	5.072
Interaction: Distance and Magnitude	-2.904	1.480	-5.897	-0.087

some evidence ($p = 0.07$) that the reduction in the bracketed duration as a location gets further away from the epicenter of an earthquake is magnified as the magnitude of the earthquake increases. Practically speaking, this means that for larger earthquakes, each kilometer you can distance yourself from the epicenter is important.

Part IV

Unit IV: Comparing the Average Response Across Groups

Chapter 23

Case Study: Organic Foods and Superior Morals

"You are what you eat" is a common phrase dating back to at least the 1820's used to suggest that if you want to be fit, you must eat healthy foods. However, does the phrase extend to our personality as well as our physique? Recent research has suggested that specific tastes (sweet vs. disgusting, for example) can influence moral processing. That is, certain foods may lead us to be nicer to those around us or lead us to be more judgemental. Organic foods are often marketed using phrases like "pure" or "honest" (Jessica Alba's Honest Company, for example); is there some relationship between the consumption of organic foods and moral behavior?

Dr. Eskine of the Department of Psychological Sciences at Loyola University sought to answer this question (Eskine 2013). He conducted a study to investigate whether exposure to certain types of food had an effect on a person's moral processing. Specifically, he randomized 62 Loyola University undergradates to one of three food types: organic, comfort, and control. Each participant received a packet containing pictures of four food items from the assigned category:

- Organic Foods: apple, spinach, tomato, carrot
- Comfort Foods: ice cream, cookie, chocolate, brownie
- Control Foods: oatmeal, rice, mustard, beans

The control foods are those which are pre-packaged and are generally considered staple items; organic foods are those which are associated with a healthy diet; and, comfort foods were sweets. After viewing the images for a set period of time, each participant received a packet containing six counter-balanced moral transgressions. An example of such a transgression is produced below:

> Bob was at a family gathering when he met Ellen, a second cousin of his that he had seen once or twice before. Bob found Ellen very

> attractive and he asked her out on a date. Ellen accepted and they began to have a romantic and sexual relationship. They often go on weekend trips to romantic hotels in the mountains.

Participants were then asked to rate the morality of the scenario on a 7-point scale (1 = "not at all morally wrong" to 7 = "very morally wrong"). The average of the morality scores across the six scenarios was used as an overall measure of their moral expectations. A higher value indicates high moral expectations (very strict) and a lower value indicates lower moral expectations (very lenient).

Dr. Eskine's analysis revealed that there was strong evidence ($p = 0.001$) that participants' moral judgments differed, on average, across the various food exposure groups. In particular, those exposed to organic foods had higher moral expectations (an average mean moral judgment of 5.58) compared to those experiencing comfort foods (average mean moral judgment of 4.89) or control foods (average mean moral judgment of 5.08). He therefore concluded that exposure to organic food did lead to higher moral expectations.

Understandably, Dr. Eskine's work caught the interest of various media outlets and researchers. Two researchers within the Department of Psychology at Dominican University in Illinois sought to replicate Dr. Eskine's work (Moery and Calin-Jageman 2016). There were several components to their research, but the first phase included a replication of Dr. Eskine's initial study with minor variants. They enrolled 123 college students into their study. The participants were presented with the same food images as in Eskine's study with the exception that celery was used instead of an apple for organic food. The same moral dilemmas were given to participants. As in the original study, the average score from the six moral dilemmas was the primary response for this study. A subset of the collected data, showing three participants from each treatment group (type of food shown), is presented below. The full dataset[1] has been made available by the researchers at the following website: https://osf.io/atkn7/wiki/home/

[1]There were multiple phases to their research. The direct replication of Dr. Eskine's work was Study 1, which is the dataset being considered in this text.

Table 23.1: Subset of data from study characterizing moral behavior following exposure to various food categories.

Participant	Food Condition	Response (Avg of Moral Questions)
18	organic	5.500
20	organic	5.500
21	organic	6.333
1	comfort	6.000
2	comfort	3.500
3	comfort	6.167
4	control	5.167
10	control	7.000
12	control	6.833

Chapter 24

Framing the Question

"Does exposure to various food types lead to different moral expectations?" The primary question from the Organic Food Case Study is about the relationship between two variables: the response (moral expectations; see Definition 3.2) and the **factor** of interest (food type).

Definition 24.1 (Factor)**:**
Also referred to as the "treamtent," a categorical variable used to explain/predict a response.

The majority of interesting research questions involve identifying or quantifying the relationship between two variables. Despite the complexity of the analyses sometimes employed to address these questions, the basic principles are the same as those studied in Unit 1. To begin, asking good questions involves defining the population of interest and characterizing the variable(s) at the population level through well-defined parameters.

The question of the Organic Food Case Study, as stated above, is ill-posed. Almost certainly, there are individuals for which exposure to organic foods may result in higher moral expectations compared to exposure to comfort foods. However, there are almost certainly individuals for which the effect is reversed — higher moral expectations are expected following exposure to comfort foods compared with organic foods. That is, we expect there to be *variability* in the effect of food types on the resulting moral expectations. The question needs to be refined.

While the study was conducted using college students, the original question seems quite broad (we discuss this discrepancy in more detail in the next chapter). Notice that the original question is not predicated on *consuming* various foods but simply *exposure* to various foods. The question itself is not limited to

only those individuals which purchase a specific type of food but concerns all individuals. More, we really see that there are three groups of interest — those which are exposed to organic foods, those exposed to comfort foods, and those exposed to the control foods. We can think of three distinct populations:

1. All individuals exposed to organic foods.
2. All individuals exposed to comfort foods.
3. All individuals exposed to control foods.

We now work to characterize the response within each of these three populations. Since the response of interest is a numeric variable (taking values between 1 and 7 with higher values indicating higher moral expectations), summarizing the variable using the mean is reasonable. That is, we might ask "does exposure to various food types lead to different moral expectations, *on average*?" Our question now compares the mean response across the groups. In particular, our question is looking for some type of difference in this mean response across the groups; our working hypothesis is then that the groups are all equivalent, on average. This could be framed in the following hypotheses:

> H_0 : the average moral expectations are the same following exposure to each of the three types of food.
> H_1 : the average moral expectations following exposure to food differ for at least one of the three types.

This is equivalent to expressing the hypotheses in terms of a relation between the two variables:

> H_0 : there is no association between the type of food an individual is exposed to and their moral expectations, on average.
> H_1 : there is is an association between the type of food an individual is exposed to and their moral expectations, on average.

We can represent these hypotheses mathematically as

> $H_0 : \mu_{\text{comfort}} = \mu_{\text{control}} = \mu_{\text{organic}}$
> H_1 : At least one μ differs from the others

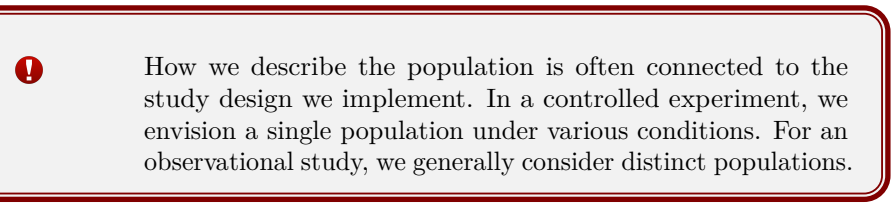
where μ_{comfort} is the mean moral expectation for individuals exposed to comfort foods, etc. The question is now well-posed — it is centered on the population and captured through parameters.

For this particular setting, there is an alternative way of thinking about the population. You might argue that there are not three distinct populations; instead, there is only a single population (all individuals) and three different exposures (organic, comfort and control foods). This is a reasonable way of characterizing the population. The hypotheses remain the same:

> $H_0 : \mu_{\text{comfort}} = \mu_{\text{control}} = \mu_{\text{organic}}$
> H_1 : At least one μ differs from the others

The difference is in our interpretation of the parameters. We would describe μ_{comfort} as the mean moral expectation when an individual is exposed to comfort foods. The distinction, while subtle is to place emphasis on switching an individual from one group to another instead of the groups being completely distinct. In fact, this latter way of thinking is more in line with how the study was conducted. Individuals were allocated to one of the exposure groups, suggesting that exposure is something that could be changed for an individual.

From an analysis perspective, there is little difference between these two ways of describing the population. The difference is primarily in our interpretation. In many cases, we can envision the population either way; however, there are a few instances where that is not possible. Suppose we were comparing the average number of offspring of mice compared to rats (a lovely thought, I know). It does not make sense to think about changing a mouse into a rat; here, it only makes sense to think about two distinct populations being compared on some metric. How we describe the population is often related to the question we are asking.



How we describe the population is often connected to the study design we implement. In a controlled experiment, we envision a single population under various conditions. For an observational study, we generally consider distinct populations.

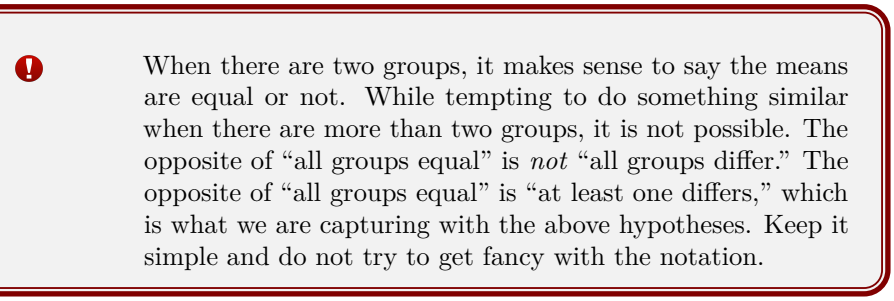
24.1 General Setting

This unit is concerned with comparing the mean response of a numeric variable across k groups. Let $\mu_1, \mu_2, \ldots, \mu_k$ represent the mean response for each of the k groups. Then, we are primarily interested in the following hypotheses:

$H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$
$H_1 :$ At least one μ differs from the others

When there are only two groups ($k = 2$), then this can be written as

$H_0 : \mu_1 = \mu_2$
$H_1 : \mu_1 \neq \mu_2$



When there are two groups, it makes sense to say the means are equal or not. While tempting to do something similar when there are more than two groups, it is not possible. The opposite of "all groups equal" is *not* "all groups differ." The opposite of "all groups equal" is "at least one differs," which is what we are capturing with the above hypotheses. Keep it simple and do not try to get fancy with the notation.

Here we are writing things in the mathematical notation, but let's not forget that every hypothesis has a context. Throughout this unit, we are looking for some signal in the *location* of the response across the groups. Our working assumption then states that the groups are all similar, *on average*. This may not be the only comparison of interest to make in practice. For example, it may not be the location that is of interest but the spread of a process. In some applications, managers would prefer to choose the process that is the most precise. These questions are beyond the scope of this unit, but the concepts are similar to what we discuss here.

Chapter 25

Study Design

Chapter 4 discussed the impact that the design of the study has on interpreting the results. Recall that the goal of any statistical analysis is to use the sample to say something about the underlying population. Observational studies are subject to confounding. In order to use the available data in order to make causal statements that apply within the population, we need to address the confounding. There are two ways of doing this:

1. Conduct a controlled experiment. While we do not limit our discussion to controlled experiments in this unit, our discussion will emphasize the elements of a well designed experiment.

2. Use observational data and account for confounders. This can be addressed through regression modeling as discussed in Chapter 21.

As discussed in Chapter 4, controlled experiments balance the groups being compared relative to the potential confounders. As a result, such studies permit causal conclusions to be drawn.

25.1 Aspects of a Well Designed Experiment

Generally speaking, there are three components to a well-designed study: replication, randomization, and comparative groups.

As we have stated repeatedly, variability is inherit in any process. We know there is variability in the population; not every subject will respond exactly the same to each treatment. Therefore, our questions do not seek to answer statements about individuals but about general trends in the population. In order to establish these general trends, we must allow that subject-to-subject variability be present within the study itself. This is accomplished through **replication**, obtaining data on multiple subjects from each group. Each subject's response would be

expected to be similar, with variability within the group due to the inherit variability in the data-generating process.

Definition 25.1 (Replication)**:**
Taking measurements on different subjects, for which you expect the results to be similar. That is, any variability is due to nautral variability within the population.

When we talk about gathering "more data," we typically mean obtaining a larger number of replicates. Ideally, replicates will be obtained through *random selection* from the underlying population to ensure they are representative. The subjects are then *randomly allocated* to a particular level of the factor under study (randomly allocated to a group). This random allocation breaks the link between the factor and any potential confounders, allowing for causal interpretations. However, if a link exists between the factor and the response, that is preserved. These are the two aspects of **randomization**.

Definition 25.2 (Randomization)**:**
Refers to the random selection *of subjects which minimizes bias and random* allocation *of subjects which permits causal interpretation.*

While students can typically describe random selection vs. random allocation, they often confuse their purpose. Random selection is to ensure the sample is representative. Random allocation balances the groups with respect to confounders.

We now have two sources of variability. That is, we have two reasons the response will differ from one subject to another. Subjects within different groups may differ because of an effect due to the group; this is the signal that we are tyring to identify with our hypotheses. Subjects within the same group will differ due to natural variability; this is the noise we observe in the data.

Random allocation ensures the groups are balanced with respect to confounders. However, there may still be a lot of variability within each group. The more variability present, the more difficult it is to detect a signal. The study will have more **power** to detect the signal if the groups are similar. This is the idea of having **comparative groups**.

Definition 25.3 (Power)**:**
Refers to the probability that a study will find a signal when one really exists in the data generating process. This is like saying "the probability a jury will declare a defendant guilty when they actually committed the crime."

Definition 25.4 (Comparative Groups)**:**
The idea that the treatment groups (levels of the factor under study) should be as similar as possible to reduce external variability in the process.

It is tempting to manually adjust the treatment groups to achieve what the researcher views as balance. This temptation should be avoided as balancing one feature of the subjects may lead to an imbalance in other features. We want to rely on randomization. However, when there is a particular feature which we would like to balance, we can employ specialized randomization techniques. For example, if we would like an equal number of Democrats and Republicans in a study, we can use stratified random sampling (see Definition 4.3) to ensure equal representation. During the random allocation, we can employ **blocking**, in which the random allocation to treatments happens within a secondary feature.

Definition 25.5 (Blocking)**:**
One way of minimizing variability contributed by an inherit characteristic. All observations that are linked through the characteristic are grouped together and random allocation occurs within *the block.*

Example 25.1: "Overseeding Golf Greens"
Golf is a major pasttime, especially in southern states. Each winter, the putting greens need to be overseeded with grasses that will thrive in cooler weather. This can affect how the ball rolls along the green. Dudeck and Peeacock (1981) reports on an experiment that involved comparing the ball roll for greens seeded with one of five varieties of rye grass. Ball roll was measured by the mean distance (in meters) that five balls traveled on the green. In order to induce a constant initial velocity, each ball was rolled down an inclined plane.

Because the distance a ball rolls is influenced by the slope of the green, 20 greens were placed into four groups in such a way that the five greens in the same group had a similar slope. Then, within each of these four groups, each of the five greens was randomly assigned to be overseeded with one of the five types of Rye grass. The average ball roll was recorded for each of the 20 greens.

The data for Example **??** is shown in Table 25.1.

It would have been easy to simply assign 4 greens to each of the Rye grass varieties; the random allocation would have balanced the slope of the greens across the five varieties. However, an additional layer was added to the design in order to control some of that additional variability. In particular, greens with similar slopes were grouped together; then, the random allocation to Rye grass varieties happened *within* groups of greens. As a result, what we see is that

Table 25.1: Data from Overseeding Golf Greens example.

Rye Grass Variety	Slope of Green Grouping	Mean Distance Traveled (m)
A	1	2.764
B	1	2.568
C	1	2.506
D	1	2.612
E	1	2.238
A	2	3.043
B	2	2.977
C	2	2.533
D	2	2.675
E	2	2.616
A	3	2.600
B	3	2.183
C	3	2.334
D	3	2.164
E	3	2.127
A	4	3.049
B	4	3.028
C	4	2.895
D	4	2.724
E	4	2.697

there is one green of each type of slope for each Rye grass variety. This has the effect of reducing variability due to nuisance characteristics of the subjects.

Blocking is often a way of gaining additional power when limited resources require your study to have a small sample size.

An extreme case of blocking occurs when you repeatedly measure the response on the same subject under different treatment conditions. For example, a pre-test/post-test study is an example of a study which incorporates blocking. In this case, the blocks are the individual subjects. The subjects then undergo each of the possible treatment options. The rationale here is to use every subject as his or her own control. The treatment groups are then as similar as possible.

We do note that blocking, while a powerful aspect of a design, has an impact on the type of analysis that can be conducted. Specifically, we must account for the blocking when conducting the analysis. We will discuss this in Chapters 32 - 38.

How did the design of the Organic Food Case Study incorporate these aspects? First, we notice that random allocation was utilized. Each of the 123 participants was randomly assigned to one of three treatment groups (type of food to which the particpant was exposed). The random allocation allows us to make causal conclusions from the data as any confounder should be balanced across the three foods. For example, subjects who adhere to a strict diet for religious purposes would naturally tend toward organic foods and higher moral expectations. However, for each subject like this exposed to organic foods, there is someone like this (on average) who was assigned to the comfort foods (on average). We also note that there is replication. Instead of assigning only one subject to each of the three treatment groups, we have several subjects within each group. This allows us to evaluate the degree to which the results vary within a particular treatment group.

The study does not make use of blocking. There are a couple of potential reasons for this; first, with such a large sample size, the researchers may not have thought it necessary. Second, it could be that there was a restriction on time. For example, researchers may have considered having students be exposed to each of the three types of food and answering different scenarios after each. However, this would take a longer amount of time to collect data. Third, it could be that researchers were not concerned about any identifiable characteristics that would generate additional variability. Regardless, the study is not worse off because it did not use blocking; it is still a very reliable design.

