Statistical Inference

July, 2023

Table of Contents

# About this Course

We are delighted that you’ve chosen to enroll in Statistical Inference, a part of the Data Science Specialization offered by Johns Hopkins Biostatistics! This course will introduce you to the essential concepts of statistical inference, which will serve as a solid foundation for the rest of your journey in the Data Science track. We strongly believe that the core essence of Data Science lies in its scientific approach.

The primary focus of this Specialization is to provide you with three key elements: Firstly, it will introduce you to the fundamental principles of working with data in a scientific manner, enabling you to derive new and reproducible insights. Secondly, it will equip you with the necessary tools to execute a data analytic strategy, starting from raw data stored in a database and culminating in a comprehensive report with interactive visualizations. Lastly, we emphasize hands-on practice, allowing you to gain practical experience and develop your skills through firsthand application of the techniques taught. This course serves as the fundamental and foundational component of the entire series. While minimizing the reliance on complex mathematics, we aim to provide students with the essential knowledge of utilizing statistics to draw inferences about populations.

We are thrilled about the prospect of expanding Data Science education at scale. Our intention is to create self-contained, fast-paced, and interactive courses that foster an engaging learning experience.

# 1 Probability & Expected Values

In this module, we’ll go over some information and resources to help you get started and succeed in the course. During this week, we’ll focus on the fundamentals including probability, random variables, expectations.

## 1.1 Introduction

Greetings and a warm welcome to the Probability class, which is a part of the Statistical Inference course within the Coursera Data Science series. I’m Brian Caffo, and I will be one of your instructors for this class. Alongside me, we have Jeff Leek and Roger Peng, who will also be co-teaching the course. We all belong to the Department of Biostatistics at the Bloomberg School of Public Health. ### Syllabus The primary instructor of this class is Brian Caffo. Brian is a professor at Johns Hopkins Biostatistics and co-directs the SMART working group.

This class is co-taught by Roger Peng and Jeff Leek. In addition, Sean Kross and Nick Carchedi have been helping greatly.

**Course Content**

In this course we will cover the following topics: 1. Probability 2. Conditional Probability 3. Expectations 4. Variance 5. Common Distributions 6. Asymptotics 7. T confidence intervals 8. Hypothesis testing 9. P-values 10. Power 11. Multiple Testing 12. Resampling

If you’d prefer to watch the videos on YouTube, you can do so through this [link](https://www.youtube.com/playlist?list=PLpl-gQkQivXiBmGyzLrUjzsblmQsLtkzJ).

### 1.1.1 Course Book:

Statistical Inference for Data Science book is now available. It’s a different sort of book published on LeanPub. If you purchase the book on LeanPub, you’ll get all editions in the future for free. You pick the price on the site. You can get it [here](https://leanpub.com/LittleInferenceBook).

Following our style for the specialization, the book is creative commons licensed to offer you maximum flexibility in how you use the materials.

You can also just read a web page rendering of the book [here](https://leanpub.com/LittleInferenceBook/read)

In addition, the book is available on [GitHub](https://github.com/bcaffo/LittleInferenceBook) if you wish to render it yourself using pandoc.

### 1.1.2 Github repository

The most up to date information on the course lecture notes will always be on the [Github repository](https://github.com/DataScienceSpecialization/courses/tree/master/06_StatisticalInference).

Please issue pull requests so that we may improve the materials. Notice that Brian’s forked github repo is sometimes out of sync with the Data Science Specialization repo managed by the other instructors. Make sure to check in Brian’s master repo for the most up to date material.

If you would just like the full set of lecture pdfs, grab them [here](https://github.com/bcaffo/courses/blob/master/06_StatisticalInference/lectures.zip?raw=true).

If you would just like the full set of Rmd files for the lecture code, get those [here](https://github.com/bcaffo/courses/blob/master/06_StatisticalInference/rmd.zip?raw=true).

### 1.1.3 Homework Problems

In the book, there are homework problems fairly similar to the quiz questions.