While it is clear that random allocation was utilized in the design, random selection was not. Students participating in the study are those from a particular lecture hall. As a result, these students were not randomly sampled from all college students (or even from the university student body). As a result, we must

really consider whether the conclusions drawn from this study would apply to all college students within the United States. Having additional information on their demographics may help determine this, but in general, this is not something that can be definitively answered. It is an assumption we are either willing to make or not. More, notice that the original question was not focused on college students; however, the sample consists only of college students. This can impact the broader generalization of our results. It is quite possible that we observe an effect in college students that is not present in the larger population. We should always be careful to ensure that the sample we are using adequately represents the population.

25.2 Collecting Observational Data

An inability to conduct a controlled experiment does not mean we neglect study design. Random sampling is still helpful in ensuring that the data is representative of the population. Similarly, ensuring there are a sufficient number of replications to capture the variability within the data is an important aspect of conducting an observational study. When collecting observational data, one of the most important steps is constructing a list of potential confounders and then collecting data on these variables. This will allow us to account for these confounders in our analysis; we cannot model what we do not collect.

Chapter 26

Presenting the Data

When a research question involves the relationship between two or more variables, such as comparing the mean response across levels of a factor, successful presentations of the data which address the question of interest need to *partition the variability*. This key idea is essential to both the data presentation and the data analysis.

We have already argued that variability makes addressing questions difficult. If every subject had the same response to a particular exposure, there would be no need for statistics. We would simply evaluate one subject and determine which treatment to give. Statistics exists because of the ambiguity created by variability in the responses. In response to this variability, our statistical graphics and models distinguish (partition) the various sources of variability. That is, with any analysis, we try to answer the question "why aren't all the values the same? What are the reasons for the difference we are observing?"

From the Organic Food Case Study, consider the primary question of interest:

> Is there evidence of a relationship between the type of food a person is exposed to and their moral expectations, on average, following exposure?

We are really asking "does the food exposure help explain the differences in the moral expectations of individuals?" We know that there are differences in moral expectations between individuals. But, are these differences solely due to natural variability (some people are just inherently, possibly due to how they were raised, more or less liberal with moral beliefs); or, is there some systematic component that explains at least a portion of the differences between individuals? We are thinking about partitioning the "why the responses differ" (the variability).

A good graphic must then tease out how much of the difference in the moral expectations is from subject-to-subject variability and how much is due to the

food exposure. First, consider a common graphic which is **not** useful in this situation (Figure 26.1).

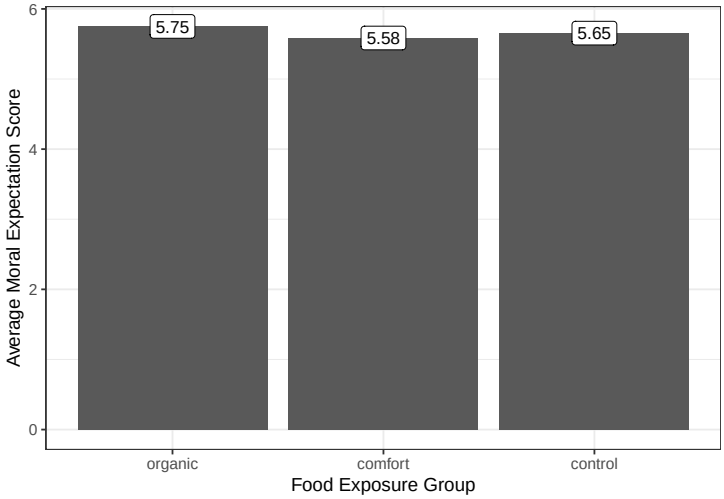


Figure 26.1: Illustration of a poor graphic using the Organic Food Case Study; the graphic does not give us a sense of variability. As a result, it is not clear how different these means really are.

To determine an appropriate graphic, we need to remember that we want to partition the variability. So, we must not only compare the differences between the groups but also allow the viewer to get a sense of the variability within the group. A common way of doing this within engineering and scientific disciplines is to construct side-by-side boxplots, as illustrated in Figure 26.2.

From the graphic, we see that the moral expectation scores seem to have nearly the same pattern in each of the exposure groups. More, the center of each of the groups is roughly the same. That is, there does not appear to be any evidence that the type of food to which a subject is exposed is associated with moral expectations, on average.

Side-by-side boxplots can be helpful in comparing large samples as they summarize the location and spread of the data. When the sample is smaller, it can be helpful to overlay the raw data on the graphic in addition to the summary provided by the boxplot. We might also consider adding additional information, like the mean within each group. An alternative to boxplots is to use violin plots which emphasize the shape of the distribution instead of summarizing it like boxplots. Yet another option is to construct density plots which are overlayed on one another. This works when there are only a small number of groups; if the number of groups is large, then placing the distributions side-by-side is much more effective. A comparison of these approaches is in Figure 26.3.

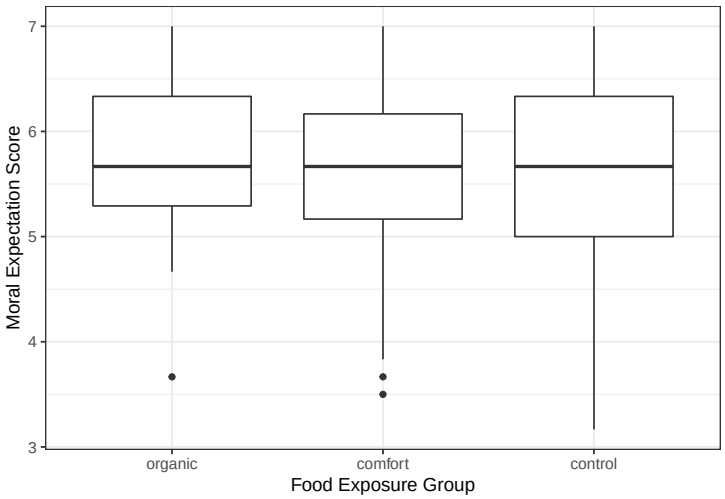


Figure 26.2: Comparison of the moral expectations for college students exposed to different types of food.

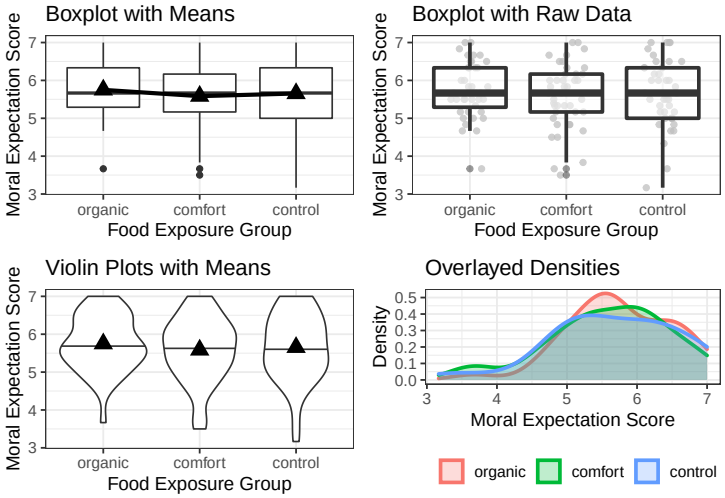


Figure 26.3: Multiple ways to effectively compare the response across multiple groups.

Each of these plots is reasonable. What makes them useful in addressing the question is that in each plot, we can compare the degree to which the groups differ relative to the variability within a group. That is, we partition the variability. With each plot, we can say that one of the reasons the groups differ is because of exposure to different food types; however, this difference is extremely small relative to the fact that regardless of which food group you were exposed to, the variability in moral expectations with that group is quite large. Since the predominant variability in the moral exposure is the variability within the groups, we would say there is no signal here. That is, there is no evidence that the average scores differ across food exposure groups.

The key to a good summary is understanding the question of interest and building a graphic which addresses this question through a useful characterization of the variability.

Chapter 27

Building the Statistical Model

In Chapter 10 we introduced the statistical modeling framework. In particular, our general model (see Equation (10.1)) was given as

$$\text{Response} = f(\text{variables, parameters}) + \text{noise}$$

As before, this model has two components:

- A deterministic component which takes the form of a function of variables and unknown parameters. It is often this component on which we would like to make inference.
- A stochastic component which captures the unexplained variability in the data generating process.

In the previous unit, we began to explore how the capabilities of such a model. In this chapter, we now discuss how to choose the function $f(\cdot)$ so that we can compare a quantitative response across the levels of a factor (our predictor).

27.1 Statistical Model for A Quantitative Response and a Categorical Predictor

For the Organic Food Case Study, we are comparing the moral expectations (quantitative response) for different food exposures (levels of a categorical variable). Our model for the data-generating process is best understood in light of the graphic we used to display the data (see Figure 27.1).

Let's consider how the value 3.67, highlighted red in Figure 27.1, was generated. As discussed previously, there are two sources of variability in the moral expec-

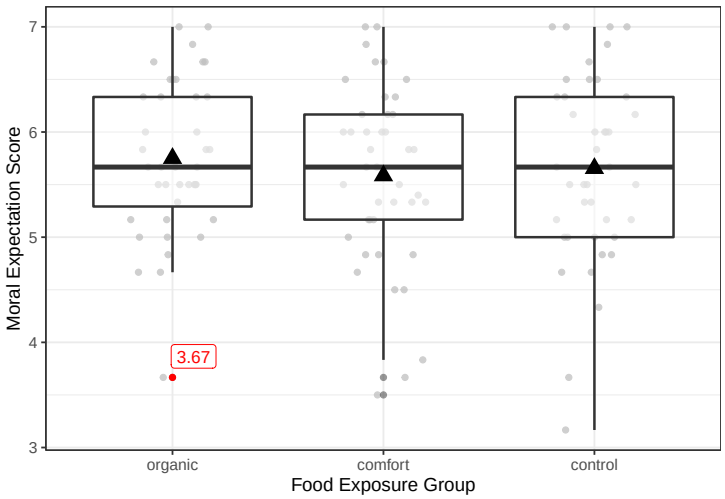


Figure 27.1: Moral expectation scores for students following exposure to various food types.

tation scores (two reasons that the values are not all the same). One source is the fact that different subjects had different exposures. That is, one reason the value 3.67 differs from others observed is because this subject belongs to the organic group and not the comfort or control exposure groups. We might initially consider something like the simple linear model discussed in Chapter 17

$$(\text{Moral Expectation Score})_i = \beta_0 + \beta_1(\text{Food Exposure Group})_i + \epsilon_i$$

However, the food exposure group is not a quantitative predictor. The solution is to use indicator variables (see Definition 17.2) to capture this categorical predictor. It turns out this is somewhat natural if we think of the function $f(\cdot)$ as a piecewise function:

$$f\left((\text{Food Exposure Group})_i\right) = \begin{cases} \mu_1 & \text{if i-th subject exposed to organic foods} \\ \mu_2 & \text{if i-th subject exposed to comfort foods} \\ \mu_3 & \text{if i-th subject exposed to control foods} \end{cases}$$

Notice that $f(\cdot)$ involves both a variable of interest as well as parameters of interest — the mean response μ_1, μ_2, μ_3 for each of the three groups. This function is perfectly acceptable, but it is cumbersome to write in a shortened form. Notice how the function works: it receives an input regarding which group, and it directs you to the appropriate parameter as an output. Using indicator variables, we can write this in a compact way

$$f\left((\text{Food Exposure Group})_i\right) = \mu_1(\text{Group})_{1,i} + \mu_2(\text{Group})_{2,i} + \mu_3(\text{Group})_{3,i}$$

where

$$(\text{Group})_{1,i} = \begin{cases} 1 & \text{if i-th subject exposed to organic foods} \\ 0 & \text{if i-th subject not exposed to organic foods} \end{cases}$$

$$(\text{Group})_{2,i} = \begin{cases} 1 & \text{if i-th subject exposed to comfort foods} \\ 0 & \text{if i-th subject not exposed to comfort foods} \end{cases}$$

$$(\text{Group})_{3,i} = \begin{cases} 1 & \text{if i-th subject exposed to control foods} \\ 0 & \text{if i-th subject not exposed to control foods} \end{cases}$$

Each of the $(\text{Group})_j$ variables is an indicator capturing whether the i-th observation belongs to the j-th group. The function $f(\cdot)$ embeds the parameters that define our question.

The deterministic component of a statistical model incorporates the parameters which govern the question of interest. It is built to explain differences in the response based on differences in group membership or other characteristics of the subjects.

Inserting this function $f(\cdot)$ into our general modeling framework, we have the following model for the data generating process:

$$(\text{Moral Expectation Score})_i = \mu_1(\text{Group})_{1,i} + \mu_2(\text{Group})_{2,i} + \mu_3(\text{Group})_{3,i} + \epsilon_i \tag{27.1}$$

The deterministic component says that every single person exposed to the same food group should have the same moral expectations, and the stochastic portion of the model allows individuals within the same group to vary. Because this model is very directly partitioning the variability in the response, it is often called an ANOVA (ANalysis Of VAriance) model. This is somewhat of a silly name since we have seen that all statistical models partition the variability in the response, and the above model is simply a regression model. But, the name has stuck.

The stochastic component of a statistical model captures the unexplained variability due to natural variability in the population or measurement error in the response.

Before proceding, let's compare the model in Equation (27.1) to when we considered a simple linear model for the data generating process. Equation (27.1) contains three parameters, each of which is attached to a "predictor" (which happens to be an indicator variable). Further, there is no "intercept" term in the model. So, our model for the data generating process relating a quantitative response and a categorical predictor is actually a special case of a general regression model without an intercept term. This is true in general.

In general, given a quantitative response variable, our model for the data generating process comparing this variable across k levels of a factor is

$$(\text{Response})_i = \sum_{j=1}^{k} \mu_j (\text{Group})_{j,i} + \epsilon_i$$

where

$$(\text{Group})_{j,i} = \begin{cases} 1 & \text{if i-th observation belongs to group j} \\ 0 & \text{if i-th observation does not belong to group j} \end{cases}$$

Just as before, we need to distinguish between the model for the data generating process and the model for the sampling distribution of the parameter estimates or the null distribution for a standarized statistic. While we need the latter for inference, the model for the data generating process is a necessary stepping stone along the way.

The parameters in this model are of course unknown. They can be estimated using the method of least squares. This actually results in exactly what we might hope — the least squares estimate of the mean for the j-th group is the sample mean of the response using only observations from the j-th group. That is, we use the observed mean response from each group as an estimate of the mean response for each group.

However, these estimates, as with any estimate, have variability associated with them. In order to make inference, we must determine a suitable model for the sampling distribution (or null distribution if appropriate). This is done by placing conditions on the stochastic portion of the model.

27.2 Conditions on the Error Distribution

In our model for the data-generating process we incorporated a component ϵ to capture the noise within each group. Since the error is a random variable (stochastic element), we know it has a distribution. We typically assume a certain structure to this distribution. The more assumptions we are willing to make, the easier the analysis, but the less likely our model is to be applicable to the actual data-generating process we have observed. The conditions we make dictate how we conduct inference (the computation of a p-value or confidence interval).

The first condition we consider is that the noise attributed to one observed individual is independent of the noise attributed to any other individual observed. That is, the amount of error in any one individual's response is unrelated to the error in any other response observed.

The second condition that is typically placed on the distribution of the errors is that the errors are identically distributed. Again, we introduced this condition in Chapters 10 and 18. In particular, if the errors are not identically distributed, it is typically because the variability of the error differs for one value of the predictor compared to another. Practically, this reveals itself as our response being more precise in one group than in another. As a result of focusing on the variability of the response for each predictor, this condition is often referred to as *homoskedasticity* instead of the errors being identically distributed.

The third condition we might consider imposing is that the errors in the response follow a Normal distribution, as discussed in Chapter 18. If this condition holds, it implies that within each group, the distribution of the response variable itself is Normally distributed.

As in regression modeling, we are not required to impose all three conditions in order to obtain a model for the sampling distribution. Historically, however, all three conditions are imposed.

At this point, you might be wondering what happened to the "mean zero" condition we imposed in regression models in which we assumed the error had the value of 0, on average, for all values of the predictor. Recall that this assumption implied that the model for the mean response was correctly specified, that no curvature was ignored. In our model above, with only a single categorical predictor with k levels (captured through k indicator variables), there is no "trend" being described. That is, instead of saying that the mean response increases (or decreases, or has any particular shape) as we move across the factors of the predictor, the model allows the mean response for each group to be completely unrelated to any other group. Since there is no "trend" term in the mean response model, we need not assume it is correctly specified.

27.3 Classical ANOVA Model

In the preceeding section, we discussed three conditions we could place on the stocastic portion of the data generating process. Placing all three conditions on the error term is what we refer to as the "Classical ANOVA Model."

Definition 27.1 (Classical ANOVA Model)**:**
For a quantitative response and categorical variable, the classical ANOVA model assumes the following data-generating process:

$$(Response)_i = \sum_{j=1}^{k} \mu_j (Group)_{j,i} + \epsilon_i$$

where

$$(Group)_{j,i} = \begin{cases} 1 & \text{if } i\text{-th observation belongs to group } j \\ 0 & \text{if } i\text{-th observation does not belong to group } j \end{cases}$$

and

1. *The errors are independent of one another.*
2. *The errors from one group have the same variability as all other groups.*
3. *The errors follow a Normal Distribution.*

It is possible to relax these assumptions; however, this is the default "ANOVA" analysis implemented in the majority of statistical packages.

27.4 Imposing the Conditions

Let's return to our model for the moral expectation score as a function of the food exposure group:

$$(\text{Moral Expectation Score})_i = \mu_1 (\text{Group})_{1,i} + \mu_2 (\text{Group})_{2,i} + \mu_3 (\text{Group})_{3,i} + \epsilon_i$$

where

Table 27.1: Summary of the model fit relating the moral expectation score of college students to the type of food to which they were exposed.

Term	Estimate	Standard Error	Lower 95% CI	Upper 95% CI
Organic Foods Group	5.750	0.131	5.490	6.010
Comfort Foods Group	5.585	0.128	5.331	5.839
Control Foods Group	5.654	0.130	5.397	5.912

$$(\text{Group})_{1,i} = \begin{cases} 1 & \text{if i-th subject exposed to organic foods} \\ 0 & \text{if i-th subject not exposed to organic foods} \end{cases}$$

$$(\text{Group})_{2,i} = \begin{cases} 1 & \text{if i-th subject exposed to comfort foods} \\ 0 & \text{if i-th subject not exposed to comfort foods} \end{cases}$$

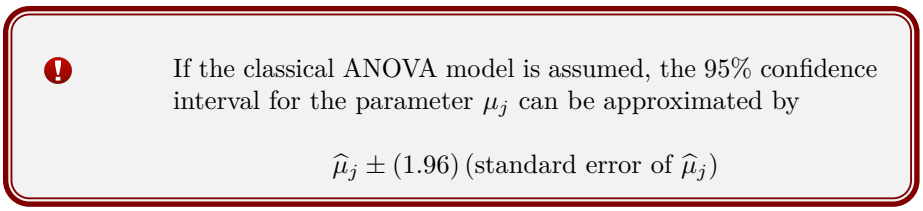
$$(\text{Group})_{3,i} = \begin{cases} 1 & \text{if i-th subject exposed to control foods} \\ 0 & \text{if i-th subject not exposed to control foods} \end{cases}$$

Using the method of least squares, we can estimate the parameters in the model; this leads to the following estimates for the average moral expectation score:

$$\text{Average moral expecation score if exposed to organic foods} = \widehat{\mu}_1 = 5.75$$
$$\text{Average moral expectation score if exposed to comfort foods} = \widehat{\mu}_2 = 5.58$$
$$\text{Average moral expectation score if exposed to control foods} = \widehat{\mu}_3 = 5.65$$

If we are willing to assume the data is consistent with the conditions for the classical ANOVA model, we are able to model the sampling distribution of these estimates and therefore construct confidence intervals. Table 27.1 summarizes the fit for the above model. In addition to the least squares estimates, it also contains the standard error of the statistic, quantifying the variability in the estimates as well as a 95% confidence interval estimating each parameter.

Under the classical ANOVA model, there is an analytical model for the sampling distribution, and it is known. As a result, the confidence interval can be computed from a formula.



If the classical ANOVA model is assumed, the 95% confidence interval for the parameter μ_j can be approximated by

$$\widehat{\mu}_j \pm (1.96)\,(\text{standard error of } \widehat{\mu}_j)$$

The confidence intervals allow us to estimate the mean moral expectation score within each group. And, while the confidence intervals are similar for each of the

groups, we have not actually addressed the question of interest. We cannot use the confidence intervals given to directly compare the groups. Instead, we must directly attack the hypotheses of interest by computing a p-value. We consider this in the next chapter.

It is common to try and compare the mean response of several groups by determining if the confidence intervals for the mean response overlap. This is a mistake. If you want to compare groups, you need to do a direct comparison through the analysis.

27.5 Recap

We have covered a lot of ground in this chapter, and it is worth taking a moment to summarize the big ideas. In order compare the mean response in each group, we took a step back and modeled the data generating process. Such a model consists of two components: a deterministic component explaining the differences between groups and a stochastic component capturing the noise in the system.

Certain conditions are placed on the distribution of the noise in our model. Depending on the set of conditions we impose will determine whether we develop an analytical model or an empirical model for the parameters in the model. We still need to discuss how we compare the mean response of the groups based on this model.

Chapter 28

Quantifying the Evidence

Figure 28.1 displays a numeric response across three groups for two different datasets. Consider the following question:

> For which dataset is there *stronger* evidence that the response is associated with the grouping variable?

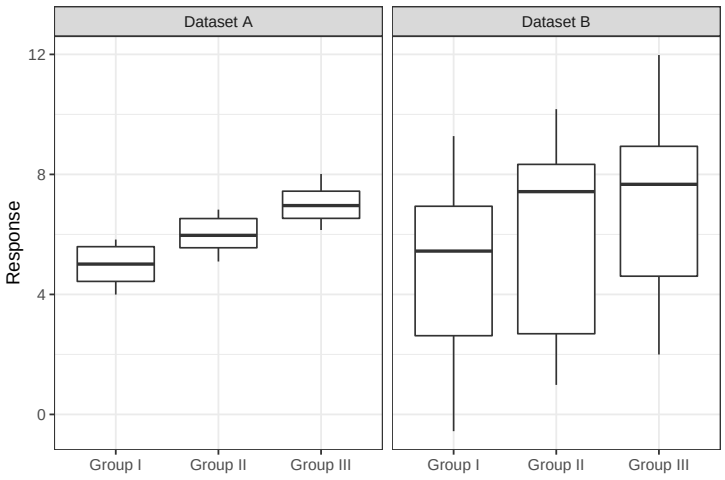


Figure 28.1: Simulated data illustrating that signal strength is determined by partitioning variability. There is a clear signal (difference in the location across groups) for Dataset A but not for Dataset B.

Nearly everyone will say that Dataset A provides stronger evidence of a relationship between the grouping variable and the response. We generated these data such that the mean for Groups I, II and III are 5, 6 and 7, respectively, *for both*

Datasets A and B. While there is a difference, on average, in the response across the groups in both cases, it is correct that Dataset A provides stronger evidence for that relationship. The real question is "what is it that leads everyone to make the same conclusion when we have not yet discussed how to analyze this data?" When we ask students why they feel Dataset A provides stronger evidence, we typically hear that it is because the "gaps" between the groups "look bigger." In essence, that is exactly right!

28.1 Partitioning Variability

Subconsciously, when we are deciding whether there is a difference between the groups, we are partitioning the variability in the response. We are essentially describing two sources of variability: the variability in the response caused by subjects belonging to different groups and the variability in the response within a group (Figure 28.2). In both Datasets A and B from Figure 28.1, the **between-group variability** is the same; the difference in the means from one group to another is the same in both cases. However, the **within-group variability** is much smaller for Dataset A compared to Dataset B.

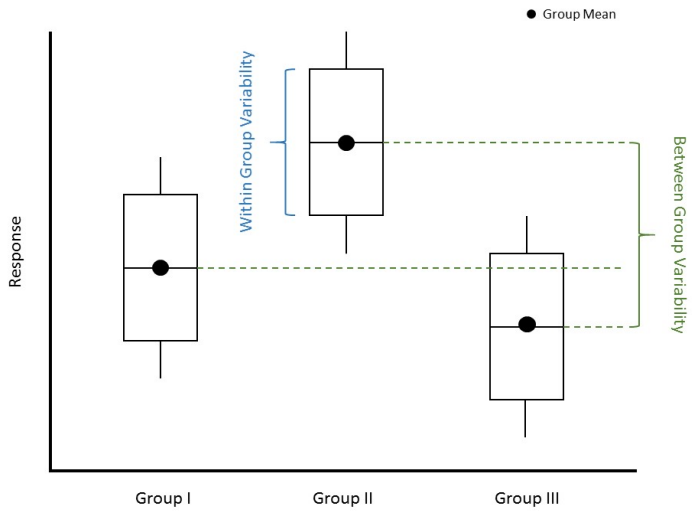


Figure 28.2: Illustration of partitioning the variability in the response to assess the strength of a signal.

Definition 28.1 (Between Group Variability)**:**
The variability in the average response from one group to another.

Definition 28.2 (Within Group Variability)**:**
The variability in the response within a particular group.

Figure 28.1 then illustrates the larger the variability between groups *relative to* the variability within groups, the stronger the signal. Quantifying the strength of a signal is then about quantifying the ratio of these two sources of variability. Let this sink in because it is completely counter-intuitive. We are saying that in order to determine if there is a difference in the mean response across groups, we have to examine variability. Further, a signal in data is measured by the variability it produces. For this reason, comparing a quantitative response across a categorical variable is often referred to as Analysis of Variance (ANOVA).

Consider the ratio of the variability between groups to the variability within groups. The larger this ratio, the stronger the evidence of a signal provided by the data.

This partitioning is a bit easier to visualize here than it was for the simple linear model, but the process is actually exactly the same.

28.2 Forming a Standardized Test Statistic

As we stated above, quantifying the strength of a signal is equivalent to quantifying the ratio of two sources of variability. This ratio forms our standardized statistic.

Based on our observations above, the standardized test statistic for comparing the mean response across multiple groups has the general form

$$T = \frac{\text{(Between Group Variability)}}{\text{(Within Group Variability)}} \tag{28.1}$$

The question we then have before us is the following: how do we measure these sources of variability? Consider again the hypothesis of interest for the Oranic Food Case Study:

$H_0 : \mu_{\text{comfort}} = \mu_{\text{control}} = \mu_{\text{organic}}$
$H_1 :$ At least one μ differs from the others

In order to form the standardized test statistic, let's again think about what constitutes evidence *against* the null hypothesis. The more the means differ from one another, the stronger the evidence. The *between-group* variability can be measured by the variance of the means; we call this the **Mean Square for Treatment (MSTrt)**.

Definition 28.3 (Mean Square for Treatment (MSTrt))**:**
This captures the between-group variability in an Analysis of Variance; it is a weighted variance among the sample means from the various groups. It represents the signal.

Since we do not know the mean response for each group (remember, each μ is a parameter), we assess the between group variability within the sample using the estimates for these parameters — the sample means. This is our signal. The larger this variance, the further apart the means are from one another (providing evidence for the alternative hypothesis); the smaller this variance, the closer the means are (consistent with the null hypothesis).

While the numerator provides some measure of the size of the signal, we need again need to consider how much noise is within the data. Again, in Figure 28.1, the variability between the means is identical for the two datasets; the signal is stronger for Dataset A because this variability is larger *with respect to the noise*. In order to capture the *within-group* variability, we pool the variances for each group; this is called the **Mean Square Error (MSE)**.

Definition 28.4 (Mean Square Error (MSE))**:**
This captures the within-group variability; it is a pooled estimate of the variance within the groups. It represents the noise.

Our test statistic in Equation (28.1) is then refined to

$$T = \frac{MSTrt}{MSE} \tag{28.2}$$

Consider testing the hypotheses $> H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$
$> H_1$: At least one μ differs from the others
The standardized test statistic of interest is

$$T = \frac{MSTrt}{MSE}$$

where

$$MSTrt = \frac{1}{k-1}\sum_{j=1}^{k} n_j \left((\text{Average response for j-th group}) - (\text{Overall average response})\right)^2$$

$$MSE = \frac{1}{n-k}\sum_{j=1}^{k} (n_j - 1)\,(\text{Variance for j-th group})^2$$

and n_j represents the sample size for the j-th group and n the overall sample size.

We note that while mathematical formulas have been provided to add some clarity to those who think algebraically, our emphasis is *not* on the computational formulas as much as the idea that we are comparing two sources of variability.

28.3 Link to Regression Analysis

The standardized statistic described in the previous section should look very familiar. That is because the ANOVA model is just a special case of a general regression model. While we developed the statistic intuitively above, we now describe how we reach the same conclusion following the development from a regression perspective.

As discussed in Chapter 19, we can partition the variability using the sums of squares. This is true in general, and we can apply it here.

$$SST = SSR + SSE$$

$$\sum_{i=1}^{n} \left((\text{Response})_i - (\text{Average Response})\right)^2 = \sum_{i=1}^{n} \left((\text{Predicted Response})_i - (\text{Average Response})\right)^2 + \sum_{i=1}^{n} \left((\text{Response})_i - (\text{Predicted Response})_i\right)^2$$

Now, keeping in mind that the least squares estimates are the sample means for each group, we can say that the "Predicted Response" is actually the sample

mean for the group to which the corresponding observation belongs. Of course, our standardized statistic is constructed using mean squares (actual variances) instead of sums of squares. In order to compute those mean squares, we must compute the corresponding degrees of freedom, which again partition just as the variability does.

Using the tip described in Chapter 19 regarding degrees of freedom, we have that the degrees of freedom for the total sum of squares (SST) is $n-1$ (n unique observations minus a single estimated mean). The degrees of freedom associated with the regression sum of squares (sometimes called the "Treatment Sum of Squares," abbreviated SSTrt in ANOVA) is $k-1$ (k averages estimated, one for each group, minus a single overall estimated mean). Finally, the degrees of freedom associated with the error sum of squares is $n-k$ (n unique observations minus k estimated group means).

We can then form the Mean Square Total $MST = SST/(n-1)$, the Mean Square for Regression (sometimes called the "Mean Square for Treatment," abbreviated MSTrt, as we did in the previous section) as $MSR = SSR/(k-1)$ and the Mean Square for Error as $MSE = SSE/(n-k)$. We then have the following standardized statistic

$$T^* = \frac{MSR}{MSE} = \frac{SSR/(k-1)}{SSE/(n-k)}$$

which is equivalent to the standardized statistic defined in the previous section. The key here is that regardless of how we approach the problem, we consider partitioning the variability in order to determine our signal to noise ratio.

Let's not forget that at its heart, when we partition the variability to perform a hypothesis test, we are really comparing two models. Consider the Organic Food Case Study. The primary question of interest is captured by the following hypotheses:

> H_0 : there is no association between the type of food an individual is exposed to and their moral expectations, on average.
> H_1 : there is is an association between the type of food an individual is exposed to and their moral expectations, on average.

which we represented mathematically as

> $H_0 : \mu_{\text{comfort}} = \mu_{\text{control}} = \mu_{\text{organic}}$
> H_1 : At least one μ differs from the others

Under the alternative hypothesis, where we place no restrictions on the parameters, we developed the following model for the data-generating process:

$$(\text{Moral Expectation Score})_i = \mu_1(\text{Group})_{1,i} + \mu_2(\text{Group})_{2,i} + \mu_3(\text{Group})_{3,i} + \epsilon_i$$

where

$$(\text{Group})_{1,i} = \begin{cases} 1 & \text{if i-th subject exposed to organic foods} \\ 0 & \text{if i-th subject not exposed to organic foods} \end{cases}$$

$$(\text{Group})_{2,i} = \begin{cases} 1 & \text{if i-th subject exposed to comfort foods} \\ 0 & \text{if i-th subject not exposed to comfort foods} \end{cases}$$

$$(\text{Group})_{3,i} = \begin{cases} 1 & \text{if i-th subject exposed to control foods} \\ 0 & \text{if i-th subject not exposed to control foods} \end{cases}$$

The null hypothesis imposes a restriction on the parameters (they must all be the same), which reduces the model for the data generating process to

$$(\text{Moral Expectation Score})_i = \mu + \epsilon_i$$

where μ is the common value of mean response for each food exposure group ($\mu \equiv \mu_1 = \mu_2 = \mu_3$). By partitioning the variability, we are really determining if the variability in the moral expectation scores explained by the different groups is a significant portion of all the variability in the moral expectation scores.

28.4 Obtaining a P-value

Standardized statistics quantify the strength of a signal, but they do not allow for easy interpretation. However, with a standardized statistic, we are able to compute a p-value to quantify how unlikely our particular sample is assuming the null hypothesis were true. That is, we need to construct a model for the null distribution of the standardized statistic. We need to know what type of signal we would expect if the null hypothesis were true. Conceptually, this is no different than it was in Unit I. We consider running the study again in a world in which all the groups are the same; for the Organic Food Case Study, this would involve

1. Obtaining a new sample of students.

2. Randomizing each student to one of the three groups at random, all showing the same foods.

3. Having each student answer a questionnaire regarding moral dilemmas.
4. Summarize the data by computing a standardized statistic.

Notice the difference in step 2 above compared to what actually happened in the real study. In the real study, each group had a different set of foods. This was to answer the question about whether there is a difference in the groups. However, in order to construct the *null distribution*, we need to force all groups to be the

same. This could be accomplished by showing every group the same set of foods. After repeating the above steps over and over again, we determine how often the recorded standardized statistics exceeded the value of the standardized statistic we obtained in our actual sample. How this null distribution is modeled depends on the conditions we are willing to place on the error term in our model.

Assuming the data is consistent with the conditions for the classical ANOVA model, we are able to construct an analytical model for the null distribution. Figure 28.3 represents this analytical null distribution of the standardized statistic. Again, these are values of the standardized statistic we would expect if there were no relationship between the food categories to which the students were exposed and their moral score. We are then interested in finding out if the observed dataset is consistent with these expectations.

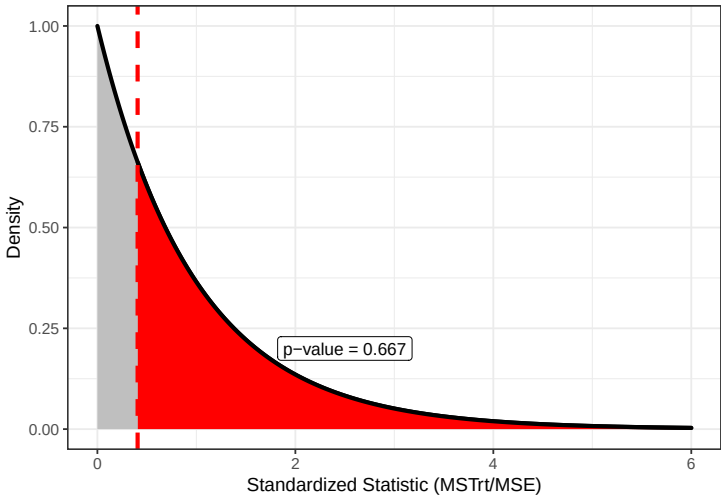


Figure 28.3: Computation of the p-value for the Organic Food Case Study under the classical ANOVA model.