If you can do them, you should be in very good shape for the quizzes. The homework assignments in this course are optional. They won’t count toward your final grade, but they are a good opportunity to practice the skills covered in the course. There are worked out solutions on youtube linked to the book. These are ordered in an odd way, as the class has been restructured. So, it’s probably best to just do them through the book.

[Homework 1](http://bcaffo.github.io/courses/06_StatisticalInference/homework/hw1.html#1) [Homework 2](http://bcaffo.github.io/courses/06_StatisticalInference/homework/hw2.html#1) [Homework 3](http://bcaffo.github.io/courses/06_StatisticalInference/homework/hw3.html#1) [Homework 4](http://bcaffo.github.io/courses/06_StatisticalInference/homework/hw4.html#1)

### 1.1.4 Differences of opinion

Keep in mind that currently data analysis is as much art as it is science - so we may have a difference of opinion - and that is ok! Please refrain from angry, sarcastic, or abusive comments on the message boards. Our goal is to create a supportive community that helps the learning of all students, from the most advanced to those who are just seeing this material for the first time.

### 1.1.5 Data Science Specialization Community Site

Since the beginning of the Data Science Specialization, we’ve noticed the unbelievable passion students have about our courses and the generosity they show toward each other on the course forums. A couple students have created quality content around the subjects we discuss, and many of these materials are so good we feel that they should be shared with all of our students.

We’re excited to announce that we’ve created a site using [GitHub Pages](http://datasciencespecialization.github.io/) to serve as a directory for content that the community has created. If you’ve created materials relating to any of the courses in the Data Science Specialization, please send us a pull request so we can add a link to your content on our site. You can find out more about contributing [here](https://github.com/DataScienceSpecialization/DataScienceSpecialization.github.io#contributing)

We can’t wait to see what you’ve created and where the community can take this site!

## 1.2 Probability

In today’s lecture, we will cover the fundamentals of probability at a beginner’s level, providing you with the necessary knowledge for your journey in the data science specialization. If you’re interested in delving deeper into this topic, I highly recommend checking out my comprehensive mathematical biostatistics boot camp series. In addition,the course notes are on GitHub.

In this module we discuss probability, the foundation of statistical analysis. Probability assigns a number between 0 and 1 to events to give a sense of the “chance” of the event. Probability has become our default model for apparently random phenomena. Our eventual goal is to use probability models, our formal mechanism for connecting our data to a population. However, before we get to probability models, we need to understand the basics of probability calculus. The next few lectures cover these basics.

**Probability** = the study of quantifying the likelihood of particular events occurring - given a random experiment, probability = population quantity that summarizes the randomness This summary is not just about the data at hand, but a conceptual quantity that exist in the population that we want to estimate.

Let’s delve into the concept of probability. In the context of a random experiment, such as rolling a die, probability quantifies the inherent randomness of the outcomes. It’s important to highlight the term “population” here. When considering a die roll, probability is seen as an intrinsic characteristic of the die itself, rather than being dependent on a specific sequence of fixed rolls. Therefore, when we discuss probability, we’re referring to a conceptual property that exists within the population we aim to estimate, rather than being directly observable in the data we have. Now, let’s define the principles that govern probability, known as probability calculus. Firstly, probability operates on the potential outcomes of an experiment. For instance, when rolling a die, the possible outcomes could be 1, the set {1, 2}, the set of even numbers {2, 4, 6}, or the set of odd numbers {1, 3, 5}, and so on. Probability is a function that assigns a number between 0 and 1 to each of these sets of possible outcomes. We must adhere to the rule that the probability of an event occurring, such as rolling the die and obtaining a particular number, must be equal to one. Additionally, the probability of the union of two mutually exclusive sets of outcomes must be equal to the sum of their individual probabilities. For example, consider the scenario where one possible outcome is obtaining either a one or a two, while another possible outcome is obtaining either a three or a four. These two sets, {1, 2} and {3, 4}, cannot occur simultaneously. The probability of the union, i.e., obtaining a one, two, three, or four, is the sum of the probabilities of obtaining a one or two, plus the sum of the probabilities of obtaining a three or four.