Notice that in our data, we observed a standardized test statistic of 0.41; based on the null distribution, we would expect a signal this strong or stronger about 66.7% of the time *when no signal existed at the population* (by chance alone). Our data is very consistent with what we would expect under the null hypothesis. There is no evidence of a relationship between the type of food a student is exposed to and their moral expectations, on average.

Of course, this p-value was based on assuming the classical ANOVA model. We could have modeled the null distribution using an empirical model assuming only that the errors were independent of one another (not imposing the conditions of homoskedasticity or normality). While the model for the null distribution would change under these revised conditions, it changes only slightly (Figure 28.4) and the final conclusion remains the same. How do we determine which p-value to

report? We must assess the conditions, which is the topic of the next chapter.

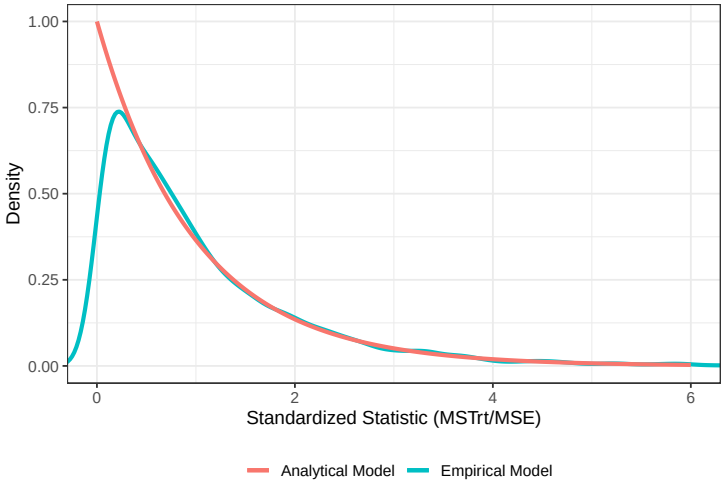


Figure 28.4: Comparison of two models for the null distribution of the standardized statistic. The empirical model for the null distribution is based on 5000 replications.

28.5 ANOVA Table

We should not lose sight of the fact that our standardized statistic is really a result of partitioning the variability and considering the variability explained by the predictor relative to the noise in the response. Our analysis of these sources of variability is often summarized in a table similar to that represented in Figure 28.5, known as an ANOVA table.

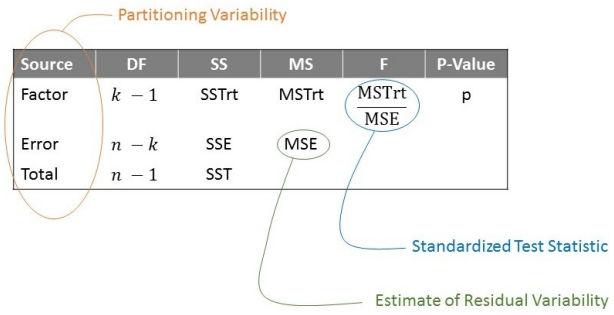


Figure 28.5: Layout of an ANOVA table which summarizes the analysis conducted. Emphasis is on partitioning the variability.

Table 28.1: ANOVA table for the Organic Food Case Study assuming the classical ANOVA model.

Source	DF	SS	MS	F	P-value
Food Exposure Group	2	0.562	0.281	0.406	0.667
Residuals	120	82.951	0.691		
Total	122	83.513			

This table is extremely familiar as we encountered it in Chapter 19. Just as before, the last entry in the table is the p-value. As with any p-value, it is computed by finding the likelihood of getting a standardized statistic as extreme or more than that observed when the null hypothesis is true. "More extreme" values of the statistic would be larger values; so, the area to the right in the null distribution is needed as highlighted in the previous section.

Let's consider the Organic Food Case Study data. Further, let's suppose that the data is consistent with all three classical ANOVA conditions. The results from the analysis (assuming the classical ANOVA model) comparing the average moral expectation score across the three food conditions are given in Table 28.1.

As long as the conditions on the error term are reasonable, then we can interpret the above p-value. Based on these results, there is no evidence that the moral expectations differ, on average, across the various food exposure groups. That is, there is no evidence of a relationship between the type of food to which we are exposed and our resulting moral expectations, on average.

The table is a way of summarizing the output from the analysis; the table itself is not very interesting, but we present it because it has the same emphasis we have in this unit — partitioning variability. The key to separating a signal from a noise is to partition the variability in the data. The total variability is partitioned into that resulting from the groups (the factor), this is the deterministic portion of the model that we can explain, and the error, the stochastic portion of the model that we cannot explain. By partitioning this variability, we are able to compute the standardized test statistic and the corresponding p-value. Practically, the only component we examine in such a table is the p-value. However, it is worth noting that the mean square error (MSE) also provides an estimate of the variance of the errors within a group, the residual variance. That is, the MSE provides an estimate of the variance in the response within a group (if we are willing to assume the variability of the errors is the same in each group).

The mean square for error (MSE) is a pooled estimate of the variability in the response within a particular group.

28.6 Simulating the Null Distribution

We note that this section is a bit more technical than other sections. This section seeks to give the reader a feel for the computational aspect of empirically modeling the null distribution. However, understanding conceptually that we are repeating the study in a world in which the null hypothesis is true is sufficient for interpreting a p-value.

Suppose we are willing to assume the data is consistent with the following two conditions:

- The error in the response for one observation is independent of the error in the resposne for all other observations.
- The errors in the response are identically distributed; specifically, the variability in the error of the response is the same within each group defined by the predictor.

Under these, we can empirically model the null distribution of our standardized statistic. The key here is to lean on our data generating process. Consider the Organic Food Case Study. *If the null hypothesis is true*, then we have that

$$\mu_{\text{organic}} = \mu_{\text{comfort}} = \mu_{\text{control}}$$

Let's define this common mean to be μ; we do not know what this value is, but it is common to all groups. Therefore, *if the null hypothesis is true*, we have that the data generating process reduces to

$$(\text{Moral Expectation Score})_i = \mu + \epsilon_i \tag{28.3}$$

We can generate data according to this model. We can replace μ by our best estimate — the sample mean response across all observations regardless of their group. It simply remains to determine how to approximate a random variable from the noise distribution. In order to do this, we need estimates of the errors — residuals. The key is to use the residuals obtained when we fit the *more complex model*:

$$(\text{Moral Expectation Score})_i = \mu_1(\text{Group})_{1,i} + \mu_2(\text{Group})_{2,i} + \mu_3(\text{Group})_{3,i} + \epsilon_i$$

Recall that a residual is the difference between the observed response and the predicted response. So, in this case, we have that the residual is given by

$$(\text{Residual})_i = (\text{Observed Moral Expectation Score})_i - (\text{Average moral expectation score for group to which i-th obser}$$

That is, the residual is the difference between the observed response and the sample mean response for the corresponding group to which the observation belongs. For example, consider the Organic Food Case Study; the data is reproduced in Figure 26.2. Based on the data available, if a subject were to be exposed to organic foods, we would expect their moral expectation score to be 5.66; this is the average observed among individuals randomized to this treatment within our study.

The key idea here is that residuals approximate the unseen error. If we randomly sample the residuals (with replacement), we are constructing a bootstrap sample of "errors" which can be used to form new responses. Specifically, a new dataset, generated under the null hypothesis, can then be constructed as

$$(\text{Bootstrap Response})_i^* = (\text{Overall Average Response}) + (\text{Sampled Residual})_i^*$$

Notice that each newly generated "bootstrap" response has the same mean (so that the null is true). We then take this new dataset and compute the standardized test statistic as before by fitting the complex model and partitioning the variability (due to the groups and the noise) and record it. Even though we know there should not be a difference among the groups (since we generated the data), we construct the analysis as if we were searching for such a difference. We repeat this process over and over again until we have constructed the null distribution. This gives us a sense of the p-value.

28.7 Recap

By partitioning the variability in the response, we are able to construct a standardized statistic for testing the hypothesis of interest. The model for the null distribution of this statistic depends upon the conditions we are willing to impose on the stochastic portion of the data generating process. Regardless of the conditions we impose, we can interpret the resulting p-value similarly. It provides an indication of whether the data suggests that the average response differs for at least one of the groups.

Of course, the interpretation of the p-value depends on the conditions we impose. We should not choose such conditions without performing some type of assessment to ensure those conditions are reasonable — that the data is consistent with the conditions. That is the focus of the next chapter.

Chapter 29

Assessing Modeling Conditions

In this unit we have discussed a model relating a quantitative response to a categorical predictor. For the Organic Food Case Study, our model had the form

$$(\text{Moral Expectation Score})_i = \mu_1(\text{Group})_{1,i} + \mu_2(\text{Group})_{2,i} + \mu_3(\text{Group})_{3,i} + \epsilon_i$$

where

$$(\text{Group})_{1,i} = \begin{cases} 1 & \text{if i-th subject exposed to organic foods} \\ 0 & \text{if i-th subject not exposed to organic foods} \end{cases}$$

$$(\text{Group})_{2,i} = \begin{cases} 1 & \text{if i-th subject exposed to comfort foods} \\ 0 & \text{if i-th subject not exposed to comfort foods} \end{cases}$$

$$(\text{Group})_{3,i} = \begin{cases} 1 & \text{if i-th subject exposed to control foods} \\ 0 & \text{if i-th subject not exposed to control foods} \end{cases}$$

Further, we considered three conditions on the distribution of the error term:

1. The error in the moral expectation score for one individual is independent of the error in the moral expectation score for all other individuals.

2. The variability in the error for the moral expectation score within a group is the same for any food exposure group.
3. The error in the moral expectation score follows a Normal distribution.

Unfortunately, we cannot just state that these are the conditions we hope hold for the data generating process and move on our merry way. Since the p-value was computed assuming these conditions hold, the p-value is only meaningful if the data is consistent with these conditions. Otherwise, the p-value is meaningless. Just as in Chapter 20, we use residuals to assess these conditions qualitatively.

29.1 Assessing Independence

> The error in the moral expectation score for one individual is independent of the error in the moral expectation score for all other individuals.

Generally, independence is assessed through the context of the data collection scheme. By carefully considering the manner in which the data was collected, we can typically determine whether it is reasonable that the errors in the response are independent of one another. Some key things to consider when examining the data collection process:

- Are there repeated observations made on the same subject? This often suggests some type of relationship between the responses and therefore would not be consistent with errors being independent.
- Is the response measured over time (time-series) such as daily temperature over the course of a month? Time-series data often exhibits strong period-to-period relationships suggesting the errors are not independent. For example, if it is hot today, it will probably be hot tomorrow as well.
- Is there a learning curve in how the data was collected? Learning curves again suggest some dependence from one observation to the next. For example, a new nurse may become better at collecting pulse readings with more practice over time.
- Measurement devices which are failing over time will introduce a dependence from one observation to the next. Imagine a bathroom scale that begins to add an additional pound each day. Then, being above average weight one day will most likely lead to an above average weight the next, due primarily to the measurement device. Generally, independence is assessed through the context of the data collection scheme. By carefully considering the manner in which the data was collected, we can typically determine whether it is reasonable that the errors in the response are independent of one another. Some key things to consider when examining the data collection process:
- Are there repeated observations made on the same subject (such as blocking)? This often suggests some type of relationship between the responses and therefore would not be consistent with errors being independent.
- Is the response measured over time (time-series) such as daily temperature over the course of a month? Time-series data often exhibits strong period-to-period relationships suggesting the errors are not independent. For example, if it is hot today, it will probably be hot tomorrow as well.

- Is there a learning curve in how the data was collected? Learning curves again suggest some dependence from one observation to the next.

These last three points illustrate a particular deviation from our condition of independence in which two observations collected close together in time are related. When we know the order in which the data was collected, we can assess whether the data tends to deviate from the condition of independence in this manner. This is done graphically through a time-series plot of the residuals. If two errors were unrelated, then the value of one residual should tell us nothing about the value of the next residual. Therefore, a plot of the residuals over time should look like noise (since residuals are supposed to be estimates of noise). If there are any trends, then it suggests the data is not consistent with independence. Of course, to construct such a plot, we need to know the order in which the data was collected.

For the Organic Food Case Study, participants were assessed simultaneously within a large lecture. Therefore, there is no ordering in time to be concerned about. Therefore, a time-series plot of the residuals would not be useful here. Considering the context, students worked individually on the questionnaire; this suggests it is reasonable to assume that the errors in the moral expectation score are unrelated to one another.

29.2 Assessing Homoskedasticity

We want the variability in the errors within a group to be the same across the groups. We can do this by examining side-by-side boxplots (or jitter plots, etc.) of the residuals within each of the groups. Figure 29.1 shows the residuals for each individual across the various groups. Notice that the boxes for each group are roughly the same size; that is, the interquartile ranges are similar. This suggests that the variability within each group is similar from one group to the next. That is, the data is consistent with this condition.

There is another (equivalent) approach to assessing this condition. If the variability in the errors for each response is the same, then the variability of the response must be the same for each group. Therefore, we can also examine the side-by-side boxplots (or jitter plots, etc.) of the response instead of the residuals. Figure 29.2 shows the moral expectation score for each individual across the various groups. Just as in the previous graphic, the interquartile ranges are similar for each of the three groups indicating the data is consistent with this condition.

29.3 Assessing Normality

Just as in Chapter 20, we emphasize the probability plot as a method for assessing whether data is consistent with being drawn from a Normal distribution.

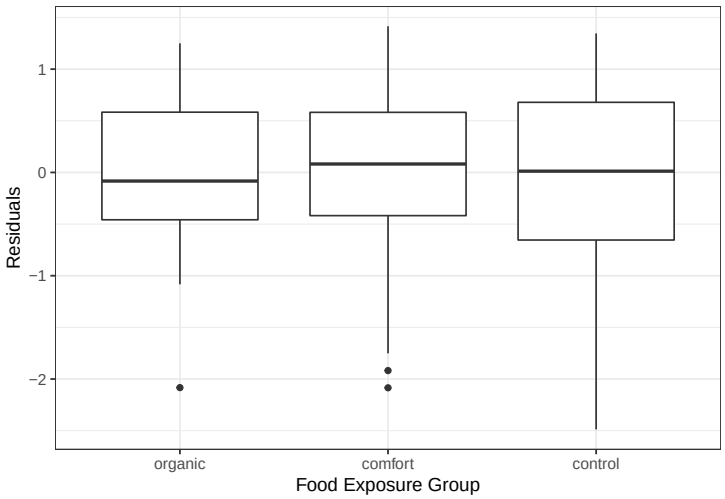


Figure 29.1: Comparison of the residuals predicting the moral expectation score for college students exposed to different types of food.

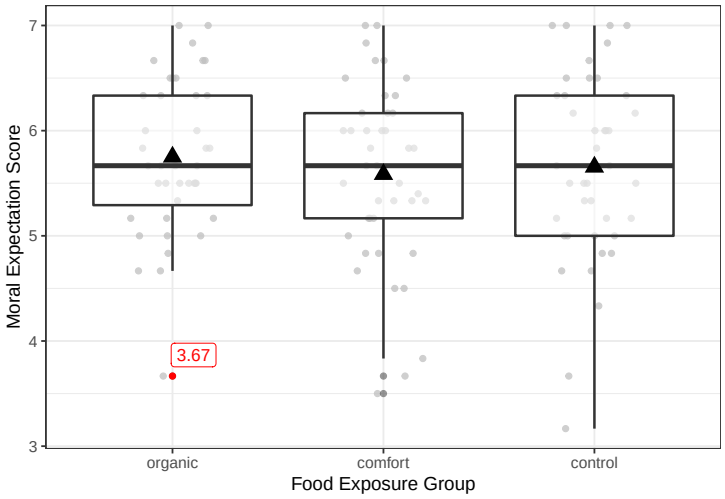


Figure 29.2: Comparison of the moral expectations for college students exposed to different types of food.

Figure 29.3 shows the probability plot for the residuals from the Organic Food Case Study.

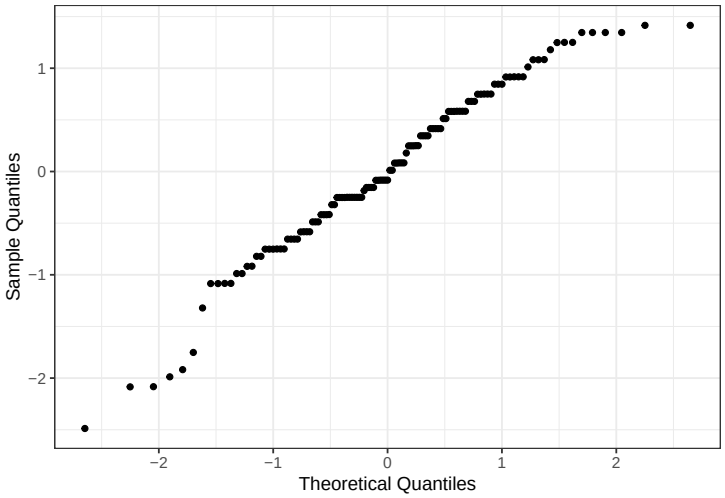


Figure 29.3: Probability plot of the residuals for the Organic Food Case Study. If the errors follow a Normal distribution, we would expect the residuals to fall along a straight line.

Overall, the points do tend to follow a straight line. There are some deviations from a linear relationship at each end of the plot, but the deviations are not extreme. Deviations in the tails are common, especially with larger datasets. And with naturally less data in the tails, it can become more difficult to establish a pattern. We are generally not concerned unless these tails form a part of a larger pattern of deviating from the linear trend. We argue that these residuals are consistent with the errors having a Normal distribution.

29.4 General Tips for Assessing Assumptions

As in Chapter 20, we want to point out three things that should be kept in mind when assessing these conditions:

1. We can never prove a condition is satisfied; we can only determine whether the data is consistent with a condition or whether it is not consistent with a condition.
2. The analysis has specific conditions placed on the error term; we choose whether to assume such a condition is reasonable by examining residuals.
3. A sample should always be consistent with the conditions you are relying on to interpret a p-value or confidence interval.

Chapter 30

Using the Tools Together

This unit introduced a framework for determining if there is an association between a quantitative response and a categorical predictor. We formed a standardized statistic for measuring the signal, and developed a model for the data-generating process which allowed us to model the null distribution of the standardized statistic. In this chapter, we pull these tools together once more to answer a research question.

The primary question we have been addressing in this unit was whether the moral expectations of students were affected by the type of food to which they were exposed. We saw that there was little evidence of a relationship between these two variables. We now use the data from the Organic Food Case Study to answer a related question:

> Do the moral expectations of males and females differ?

30.1 Framing the Question (Fundamental Idea I)

As stated, the above question is ill-posed. We have not identified a variable or parameter of interest. We refine this question to be

> Does the average moral expectation score of males differ from that of females?

This question could also be stated as the following set of hypotheses:

> Let μ_1 and μ_2 represent the average moral expectation score for males and females, respectively.
> $H_0 : \mu_1 = \mu_2$
> $H_1 : \mu_1 \neq \mu_2$

30.2 Getting Good Data (Fundamental Idea II)

As we are working with previously collected data, our goal in this discussion is not how best to collect the data but making note of the limitations of the data as a result of how it was collected. We previously described the Organic Food Case Study as an example of a controlled experiment. This was true... with regard to the primary question of interest (moral expectations and food exposure). However, the subjects were *not* randomly assigned to gender here; therefore, with regard to this question of interest, the data was an observational study.

It is common for young researchers to believe that if initially a controlled experiment was performed that the data always permits a causal interpretation. However, we must always examine the data collection with respect to the question of interest. Such "secondary analyses" (using data collected from a study to answer a question for which the data was not initially collected) are generally observational studies. As a result, there may be other factors related to gender and moral expectations that drive any results we may see.

30.3 Presenting the Data (Fundamental Idea III)

Our question here is examining the relationship between a quantitative response (moral expectation score) and a categorical predictor (gender). Figure 30.1 compares the distribution of the moral expectation score for the two groups. Note that 3 students did not specify their gender; these subjects will be removed from the analysis.

Based on the above graphic, it appears the females tend to have higher moral expectations by about 1 point, compared to males. We also observe that there are many more females in our sample compared to males, which is probably a result of the type of class and the demographic makeup of the university at which the study was conducted.

30.4 Quantifying the Variability in the Estimate (Fundamental Idea IV)

In order to measure the size of the signal, we can compute the standardized statistic

$$T = \frac{MSTrt}{MSE}$$

which is 6.52 for the sample we have observed. Of course, if we were to collect a new sample, we would expect this value to change. If we want to quantify the variability in this statistic, we need a model for its sampling distribution. More, what we are really interested in is the sampling distribution of this statistic if

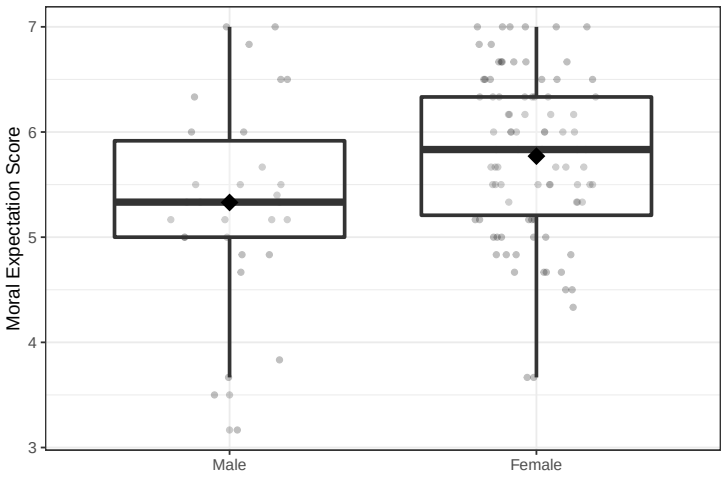


Figure 30.1: Comparison of the moral expectations of males and females. The average value is added for each group. Students who did not specify their gender were removed from the analysis.

the average moral expectation score were the same for the two genders; that is, we are interested in the null distribution of this standardized statistic. With the null distribution, we could ascertain how unlikely our sample is to occur by chance alone (allowing us to quantify the strength of evidence in the data).

In order to model the null distribution, we consider the following model for the data-generating process:

$$(\text{Moral Expectation Score})_i = \mu_1(\text{Male})_i + \mu_2(\text{Female})_i + \epsilon_i \tag{30.1}$$

where

$$(\text{Male})_i = \begin{cases} 1 & \text{if i-th subject is male} \\ 0 & \text{if i-th subject is female} \end{cases}$$

$$(\text{Female})_i = \begin{cases} 1 & \text{if i-th subject is female} \\ 0 & \text{if i-th subject is male} \end{cases}$$

and we impose the following conditions on the error term:

1. The error in the moral expectation score for one individual is independent of the error in the moral expectation score for any other individual.
2. The variance of the error in the moral expectation scores for males is the same as the variance of the error in moral expectation scores for females.

3. The error in the moral expectation score for individuals follows a Normal Distribution.

Under these three assumptions, we are able to construct a model for the null distribution of the standardized statistic. Figure 30.2 illustrates the null distribution assuming these conditions are satisfied.

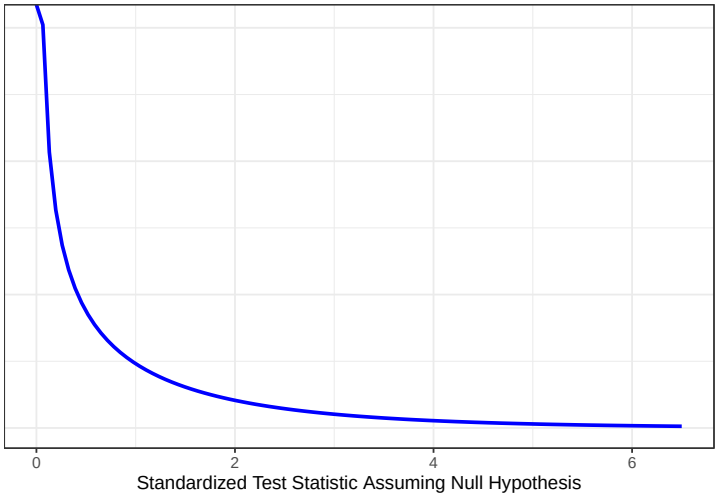


Figure 30.2: Model for the standardized test statistic measuring the signal comparing the moral expectation scores for males and females in the Organic Food Case Study. This model is constructed assuming the classical ANOVA conditions are satisfied.

Before we can use this model to make any conclusions regarding our question of interest, we need to address the fact that we have assumed certain conditions are satisfied. We need to assess whether the data is consistent with these assumptions. This requires examining the residuals for the model.

First, we discuss the assumption of independence. Since the data was collected at a single point in time, known as a *cross-sectional study*, constructing a time-series plot of the residuals would not provide any information regarding this assumption. Instead, we rely on the context of the problem to make some statements regarding whether the data is consistent with this condition (whether making this assumption is reasonable). It is reasonable that the errors are independent. One case in which this might be violated is if students discussed their answers to the questions as they filled out the survey; then, it is plausible that one student influenced another's responses. As this is unlikely given the description of the data collection, we feel it is reasonable to assume independence.

Again, note that there is a condition of independence; we are simply saying whether we are willing to assume the condition is satisfied. There is no way to ensure the condition holds.

In order to assess the condition of constant variance, let us look back at the box plots given in Figure 30.1. As the spread of the moral expectation score for each of the two genders is roughly the same, it is reasonable to assume the variability of the errors in each group is the same.

Finally, to assess the condition that the distribution of the errors is Normal, we consider a probability plot of the residuals (Figure 30.3). Given that the residuals tend to display a linear relationship, it is reasonable that the residuals represent a sample from a Normal Distribution. That is, it is reasonable that the errors follow a Normal Distribution.

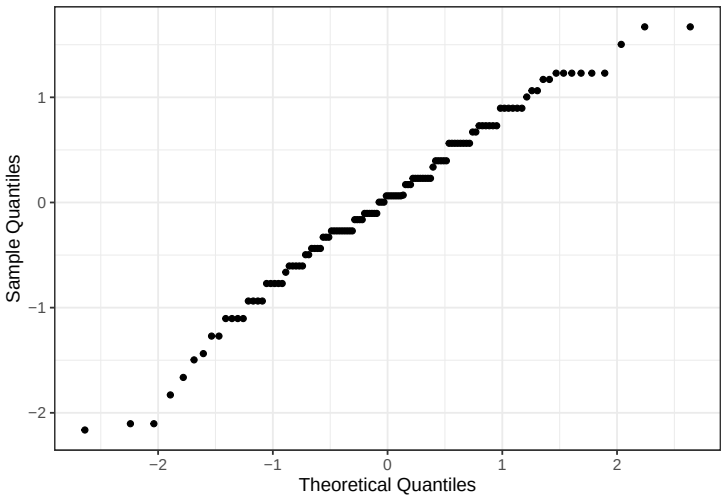


Figure 30.3: Probability plot assessing the assumption that the errors for our model comparing the moral expectation score across gender follow a Normal Distribution.

Given that we are comfortable assuming the conditions on the error term are reasonable, we can make use of the analytical model for the null distribution in Figure 30.2.

30.5 Quantifying the Evidence (Fundamental Idea V)

Now that we have a model for the null distribution, we can determine how extreme our particular sample was by comparing the standardized statistic for our sample with this null distribution. We can measure this through computation of a p-value, the probability that we would observe a standardized statistic of this magnitude or higher by chance alone if there were no difference in the mean moral expecation scores of males and females. This is summarized in Table 30.1 below.

Table 30.1: ANOVA table summarizing the comparison of the moral expectation score across gender within the Organic Food Case Study.

Source	DF	SS	MS	F	P-value
Gender	1	4.363	4.363	6.517	0.012
Residuals	118	79.008	0.670		
Total	119	83.372			

From the results, we can conclude that there is evidence ($p = 0.012$) of a relationship between the moral expectations of a student and their gender. Looking back at Figure 30.1, females tend to have higher moral expectations on average.

30.6 Conclusion

Throughout this unit, we have examined a framework for examining the association between a quantitative response and a categorical predictor. This reinforces a couple of big ideas we have seen throughout this text:

- The key to measuring a signal is to partition the variability in the response.
- A standardized statistic is a numeric measure of the signal strength in the sample.
- Modeling the data-generating process provides us a way of modeling the sampling distribution of the parameter estimates and the null distribution of a standardized statistic.
- Conditions are often placed on the noise portion of the model for the data-generating process; before assuming these conditions are met, we should graphically assess whether the data is consistent with these conditions.

Part V

Unit V: Comparing the Average Response Across Correlated Groups

Chapter 31

Case Study: Paying a Premium for the Experience

Around 2010 Americans were in love with frozen yogurt. Self-serve frozen yogurt shops were popping up in towns across the country. By 2016, the craze had begun to subside.[1] What happened to this once booming industry? One possibility is that consumers began to believe that they were paying a premium for the experience; that is, consumers were paying an increased price to purchase a product in a self-serve shop that could be purchased for much less at a local grocery store. Under this theory, the increased price point reflected the experience of eating at the yogurt shop, not an improvement in the quality of the product purchased. While we cannot fully determine why self-serve shops began to disappear, we can assess whether consumers identify a difference in the quality of yogurt from self-serve shops compared with their local grocier.

A group of college students taking a Practice of Science class at a small university conducted a study in which nine consumers were given a cup of vanilla yogurt from each of three different locations:

- East-Side Yogurt: a local frozen yogurt self-serve shop on the east side of town.
- South-Side Yogurt: a local frozen yogurt self-serve shop on the south side of town.
- Name Brand: frozen yogurt from a name-brand regional dairy available at local grociers.

[1] https://www.washingtonpost.com/business/economy/baked-goods-coffee-and-cash-rise-from-the-ashes-of-the-frozen-yogurt-craze/2015/12/05/3c1e7d72-99fd-11e5-b499-76cbec161973_story.html?noredirect=on&utm_term=.5012f2fabf08

The order in which each participant tasted the yogurt was determined randomly. Each cup was labeled A, B or C to prevent participants from knowing which location each cup represented. The participants were asked to rate the taste, the texture, and the appearance of each cup on a 10-point scale (higher values representing a more appetizing score).

The full dataset is presented below.

Table 31.1: Subset of data from blind taste test comparing the qualities of frozen yogurt across three vendors.

Participant ID	Taste Rating	Texture Rating	Appearance Rating	Type
1	5	7	8	Name Brand
1	7	7	8	South Side Yogurt
1	8	7	8	East Side Yogurt
2	8	5	8	Name Brand
2	6	7	9	South Side Yogurt
2	9	8	10	East Side Yogurt
3	8	6	6	Name Brand
3	6	9	9	South Side Yogurt
3	9	5	8	East Side Yogurt
4	8	7	8	Name Brand
4	6	7	8	South Side Yogurt
4	9	9	8	East Side Yogurt
5	8	5	5	Name Brand
5	4	7	8	South Side Yogurt
5	9	9	8	East Side Yogurt
6	4	5	8	Name Brand
6	8	9	8	South Side Yogurt
6	2	7	6	East Side Yogurt
7	9	7	9	Name Brand
7	9	8	9	South Side Yogurt
7	10	10	5	East Side Yogurt
8	5	2	6	Name Brand
8	8	7	7	South Side Yogurt
8	7	8	7	East Side Yogurt
9	8	3	8	Name Brand
9	4	8	7	South Side Yogurt
9	2	8	7	East Side Yogurt

Chapter 32

Framing the Question

"Are vendors of yogurt rated differently based on taste?" As in the previous two units, the primary question in the Frozen Yogurt Case Study is about the relationship between two variables: the response (taste of product on scale of 1 to 10; see Definition 3.2) and the factor of interest (vendor of yogurt; see Definition 24.1).

The question we have posed, as stated above, is ill-posed. Instead of asking about individual tastes, we want to know if, on average, there is a difference in the taste of yogurt between vendors. That is, we want to test the following hypotheses:

> H_0 : the average taste rating is the same for each of the three vendors.
> H_1 : the average taste rating differs for at least one of the three vendors.

Mathematically, we write

> $H_0 : \mu_{\text{East-Side}} = \mu_{\text{South-Side}} = \mu_{\text{Name-Brand}}$
> H_1 : At least one μ differs from the others

where each μ represents the average taste rating for yogurt from the corresponding vendor. Our question is now centered on the population and captured through parameters, making it a well-posed question. In fact, this seems to be a question we have already addressed. In a way, it is.

In this unit, we will be tackling the same types of questions we did in Unit IV — we are comparing the mean of a quantitative response across the levels of a categorical predictor. The difference is that the observations we have observed are not independent of one another, and we must account for this lack of independence in the analysis.

32.1 General Setting

This unit is concerned with comparing the mean response of a numeric variable across k groups. Let $\mu_1, \mu_2, \ldots, \mu_k$ represent the mean response for each of the k groups. Then, we are primarily interested in the following hypotheses:

$H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$
$H_1 :$ At least one μ differs from the others

When there are only two groups ($k = 2$), then this can be written as

$H_0 : \mu_1 = \mu_2$
$H_1 : \mu_1 \neq \mu_2$

Here we are writing things in the mathematical notation, but let's not forget that every hypothesis has a context. Throughout this unit, we are looking for some signal in the *location* of the response across the groups. Our working assumption then states that the groups are all similar, *on average*.

Chapter 33

Correlated Data

Chapter 25 discussed three aspects of a well-designed study: replication, randomization, and comparative groups. Of particular interest for us in this unit is the concept of blocking for creating groups which are as similar as possible to reduce external variability. Restating Definition 25.5:

> Blocking is one way of minimizing variability contributed by an inherent characteristic. All observations that are linked through the characteristic are grouped together and random allocation (if applicable) occurs *within* the block.

A block is formed by subjects which have some underlying commonality. An extreme case occurs when you repeatedly measure the response on the same subject under different treatment conditions. This is exactly what happened in the Frozen Yogurt Case Study. Each subject was measured three times, once under each of the conditions. In order to really comprehend the effect of this, consider an alternative study design:

> Take each of the nine subjects and randomly assign each to one of the three yogurt vendors (3 subjects to each yogurt vendor). Each subject rates the yogurt assigned.

This alternative study design is completely valid and feasible, but there seems an intuitive advantage to having each subject rate not just one yogurt, but instead rate all the yogurts being tested. This is indeed the case; by making the subjects taste each of the three vendor yogurts, then the three groups are as similar as possible (the same group exposed to each of the three treatments). This increases the power of the study (given the same number of subjects), but it also has an effect on the analysis we conduct.