Interestingly, these simple rules encompass all the necessary principles to establish the general rules that govern probability. This significant discovery was made by the Russian mathematician Kolmogorov. Let’s explore some of the essential rules that probability must abide by. While I have already mentioned a few, others naturally follow from the previously stated rules.

1. The probability of an event not occurring, or “nothing” happening, is zero. In the case of rolling a die, something is bound to occur, and you will obtain a number.
2. Conversely, the probability of an event occurring, such as rolling a specific number on the die, is equal to one.
3. It is intuitive to understand that the probability of an event happening is equal to one minus the probability of the opposite event occurring. For example, the probability of rolling an even number on a die is equal to one minus the probability of rolling an odd number. This is because the set of odd numbers is considered the opposite of obtaining an even number in the context of rolling a die.
4. The probability of at least one of two or more mutually exclusive events, which cannot occur simultaneously, is the sum of their individual probabilities. This aligns with the definition we discussed earlier.
5. Another consequence of probability calculus is that if event A implies the occurrence of event B, then the probability of event A is less than or equal to the probability of event B. Although this may sound complex when explained verbally, it becomes clearer when visualized using a Venn diagram.



Figure : Figure 1.1: Event A being sub section of B event

In the diagram, event A is represented by a circle contained within event B. When we consider the probability of A, we assign a number to the area within circle A. Similarly, when discussing event B, we refer to the probability assigned to the entire circle, which includes the area of A. Therefore, it logically follows that the probability of B is larger than or equal to the probability of A. This concept is often intuitive and easily understood once visualized. For instance, the probability of rolling a 1 (set A) is less than the probability of rolling a 1 or a 2 (set B).

1. For any two events, the probability of at least one occurring is equal to the sum of their probabilities minus the probability of their intersection.



Figure : Figure 1.2: Events A and B with intersection

Again, visualizing this with a Venn diagram helps in understanding it better. Consider set A and set B. When we add their individual probabilities, we are effectively adding the intersection region twice, once when considering A and once when considering B. Since we have counted the intersection twice, to obtain the probability of their union, we need to subtract the intersection once. This rule highlights that we cannot simply add probabilities if there exists a non-trivial intersection between the events.

Now, let’s illustrate an example to demonstrate why we cannot simply add probabilities when the events are not mutually exclusive. According to the National Sleep Foundation, approximately 3% of the American population has sleep apnea, while around 10% of the North American and European population has restless leg syndrome. Let’s assume, for the sake of argument, that these probabilities are derived from the same population. The question is, can we add these probabilities together to conclude that about 13% of people in this population have at least one of these sleep problems? The answer is no. The reason is that these events, sleep apnea and restless leg syndrome, can occur simultaneously and are not mutually exclusive. There is a non-trivial portion of the population that experiences both conditions concurrently.

To elaborate further, let’s define event A as the occurrence of sleep apnea in a person drawn from this population, and event B as the occurrence of restless leg syndrome. In this case, we believe that the intersection of these two events (the occurrence of both conditions) is non-trivial. If we were to naively add the probabilities of A and B, we would essentially count the intersection twice, which would result in an overestimate. To determine the probability of the union (at least one of the conditions), we need to subtract the intersection once, recognizing that it was mistakenly included twice in the initial addition.

### 1.2.1 Probability mass functions and probability density functions

Probability calculus provides a valuable framework for understanding the fundamental rules that govern probability and serves as the basis for all probabilistic thinking. However, when it comes to numeric outcomes of experiments, we require a more practical approach. This is where densities and mass functions for random variables come into play, serving as a convenient starting point. These concepts will be sufficient for our purposes, which is collecting data that will be utilized to estimate properties of the population.

One of the most well-known examples of a density function is the bell curve, also known as the normal distribution. In this class, you will gain a deeper understanding of what it truly means for data to follow a bell curve. You will learn about the significance and interpretation of the bell curve. Importantly, you will also realize that when discussing probabilities associated with the bell curve or the normal distribution, we are referring to population quantities, not statements solely based on the observed data.