Suppose one of the subjects in the study does not really enjoy frozen yogurt (more of an ice cream fan); then, their ratings on the taste will tend to be lower than other subjects *for each of the vendors*. Similarly, a huge frozen yogurt fan

will tend to have taste ratings which are higher than other subjects for each of the vendors. If you are told the taste rating for the name-brand vendor given by the subject who does not really enjoy frozen yogurt, you have a pretty good guess of what their rating will be on the other vendors. There is a *correlation* between their responses across the factor levels; that is, the responses are not independent of one another. This relationship is what provides power in the study, but it is also what needs to be accounted for in our analysis.

In the Frozen Yogurt Case Study, the order in which the yogurt from each vendor was given to a subject was randomized. That is, the randomization did not occur at the subject-level but within the subject. When randomization occurs within the block, the study is referred to as a **randomized complete block design**.

Definition 33.1 (Randomized Complete Block Design)**:**
A controlled experiment utilizing blocking. Each treatment is randomized to units within blocks in such a way that every treatment is present within the block and the same number of units are assigned to each treatment.

Block designs need not be from controlled experiments. For example, pre-post tests are an example of a block design in which each subject is tested prior to and following some intervention. The subjects act as the blocks; however, the "treatment" groups (pre and post) are not randomized. This would be an example of an observational study with blocks.

The Frozen Yogurt Case Study is a common example in which the blocks are formed by taking repeated measurements on the subjects. Blocked designs can extend further. Example **??** illustrates that this need not be the case. In that example, the blocks were composed of separate units (golf greens) which had a similar characteristic (slope of green) which created the block.

Chapter 34

Presenting Correlated Data

Consider the graphical summary in Figure 34.1 of the data from the Frozen Yogurt Case Study.

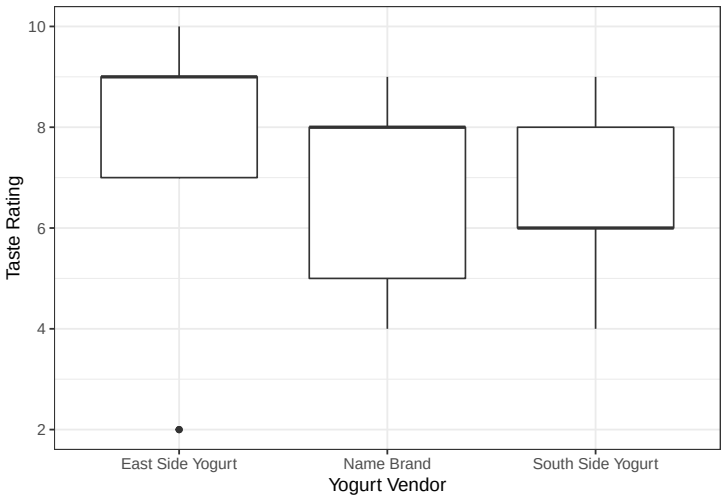


Figure 34.1: Illustration of a poor graphic summarizing correlated data; the graphic hides the fact that there were repeated measures on the subject. It is not clear that the responses are in any way correlated.

Summarizing correlated data can be quite difficult. If there are only a few blocks, indicating the various blocks with color can be helpful. Figure 34.2 uses color to distinuish responses from the same subject.

Even with only nine blocks, it can be difficult to distinguish one subject's response from another in Figure 34.2. Another technique is to connect the responses from

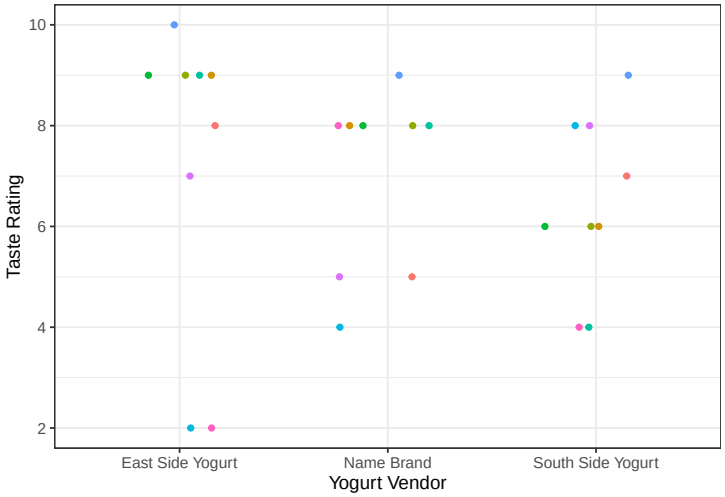


Figure 34.2: Results from a blind taste test comparing how subjects rated the taste of yogurt from three different vendors. Ratings from the same subject are displayed using the same color.

a single subject; this is illustrated in Figure 34.3. This plot is disappointing due to the number of subjects who rated a yogurt similarly (more than one 9 rating was received for the name brand vendor as an example).

There is no universally adopted gold standard for summarizing correlated data. The key here is that the correlation in the data should not be ignored and should be illustrated in the summary while still addressing the primary question of interest.

A good graphic should aid in partitioning the variability; with correlated responses, this includes indicating values which are related so that we can visually assess the variability between independent groups and within related groups.

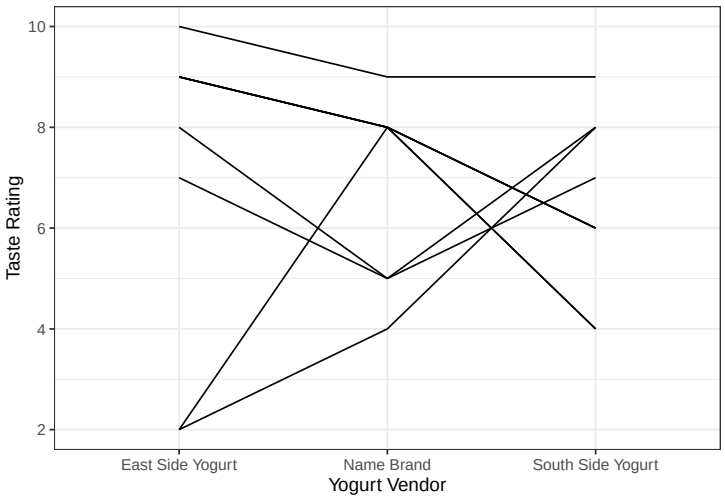


Figure 34.3: Results from a blind taste test comparing how subjects rated the taste of yogurt from three different vendors. Ratings from the same subject are connected.

Chapter 35

Analyzing Correlated Responses

Our question of interest in this unit is the same as that in our previous unit:

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_k \qquad \text{vs.} \qquad H_1 : \text{At least one } \mu_j \text{ differs}$$

It seems reasonable to begin with the model for describing a quantitative response as a function of a categorical predictor described in Chapter 27. In this chapter, we extend this model to account for the correlation between responses.

35.1 Statistical Model for Correlated Responses

For the Frozen Yogurt Case Study, we are comparing the average taste rating for different vendors. In the previous unit, we would have constructed the following model for the data generating process:

$$(\text{Taste Rating})_i = \mu_1(\text{East Side})_i + \mu_2(\text{South Side})_i + \mu_3(\text{Name Brand})_i + \epsilon_i$$

where

$$(\text{East Side})_i = \begin{cases} 1 & \text{if i-th rating associated with east side yogurt vendor} \\ 0 & \text{if i-th rating not associated with east side yogurt vendor} \end{cases}$$

$$(\text{South Side})_i = \begin{cases} 1 & \text{if i-th rating associated with south side yogurt vendor} \\ 0 & \text{if i-th rating not associated with south side yogurt vendor} \end{cases}$$

$$(\text{Name Brand})_i = \begin{cases} 1 & \text{if i-th rating associated with name brand yogurt vendor} \\ 0 & \text{if i-th rating not associated with name brand yogurt vendor} \end{cases}$$

are indicator variables to capture the various factor levels. In order to use this model, the first condition we imposed on the error term was that the error in the rating for one observation is independent of the error in the rating for all other observations. However, for the Frozen Yogurt Case Study, we know this condition is violated. If the errors were independent of one another, it would imply the responses are independent of one another. But, since each subject rated each of the three vendors, the ratings from the same subject are related.

It should not come as a surprise that the way to address this complication is to *partition the variability* in the response further. Essentially, we know of another reason that the responses vary in the way that they do: observations from the same subject should be related. We want to tease this apart, and that is done by adding additional terms into the model for the data generating process.

Consider the following model:

$$\begin{aligned} (\text{Taste Rating})_i = \mu_1(\text{East Side})_i + \mu_2(\text{South Side})_i + \mu_3(\text{Name Brand})_i \\ + \beta_2(\text{Subject 2})_i + \beta_3(\text{Subject 3})_i + \beta_4(\text{Subject 4})_i \\ + \beta_5(\text{Subject 5})_i + \beta_6(\text{Subject 6})_i + \beta_7(\text{Subject 7})_i \\ + \beta_8(\text{Subject 8})_i + \beta_9(\text{Subject 9})_i + \epsilon_i \end{aligned}$$

where

$$(\text{Subject j})_i = \begin{cases} 1 & \text{i-th observation taken from Subject j} \\ 0 & \text{i-th observation not taken from subject j} \end{cases}$$

is an indicator of whether the observation comes from a particular subject. It may at first appear as if we forgot the indicator for Subject 1; it is not needed. Just as with any model, it is often easiest to see what is happening by thinking about the form of the model under specific cases. How do we describe observations (remember there is more than one) for Subject 2? Subject 2 adheres to the following model:

$$(\text{Taste Rating})_i = \mu_1(\text{East Side})_i + \mu_2(\text{South Side})_i + \mu_3(\text{Name Brand})_i + \beta_2 + \epsilon_i$$

We could do something similar for each of Subjects 3 through 9. What about Subject 1? Well, Subject 1 would not be Subject 2 or 3, etc. So, the indicator variable $(\text{Subject } 2)_i$ for observations corresponding to Subject 1 would be 0; as would the indicators $(\text{Subject } 3)_i$, $(\text{Subject } 4)_i$, etc. That is, Subject 1 adheres to the following model:

$$(\text{Taste Rating})_i = \mu_1(\text{East Side})_i + \mu_2(\text{South Side})_i + \mu_3(\text{Name Brand})_i + \epsilon_i$$

This affects how we interpret our parameters. In our model μ_1 is no longer the average rating given to East Side Yogurt; it is the average rating given to East Side Yogurt *by Subject 1*. It is the same concept as the "reference group" (see Definition 17.3) discussed in the regression unit.

If there are b blocks, we need only include $b - 1$ indicator variables and corresponding parameters to capture all the blocks. The remaining block is the "refernece group" and is captured by the parameters comparing the factor levels under study.

This may seem like it affects our questions of interest. After all, the hypothesis

$$H_0 : \mu_1 = \mu_2 = \mu_3$$

says that the "average taste rating for Subject 1 is the same for all vendors" instead of the "average taste rating across all subjects is the same for all vendors." The latter is the hypothesis we want to test, but we have the parameters specified in terms of the first subject only. Notice, however, that subjects differ only by a constant (the β's). Therefore, if the mean response for one subject is the same for all vendors, then it must be that the mean response across vendors is the same for all subjects, addressing our question of interest.

To formalize this mathematically, consider a case in which there are two groups and two blocks. Then, we have a model of the form

$$(\text{Response})_i = \mu_1(\text{Group 1})_i + \mu_2(\text{Group 2})_i + \beta_2(\text{Block 2})_i + \epsilon_i$$

Suppose we want the mean response across all blocks. Then, that would be

$$(1/2)(\text{Mean from Block 1}) + (1/2)(\text{Mean from Block 2})$$

But, we can write this in terms of the parameters above.

$$(\text{Mean for Group 1}) = (1/2)(\mu_1) + (1/2)(\mu_1 + \beta_2)$$
$$(\text{Mean for Group 2}) = (1/2)(\mu_2) + (1/2)(\mu_2 + \beta_2)$$

If the mean response for each group is the same, then

$$\mu_1 + (1/2)\beta_2 = \mu_2 + (1/2)\beta_2$$

But, this is only true if $\mu_1 = \mu_2$. So, testing that the mean response is the same in the first block is equivalent to testing if the mean response is the same for all blocks.

This model essentially says there are three reasons that the taste ratings differ from one observation to another:

- Ratings applied to different vendors differ.
- Ratings from different subjects differ.
- Unexplained differences due to inherent variability.

In general, this type of model, often described as a "Repeated Measures ANOVA" model, partitions the variability in the response into three general categories: differences between groups, differences between blocks, differences within blocks.

In general, given a quantitative response variable, our model for the data generating process comparing this variable across k levels of a factor in the presence of b blocks is

$$(\text{Response})_i = \sum_{j=1}^{k} \mu_j (\text{Group})_{j,i} + \sum_{m=2}^{b} \beta_m (\text{Block})_{m,i} + \epsilon_i$$

where

$$(\text{Group})_{j,i} = \begin{cases} 1 & \text{if i-th observation belongs to group j} \\ 0 & \text{if i-th observation does not belong to group j} \end{cases}$$

$$(\text{Block})_{m,i} = \begin{cases} 1 & \text{if i-th observation belongs to block m} \\ 0 & \text{if i-th observation does not belong to block m} \end{cases}$$

are indicators capturing the factor grouping and blocks. This is often referred to as a "Repeated Measures ANOVA" model.

In the past, the stochastic portion of the model ϵ_i captured the subject-to-subject variability. It no longer has the same role in this case. It now captures the variability in repeated measures on the same subject. That is, it captures the fact that if we repeatedly taste the same yogurt, we might rate it differently each time because of our mood or some other external factor that we have not captured. The subject-to-subject variability is captured by the β parameters in the model.

In a model without repeated measures (blocks), the error term captures the subject-to-subject variability. In a model with repeated measures, the error term captures the variability between observations on the same subject.

There is something else that is unique about the repeated measures ANOVA model. We do not really care about all the parameters in the model. Our question of interest is based on the parameters μ_1, μ_2, μ_3. We would never be interested in testing something of the form

$$H_0 : \beta_2 = \beta_3 \qquad \text{vs.} \qquad H_1 : \beta_2 \neq \beta_3$$

as this would be comparing Subject 2 to Subject 3. Such a comparison would not be useful because it does not help researchers to know that two different

subjects have different preferences for yogurt taste. Said another way, we did not put the parameters $\beta_2, \ldots, \beta_9$ into the model because they helped us address a particular question. Instead, we put them in the model because they captured the observed relationship in the responses. This is the difference between **fixed effects** and **random effects**.

Definition 35.1 (Fixed Effect)**:**
A predictor in the model for which we are interested in specific values observed and the relationship it has with the response. It is generally part of our question of interest.

Definition 35.2 (Random Effect)**:**
A predictor in the model used to capture the correlation induced due to an inherent characteristic that varies across the population. We are generally not interested in specific values observed but see these as a random sample from some underlying population of possibilities.

While the theory underlying the analysis of such models makes use of more technical definitions of these terms, these are sufficient for our purposes in the text and understanding the role of these two types of terms. Notice that if we were to repeat the study, we would use the same three vendors, since they are a fundamental part of the question. However, we would not need to use the same subjects in the sample; we would be satisfied with any random sample from the population. So, the values "East Side Yogurt," "South Side Yogurt," and "Name Brand" (at least, the three vendors these represent) are of specific interest. However, we do not care about "Subject 2" and "Subject 3." These can be any two individuals from the population. Therefore, for the Frozen Yogurt Case Study, the vendor is the fixed effect, while subject is the random effect.

We are rarely interested in comparing one block to another. The effect for the block is placed in the model in order to account for the correlation between responses; the block effect is then generally a random effect.

Just as before, we need to distinguish between the model for the data generating process and the model for the sampling distribution of the parameter estimates or the null distribution for a standardized statistic. While we need the latter for inference, the model for the data generating process is a necessary stepping stone along the way.

The parameters in this model are of course unknown. They can be estimated using the method of least squares. However, these estimates, as with any estimate,

have variability associated with them. In order to make inference, we must determine a suitable model for the sampling distribution (or null distribution if appropriate). This is done by placing conditions on the stochastic portion of the model.

35.2 Conditions on the Error Distribution

In our model for the data-generating process we incorporated a component ϵ to capture the noise within each block. Since the error is a random variable (stochastic element), we know it has a distribution. We typically assume a certain structure to this distribution. The more assumptions we are willing to make, the easier the analysis, but the less likely our model is to be applicable to the actual data-generating process we have observed. The conditions we make dictate how we conduct inference (the computation of a p-value or confidence interval).

The first condition we consider is that the noise attributed to one observed response for an individual is independent of the noise attributed to the observed response for any other individual. This may seem counter-intuitive; this entire unit exists because we felt there was a correlation among the responses. However, this condition is stating that once we account for the correlation induced by the blocks by incorporating the random effect into the model, the remaining noise is now independent. We essentially partitioned out the correlated component, and what remains is now just independent noise.

The second condition that is typically placed on the distribution of the errors is that the errors are identically distributed. Again, we introduced this condition in Chapters 10 and 18. In particular, if the errors are not identically distributed, it is typically because the variability of the error differs for one value of the predictors compared to another. Practically, this reveals itself as our response being more precise for some collection of the predictors. As a result of focusing on the variability of the response for each predictor, this condition is often referred to as *homoskedasticity* instead of the errors being identically distributed.

The third condition we might consider imposing is that the errors in the response follow a Normal distribution, as discussed in Chapter 18. If this condition holds, it implies that within block, the distribution of the response for a particular group is itself is Normally distributed. While this was a bit easier to visualize in the ANOVA model, it becomes difficult to visualize here. That is because we are talking about the taste ratings for the Name Brand yogurt made by Subject 1 following a Normal distribution; however, we only observed a single response from Subject 1 related to the Name Brand. This is similar to when we placed conditions on the general regression model.

As in regression modeling, we are not required to impose all three conditions in order to obtain a model for the sampling distribution. Historically, however, all three conditions are imposed.

35.3 Conditions on the Random Effects

The random effects we placed in the model partitioned the original error term further; the random effects capture the correlation while the remaining portion captures the noise in the block. This means that in addition to conditions on the error term, we must also place conditions on the random effects, since they represent a random sample from a population. That is, the random effects also have a distribution which must be constrained.

The easiest way to think about the random effects is the "bump" attributed to that block. Again, think about a person who just is not a fan of frozen yogurt. Then, regardless of which vendor their yogurt comes from, their taste rating will tend to "bump" down compared to others. The first condition we impose is that this "bump" is the same for all observations from this individual. That is, their taste for frozen yogurt does not shift during the study. More generally, we are saying that the random effect associated with a particular block is always the same.

The second condition we consider is that the bump for one subject has nothing to do with the bump for any other subject. Practically, my taste for frozen yogurt is unaffected by anyone else's taste for frozen yogurt. This can be accomplished in the study by ensuring that each person is alone when they do their taste ratings so that they are not influenced by others' reactions. More generally, the random effect for one block is independent of the random effect for any other block.

It is generally assumed the random effects follow a Normal distribution and that they are also independent of the error.

35.4 Classical Repeated Measures ANOVA Model

In the preceeding sections, we discussed conditions we could place on the stocastic portions of the data generating process. Placing all conditions on the error term and random effects is what we refer to as the "Classical Repeated Measures ANOVA Model."

Definition 35.3 (Classical Repeated Measures ANOVA Model)**:**
For a quantitative response and categorical variable with k groups observed each in b blocks, the classical Repeated Measures ANOVA model assumes the following data-generating process:

$$(Response)_i = \sum_{j=1}^{k} \mu_j (Group)_{j,i} + \sum_{m=2}^{b} \beta_m (Block)_{m,i} + \epsilon_i$$

where

$$(Group)_{j,i} = \begin{cases} 1 & \text{if i-th observation belongs to group j} \\ 0 & \text{if i-th observation does not belong to group j} \end{cases}$$

$$(Block)_{m,i} = \begin{cases} 1 & \text{if i-th observation belongs to block m} \\ 0 & \text{if i-th observation does not belong to block m} \end{cases}$$

are indicators capturing the factor grouping and blocks, and

1. *The errors are independent of one another.*
2. *The errors are identically distributed.*
3. *The errors follow a Normal Distribution.*
4. *The random effects are identical for all observations within a block.*
5. *The random effects are independent of one another.*
6. *The random effects are independent of the errors.*
7. *The random effects follow a Normal Distribution.*

It is possible to relax these assumptions; however, this is what is commonly implemented in practice.

35.5 Recap

We have covered a lot of ground in this chapter, and it is worth taking a moment to summarize the big ideas. In order compare the mean response in each group, needed to account for the correlation induced by the blocks when developing the model for the data generating process. Such a model further partitions the error term in the model into a random effect which captures the variability across the blocks and the remaining noise captures the variability within a block.

Certain conditions are placed on the distributions of these stochastic portions. Depending on the set of conditions we impose will determine whether we develop an analytical model or an empirical model for the parameters in the model. We still need to discuss how we compare the mean response of the groups based on this model.

Chapter 36

Quantifying the Evidence

Recall that at its heart, hypothesis testing is about comparing two models:

- A more complex model for the data generating process which does not place any constraints on the parameters and
- A simpler model for the data generating process which places some constraints on the parameters.

We have seen throughout the text that the key to hypothesis testing is to partition the variability in the response. By doing so, we have been able to form a standardized statistic which measures the degree to which the data departs from what we could expect under the simpler model (therefore favoring more complexity). In this chapter, we present the general framework for making such comparisons which we alluded to in Chapters 12 and 21.

36.1 Partitioning Variability

Consider our model for the Frozen Yogurt Case Study:

$$\begin{aligned}(\text{Taste Rating})_i = \mu_1(\text{East Side})_i + \mu_2(\text{South Side})_i + \mu_3(\text{Name Brand})_i \\ + \beta_2(\text{Subject 2})_i + \beta_3(\text{Subject 3})_i + \beta_4(\text{Subject 4})_i \\ + \beta_5(\text{Subject 5})_i + \beta_6(\text{Subject 6})_i + \beta_7(\text{Subject 7})_i \\ + \beta_8(\text{Subject 8})_i + \beta_9(\text{Subject 9})_i + \epsilon_i\end{aligned}$$

where

$$(\text{East Side})_i = \begin{cases} 1 & \text{if i-th rating associated with east side yogurt vendor} \\ 0 & \text{if i-th rating not associated with east side yogurt vendor} \end{cases}$$

$$(\text{South Side})_i = \begin{cases} 1 & \text{if i-th rating associated with south side yogurt vendor} \\ 0 & \text{if i-th rating not associated with south side yogurt vendor} \end{cases}$$

$$(\text{Name Brand})_i = \begin{cases} 1 & \text{if i-th rating associated with name brand yogurt vendor} \\ 0 & \text{if i-th rating not associated with name brand yogurt vendor} \end{cases}$$

$$(\text{Subject j})_i = \begin{cases} 1 & \text{i-th observation taken from Subject j} \\ 0 & \text{i-th observation not taken from subject j} \end{cases}$$

We are interested in testing the hypotheses

$$H_0 : \mu_1 = \mu_2 = \mu_3 \qquad \text{vs.} \qquad H_1 : \text{At least one } \mu_j \text{ differs}$$

In previous units, we would have partitioned the variability in the taste ratings as

$$SS_{\text{Taste Ratings}} = SS_{\text{Vendors}} + SS_{\text{Error}}$$
$$SST = SSTrt + SSE$$

However, we have added an additional component to the model; we know that there is variability between the subjects (blocks). Therefore, we add a refinement to our partition:

$$SS_{\text{Taste Ratings}} = SS_{\text{Vendors}} + SS_{\text{Subjects}} + SS_{\text{Error}}$$
$$SST = SSTrt + SSB + SSE$$

Here, SSB refers to the "block sum of squares" capturing the variability due to the difference in the response between blocks. Let's not get lost in the details here; what we want to focus on is that the error sum of squares still captures the "unexplained variability" in the response. So, the smaller that is, the more the model is explaining.

Now, our goal is to compare two models. Under the more complex model (in which we allow the average ratings to differ between the vendors), we partition the variability as stated above. However, under the simpler model (in which we say the average rating is the same for all vendors), our data generating process becomes

$$\begin{aligned}(\text{Taste Rating})_i = \mu &+ \beta_2(\text{Subject 2})_i + \beta_3(\text{Subject 3})_i + \beta_4(\text{Subject 4})_i \\ &+ \beta_5(\text{Subject 5})_i + \beta_6(\text{Subject 6})_i + \beta_7(\text{Subject 7})_i \\ &+ \beta_8(\text{Subject 8})_i + \beta_9(\text{Subject 9})_i + \epsilon_i\end{aligned}$$

where μ is the common mean taste ratings for Subject 1. The model still has the terms which capture the variability between blocks because even if there is no difference in the vendors, there is still a correlation in the responses from the same subject. This reduced model simplifies the partition of the variability into

$$SST = SSB + SSE$$

That is, the only reason for variability in the taste ratings is randomness — the randomness from one subject to another (block effect) and the unexplained variability within a subject (error). Since the block effect exists in both models, moving from the simple model to the more complex model transfers some of the "error" variability into "treatment" variability. Therefore, the SSE for the simple model will *always* be larger than that for the more complex model. The question is whether the difference is significant enough that we believe there must be a difference between the vendors.

Comparing the difference in the unexplained variability between two models allows us to assess if the data is inconsistent with the simpler of the two models.

Of course, this is just a signal. We must examine this difference in light of the noise in the data in order to form a standardized statistic.

36.2 Forming a Standardized Test Statistic

As we have seen in the past two units, a standardized statistic is really a ratio of variability. That hasn't changed; it is just how we form that variability. The variability due to the "treatment" comes from subtracting:

$$SSTrt = SSE_{\text{Simple}} - SSE_{\text{Complex}}$$

If we take the variability due to error that we had in the simple model (under the null hypothesis) and subtract out the variability due to error that we had in the complex model (under the alternative hypothesis), that must represent the amount of variability we "transfer" into the treatment. In order to make this a true variance, we need to divide by an appropriate set of degrees of freedom.

Using the tip described in Chapter 19 regarding degrees of freedom, we have that the degrees of freedom for the total sum of squares (SST) is $n-1$ (n unique observations minus a single estimated mean). The degrees of freedom associated with the treatment sum of squares is $k-1$ (k averages estimated, one for each group, minus a single overall estimated mean). The degrees of freedom associated with the block sum of squares is $b-1$ (b averages estimated, one for each block, minus a single overall estimated mean). Finally, the degrees of freedom associated with the error sum of squares is $n-k-b+1$ (n unique observations minus k estimated group means and minus $b-1$ block means since we do not include an estimate for the first block).

Therefore, we have that the mean square for treatment is given by

$$MSTrt = \frac{SSTrt}{k-1} = \frac{SSE_{\text{Simple}} - SSE_{\text{Complex}}}{(n-b)-(n-k-b+1)}$$

We can use the mean square for error from the more complex model to capture the noise. Therefore, our standardized statistic becomes

$$T = \frac{MSTrt}{MSE} = \frac{\frac{1}{k-1}SSTrt}{\frac{1}{n-k-b+1}SSE}$$

just as in the ANOVA model. The difference is that we really think of this as getting the difference in the error sum of squares for two different models. Further, this process of comparing the simpler model to the more complex model is a very general procedure.

Consider testing the following general hypotheses from a regression model > H_0 : Model with restrictions on parameters is sufficient for explaining the response
> H_1 : Model without restrictions on parameters is needed for explaining the response
The standardized test statistic of interest is

$$T = \frac{\frac{SSE_{\text{Simple}} - SSE_{\text{Complex}}}{df_{\text{Error Simple}} - df_{\text{Error Complex}}}}{MSE_{\text{Complex}}}$$

where "Simple" refers to the model under the null hypothesis and "Complex" the model under the alternative, MSE refers to the mean square for error and SSE srefers to the error sum of squares and df to the associated degrees of freedom.

We note that while mathematical formulas have been provided to add some clarity to those who think algebraically, our emphasis is *not* on the computational formulas as much as the idea that we are comparing two sources of variability.

Table 36.1: ANOVA table for the Frozen Yogurt Case Study assuming the classical repeated measures ANOVA model.

	Source	DF	SS	MS	F	P-value
Type	Vendor	2	2.889	1.444	0.319	0.731
'Participant ID'	Subject (Block)	8	53.333	6.667	1.472	0.242
Residuals	Error	16	72.444	4.528		
...4	Total	26	128.667			

We can then model the null distribution of this standardized statistic under the conditions we place on the stochastic portion of the model. This allows us to compute a p-value.

36.3 ANOVA Table

We should not lose sight of the fact that our standardized statistic is really a result of partitioning the variability and considering the variability explained by the predictor relative to the noise in the response. We can summarize this comparison using an ANOVA table.

Let's consider the Frozen Yogurt Case Study data. We will further suppose that the data is consistent with all classical repeated measures ANOVA conditions. The results from the corresponding analysis comparing the average taste ratings across the three vendors are given in Table 36.1.

As long as the conditions are reasonable, then we can interpret the above p-value. Based on these results, there is no evidence that the taste ratings differ, on average, across the various yogurt vendors. That is, while we cannot prove that the average ratings are the same for all vendors, the data is consistent with the three yogurt vendors having the same taste ratings, on average. This is in line with the idea that consumers were paying a premium for the experience of going to a yogurt-shop; they viewed the product similarly with what could be purchased at a local grocier. Note that while it is standard for an ANOVA table to provide a p-value for the blocks, we do not examine this p-value; it is rare that we are interested in comparing subjects within the population directly.

The table is a way of summarizing the output from the analysis; the table itself is not very interesting, but we present it because it has the same emphasis we have in this unit — partitioning variability. The key to separating a signal from a noise is to partition the variability in the data. The total variability is partitioned into that resulting from the vendors (the factor), the differences between subjects (the blocks), and the error. By partitioning this variability, we are able to compute the standardized test statistic and the corresponding p-value.

36.4 Recap

By partitioning the variability in the response, we are able to construct a standardized statistic for testing the hypothesis of interest. The model for the null distribution of this statistic depends upon the conditions we are willing to impose on the stochastic portion of the data generating process. Regardless of the conditions we impose, we can interpret the resulting p-value similarly. It provides an indication of whether the data suggests that the average response differs for at least one of the groups.

Of course, the interpretation of the p-value depends on the conditions we impose. We should not choose such conditions without performing some type of assessment to ensure those conditions are reasonable — that the data is consistent with the conditions. That is the focus of the next chapter.

Chapter 37

Assessing Modeling Assumptions

In this unit we have discussed a model relating a quantitative response to a categorical predictor in the presence of blocks which induce correlation among the responses. For the Frozen Yogurt Case Study, our model had the form

$$\begin{aligned}(\text{Taste Rating})_i = \mu_1(\text{East Side})_i + \mu_2(\text{South Side})_i + \mu_3(\text{Name Brand})_i \\ + \beta_2(\text{Subject 2})_i + \beta_3(\text{Subject 3})_i + \beta_4(\text{Subject 4})_i \\ + \beta_5(\text{Subject 5})_i + \beta_6(\text{Subject 6})_i + \beta_7(\text{Subject 7})_i \\ + \beta_8(\text{Subject 8})_i + \beta_9(\text{Subject 9})_i + \epsilon_i\end{aligned}$$

where

$$(\text{East Side})_i = \begin{cases} 1 & \text{if i-th rating associated with east side yogurt vendor} \\ 0 & \text{if i-th rating not associated with east side yogurt vendor} \end{cases}$$

$$(\text{South Side})_i = \begin{cases} 1 & \text{if i-th rating associated with south side yogurt vendor} \\ 0 & \text{if i-th rating not associated with south side yogurt vendor} \end{cases}$$

$$(\text{Name Brand})_i = \begin{cases} 1 & \text{if i-th rating associated with name brand yogurt vendor} \\ 0 & \text{if i-th rating not associated with name brand yogurt vendor} \end{cases}$$

$$(\text{Subject j})_i = \begin{cases} 1 & \text{i-th observation taken from Subject j} \\ 0 & \text{i-th observation not taken from subject j} \end{cases}$$

Further, we considered three conditions on the distribution of the error term:

1. The error in the taste ratings within one individual is independent of the error in the taste ratings within any other individual.
2. The error for the taste rating is identically distributed.
3. The error in the taste rating follows a Normal distribution.

In addition, we considered four conditions on the distribution of the random effects:

1. Each subject's effect is identical for all vendors.
2. The effect of one subject is independent of the effect of any other subject.
3. The effect of each subject is independent of the error in the taste ratings.
4. The effect of each subject follows a Normal distribution.

We make a distinction in these conditions because the latter four conditions are not easily assessed. These are generally stated and assumed. However, we can assess the conditions on the error in a similar way to previous units. Just as in Chapters 20 and 29, we use residuals to assess these conditions qualitatively.

37.1 Assessing Independence

> The error in the taste ratings within one individual is independent of the error in the taste ratings within any other individual.

When a study design incorporates a block, it is rare that the researchers report the order in which the data was collected. This tends to be because the data is collected in the most convenient manner, as opposed to randomizing the order of the data collection. In such cases, we must really rely on the context to determine if it is reasonable to assume this condition. When the order is known, we can use a time-series plot of the residuals. As in the past, this particular plot only assesses one particular deviation from this condition, but it is the most common.

If two errors were unrelated, then the value of one residual should tell us nothing about the value of the next residual. Therefore, a plot of the residuals over time should look like noise (since residuals are supposed to be estimates of noise). If there are any trends, then it suggests the data is not consistent with independence. Of course, to construct such a plot, we need to know the order in which the data was collected.

For the Frozen Yogurt Case Study, participants were assessed simultaneously within the class. Therefore, there is no ordering in time to be concerned about. As such, a time-series plot of the residuals would not be useful here. Considering the context, the students were the ones who had designed the study (it was carried out by their instructor); therefore, they were concerned about the quality of the data collection. The students did their best to not influence any other's ratings. It is reasonable to assume the data is consistent with this condition.

37.2 Assessing Identical Distribution

We want to assess the variability in the residuals in order to determine if the data is consistent with the errors having an identical distribution. Unlike Chapter 29, we cannot simply make a boxplot of the errors across the three groups. Once there is more than a single predictor in the model, we resort back to the general strategy discussed in the regrssion unit and construct a plot of the residuals against the predicted values. Figure 37.1 shows the residuals for each individual across the predicted taste rating for that individual observation. Notice that as the predicted taste ratings increase, the variability in the residuals tends to decrease. This would suggest the data is not consistent with this condition. If it were, we would not expect to see this fan shape.

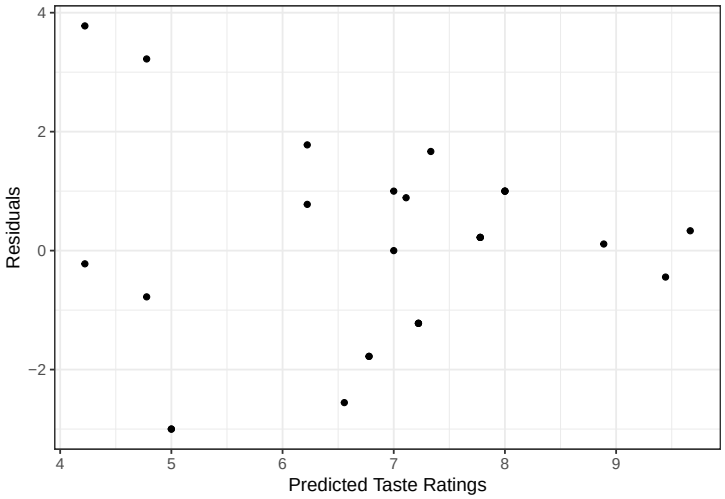


Figure 37.1: Comparison of the residuals from comparing the taste ratings across yogurt vendors accounting for subject-variability.

This plot does suggest the residuals tend to be centered around 0. You may think "hold on, I don't remember discussing the mean-0 condition." We did this indirectly. When we assume that the random effect for each subject is the same across the vendors, this is essentially saying that the effect of the vendor is not dependent upon the subject we are working with (no interaction, see Definition 21.2). Since our model does not allow for the effect of the vendor to depend upon the subject, we are making an assumption about the form of the model, which is exactly what the mean-0 condition in regression does. While we have used residuals to assess this condition, we can also assess this based on context in the case of blocks. It is reasonable to assume that the average taste ratings for a particular vendor are similar across subjects.

37.3 Assessing Normality

Just as before, we emphasize the probability plot as a method for assessing whether data is consistent with being drawn from a Normal distribution.

Figure 37.2 shows the probability plot for the residuals from the Frozen Yogurt Case Study.

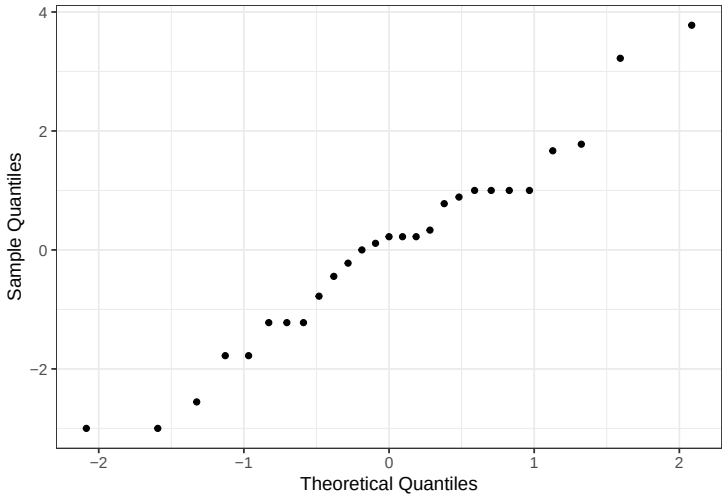


Figure 37.2: Probability plot of the residuals for the Frozen Yogurt Case Study. If the errors follow a Normal distribution, we would expect the residuals to fall along a straight line.

Overall, the points do tend to follow a straight line. It seems reasonable the data is consistent with the errors following a Normal distribution.

37.4 General Tips for Assessing Assumptions

As in Chapter 20, we want to point out three things that should be kept in mind when assessing these conditions:

1. We can never prove a condition is satisfied; we can only determine whether the data is consistent with a condition or whether it is not consistent with a condition.
2. The analysis has specific conditions placed on the error term; we choose whether to assume such a condition is reasonable by examining residuals.
3. A sample should always be consistent with the conditions you are relying on to interpret a p-value or confidence interval.

Chapter 38

Using the Tools Together

This unit introduced a framework for determining if there is an association between a quantitative response and a categorical predictor when the responses are correlated due to blocks. We formed a standardized statistic for measuring the signal, and developed a model for the data-generating process incorporating the block effect which allowed us to model the null distribution of the standardized statistic. In this chapter, we pull these tools together once more to answer a research question.

For the Frozen Yogurt Case Study, we found no evidence that people rated the taste differently, on average, for any of the vendors. However, the students conducting the study also recorded the how the participants rated the texture and appearance of the yogurt. In this chapter, we will use the data to answer the following question:

> Is there evidence that the appearance of the yogurt differs across vendors?

38.1 Framing the Question (Fundamental Idea I)

As stated, the above question is ill-posed. We have not identified a parameter of interest. We refine this question to be

> Is there evidence that, on average, the appearance rating differs for at least one of the vendors?

This question could also be stated as the following set of hypotheses:

> Let $\mu_{\text{East Side}}$, $\mu_{\text{South Side}}$ and $\mu_{\text{Name Brand}}$ represent the average appearance rating (on a scale of 1-10) of vanilla yogurt from each of the three vendors.

$H_0 : \mu_{\text{East Side}} = \mu_{\text{South Side}} = \mu_{\text{Name Brand}}$
H_1 : At least one mean differs

38.2 Getting Good Data (Fundamental Idea II)

As we are working with previously collected data, our goal in this discussion is not how best to collect the data but making note of the limitations of the data as a result of how it was collected. As before, each participant sampled yogurt from each of the three vendors, creating natural blocks. That is, each subject forms a unique block. Since it is quite reasonable that appearance preferences vary substantially between individuals, forming blocks out of subjects should allow us to increase the power of the study because we are accounting for a substantial source of variability in the appearance ratings.

The study was was a controlled experiment since the order in which the samples from each vendor were presented to the participants was randomized. While the study made use of random allocation, it did not make use of random selection. The participants were students taking a particular course; however, it may be reasonable to assume they are representative of college students in the area. The sample size was also limited as only students in this course were included in the study.

If you compare the above paragraph to the corresponding section in Chapter 30, you might be confused because in that section, we described that changing the question resulted in the study no longer being a controlled experiment. However, here, we changed the question of interest and retained the fact that the study was controlled. Why? The question of whether a study is controlled is always in regard to whether random allocation was used. In general, if you change the response but keep the primary factor of interest unchanged, the study will remain a controlled experiment. If you change the factor under study, it will no longer be controlled.

38.3 Presenting the Data (Fundamental Idea III)

Our question here is examining the relationship between a quantitative response (appearance rating) and a categorical predictor (vendor) in the presence of blocks (subjects). Figure 38.1 compares the distribution of the appearance rating for the three vendors.

Based on the above graphic, there appears to be less variability among the appearance for the South Side Yogurt vendor, but the average rating appears similar for all three vendors.

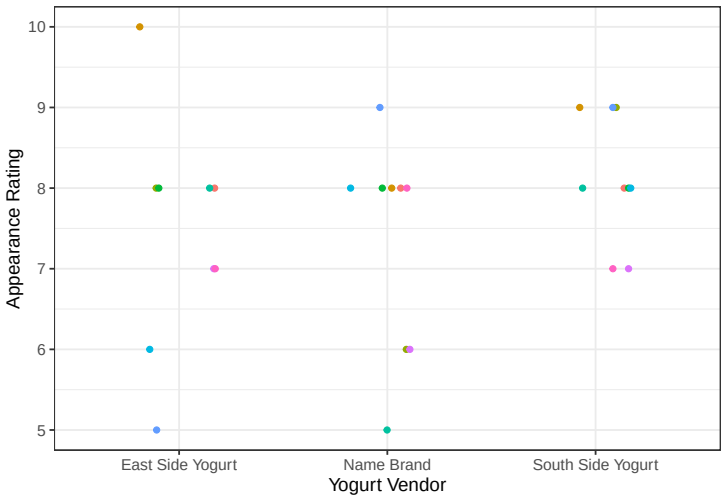


Figure 38.1: Comparison of the appearance ratings for yogurt from three vendors. Color is used to distinguish ratings from the same subject.

38.4 Quantifying the Variability in the Estimate (Fundamental Idea IV)

In order to measure the size of the signal, we can compute the standardized statistic

$$T = \frac{MSTrt}{MSE}$$

But, we need to be sure that these mean squares are computed from a model which accounts for the correlation in the responses. In particular, we consider the following model:

$$\begin{aligned}(\text{Appearance Rating})_i = \mu_1(\text{East Side})_i + \mu_2(\text{South Side})_i + \mu_3(\text{Name Brand})_i \\ + \beta_2(\text{Subject 2})_i + \beta_3(\text{Subject 3})_i + \beta_4(\text{Subject 4})_i \\ + \beta_5(\text{Subject 5})_i + \beta_6(\text{Subject 6})_i + \beta_7(\text{Subject 7})_i \\ + \beta_8(\text{Subject 8})_i + \beta_9(\text{Subject 9})_i + \epsilon_i\end{aligned}$$

where

$$(\text{East Side})_i = \begin{cases} 1 & \text{if i-th rating associated with east side yogurt vendor} \\ 0 & \text{if i-th rating not associated with east side yogurt vendor} \end{cases}$$

$$(\text{South Side})_i = \begin{cases} 1 & \text{if i-th rating associated with south side yogurt vendor} \\ 0 & \text{if i-th rating not associated with south side yogurt vendor} \end{cases}$$

$$(\text{Name Brand})_i = \begin{cases} 1 & \text{if i-th rating associated with name brand yogurt vendor} \\ 0 & \text{if i-th rating not associated with name brand yogurt vendor} \end{cases}$$

$$(\text{Subject j})_i = \begin{cases} 1 & \text{i-th observation taken from Subject j} \\ 0 & \text{i-th observation not taken from subject j} \end{cases}$$

We note here that μ_1 is not the same as $\mu_{\text{East Side}}$; however, testing

$$H_0 : \mu_1 = \mu_2 = \mu_3$$

is equivalent to testing

$$H_0 : \mu_{\text{East Side}} = \mu_{\text{South Side}} = \mu_{\text{Name Brand}}.$$

We observe a standardized statistic of 1.06. Of course, if we were to collect a new sample, we would expect this value to change. If we want to determine if this value is something we would expect when the appearance were similar for all vendors, we need a model for its null distribution. To do so, we impose the following conditions:

1. The error in the appearance rating for any one observation is independent of the error in the appearance rating for any other observation.
2. The error in the appearance rating has the same distribution for all observations.
3. The error in the appearance rating follows a Normal distribution.
4. The effect of each individual subject on the appearance rating is the same for all observations from that subject.
5. The effect of each individual subject on the appearance rating is independent of the effect of any other individual subject.
6. The effect of each individual subject on the appearance rating is unrelated to the error in the appearance rating for any observation.
7. The effect of each individual subject on the appearance rating follows a Normal distribution.

Under these three assumptions, we are able to construct a model for the null distribution of the standardized statistic. Figure 38.2 illustrates the null distribution assuming these conditions are satisfied.

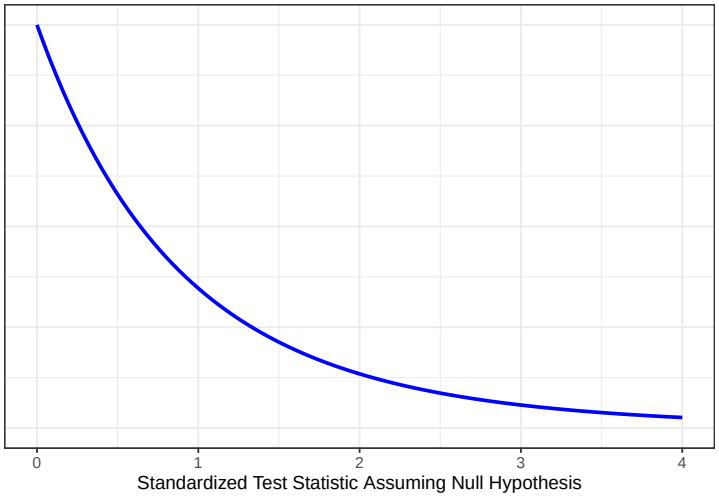


Figure 38.2: Model for the standardized test statistic measuring the signal comparing the appearance ratings of yogurt from three vendors while accounting for the repeated measurements taken on subjects. This model is constructed assuming the classical repeated measures ANOVA conditions are satisfied.

Before we can use this model to make any conclusions regarding our question of interest, we need to address the fact that we have assumed certain conditions are satisfied. We need to assess whether the data is consistent with these assumptions. This requires examining the residuals for the model.

First, we discuss the assumption of independence. Since each round of tasting involved all students tasting simultaneously, there is no natural ordering to the data. Instead, we rely on the context of the problem to make some statements regarding whether the data is consistent with this condition (whether making this assumption is reasonable). It is reasonable that the errors are independent. One case in which this might be violated is if students had visible reactions (grimmaced for example) when the yogurt was placed in front of them; if others noticed, it might bias their own ratings of the appearance. As the participants also designed the study and had a vested interest in the quality of the data, it is unlikely there were such issues, and we feel it is reasonable to assume independence.

Again, note that there is a condition of independence; we are simply saying whether we are willing to assume the condition is satisfied. There is no way to ensure the condition holds.

In order to assess if the errors are independent and to some degree whether the random effects are constant for all observations from a subject, we examine a plot of the residuals against the predicted values for each observation (Figure

38.3). As the spread of the plot is relatively constant, and the errors tend to center around 0, the data is consistent with these conditions.

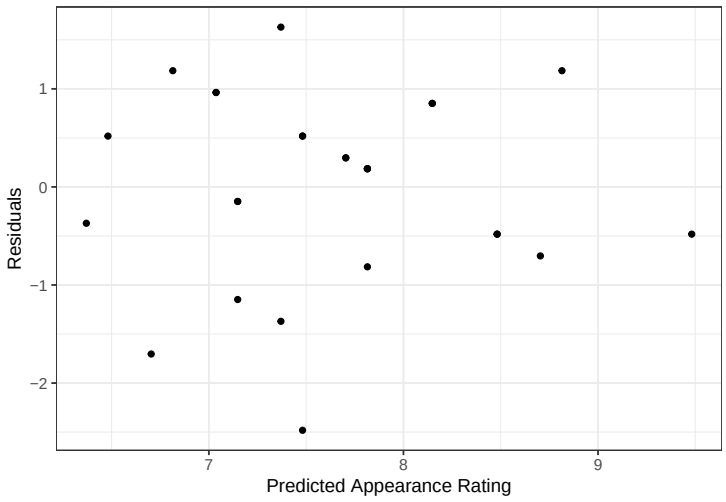


Figure 38.3: Plot of the residuals against the predicted values from a model comparing the appearance rating across vendors while accounting for the subject effect.

Finally, to assess the condition that the distribution of the errors is Normal, we consider a probability plot of the residuals (Figure 38.4). Given that the residuals tend to display a linear relationship, it is reasonable that the residuals represent a sample from a Normal Distribution. That is, it is reasonable that the errors follow a Normal Distribution.

Given that we are comfortable assuming the conditions on the error term are reasonable, and we assume the conditions on the random effects are also reasonable, we can make use of the analytical model for the null distribution in Figure 38.2.

38.5 Quantifying the Evidence (Fundamental Idea V)

Now that we have a model for the null distribution, we can determine how extreme our particular sample was by comparing the standardized statistic for our sample with this null distribution. We can measure this through computation of a p-value, the probability that we would observe a standardized statistic of this magnitude or higher by chance alone if there were no difference in the mean appearance ratings between the three vendors. This is summarized in Table 38.1 below.

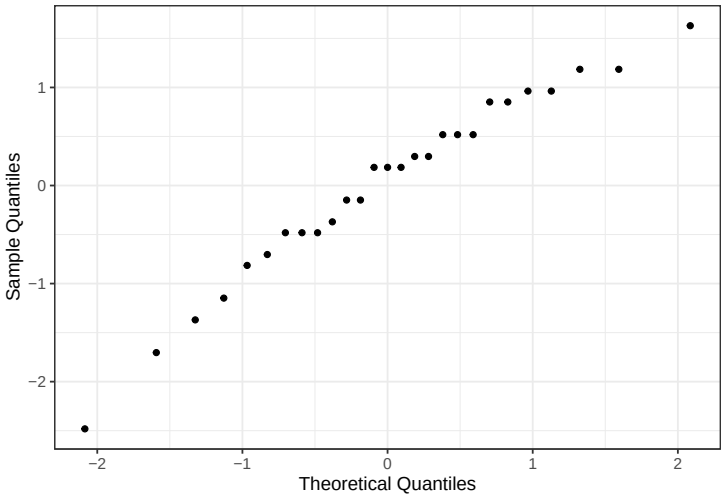


Figure 38.4: Probability plot assessing the assumption that the errors for our model comparing appearance rating across vendors follow a Normal Distribution.

Table 38.1: ANOVA table summarizing the comparison of the appearance ratings across vendors for the Frozen Yogurt Case Study.

Source	DF	SS	MS	F	P-value
Vendor (Treatment)	2	3.185	1.593	1.055	0.371
Subject (Block)	8	10.963	1.370	0.908	0.534
Error	16	24.148	1.509		
Total	26	38.296			

From the results, we can conclude that there is no evidence ($p = 0.371$) of a relationship between the appearance rating and the yogurt vendor.

38.6 Conclusion

Throughout this unit, we have examined a framework for examining the association between a quantitative response and a categorical predictor when there is correlation among the responses. This reinforces a couple of big ideas we have seen throughout this text:

- The key to measuring a signal is to partition the variability in the response.
- A standardized statistic is a numeric measure of the signal strength in the sample.
- Modeling the data-generating process provides us a way of modeling the sampling distribution of the parameter estimates and the null distribution of a standardized statistic.
- Conditions are often placed on the noise portion of the model for the data-generating process; before assuming these conditions are met, we should graphically assess whether the data is consistent with these conditions.

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