Before delving into data analysis, it is crucial to develop our intuition for understanding population quantities. A random variable represents the numerical outcome of an experiment. In our study, we will encounter two types of random variables: discrete and continuous. Discrete random variables are those that can be counted, such as the number of web hits or the possible outcomes of rolling a die. They can even include non-numeric attributes like hair color, which can be assigned numeric values (e.g., 1 for blonde, 2 for brown, 3 for black, etc.). For discrete random variables, we assign probabilities to each possible value they can take. On the other hand, continuous random variables can assume any value within a range or continuum. When working with continuous random variables, we assign probabilities to ranges of values they can take.

Let’s consider some simple examples that can be viewed as random variables, as these examples will aid in building our intuition throughout the course. One prominent example is the flip of a coin, where we can assign values of “heads” or “tails” (or 0 and 1) to represent the outcomes. This is a discrete random variable since it can only take two distinct levels. Another example of a discrete random variable is the outcome of rolling a die. It can only take one of six possible values, making it a discrete random variable with simple probability mechanics. A more complex random variable would be, the amount of website traffic or the number of web hits on a given day. While we’ll likely treat it as discrete, it’s interesting because it doesn’t have an upper bound. In such cases, we might employ the Poisson distribution to model it. The hypertension status of a randomly selected subject from a population can also be a random variable. We may assign a value of 1 to indicate the presence of hypertension or a diagnosis, and 0 otherwise. This random variable would typically be modeled as discrete.

An example of continuous random variable would be measuring a subject’s body mass index (BMI). In this case, BMI would be considered a continuous random variable, as it can assume any value within a range. Intelligence quotients (IQ) are often modeled as continuous random variables.

When working with discrete random variables, we assign a probability to each possible value they can take. We represent this assignment using a function called the probability mass function (PMF). The PMF takes any value of the discrete random variable and assigns the probability of it taking that specific value.

For example, in the case of a die roll, the PMF would assign a probability of one-sixth to the value one, one-sixth to the value two, one-sixth to the value three, and so on.

To ensure that the PMF satisfies the basic rules of probability, we have two requirements. First, the PMF must always be greater than or equal to zero since probabilities range from zero to one, inclusive. Second, the sum of the probabilities assigned to all possible values of the random variable must add up to one. In the case of a die roll, if we add the probabilities of getting one, two, three, four, five, and six, the sum should equal one. This ensures that the probability of any possible outcome occurring is accounted for.

Therefore, the PMF of a discrete random variable must adhere to these two rules to accurately represent probabilities.

We will primarily focus on using probability mass functions (PMFs) that are particularly useful in our context. Two examples of such PMFs are the binomial distribution, commonly used for coin flips, and the Poisson distribution, commonly used for counting events. However, let’s discuss one of the most well-known PMFs, the Bernoulli distribution, which is often used to model the outcome of a coin flip.

Let’s denote the random variable representing the coin flip outcome as capital X, where X = 0 represents tails and X = 1 represents heads. In this notation, an uppercase letter represents a potential value of the random variable that may or may not occur. On the other hand, a lowercase x serves as a placeholder for a specific value that we will substitute.

The PMF for the Bernoulli distribution is represented as . When we substitute x = 0 into this PMF, we obtain a probability of one-half. Similarly, when we substitute x = 1, we also get a probability of one-half. This means that the probability of the random variable X taking the value 0 is one-half, and the probability of it taking the value 1 is also one-half.

When we introduce an unfair coin, we can adjust our approach by considering a parameter, theta, representing the probability of getting a head. The probability of getting a tail would then be 1 minus theta, where theta is a number between 0 and 1. In this case, the probability mass function can be written as follows:

. By substituting x = 1 into this PMF, we obtain the probability . Similarly, when we substitute x = 0, we get the probability . This implies that for this population distribution, the probability of the random variable X taking the value 0 is , and the probability of it taking the value 1 is .

This approach is particularly useful for modeling the prevalence of a certain condition or event. For instance, if we want to model the prevalence of hypertension, we can assume that the population or sample we are studying can be likened to the outcomes of biased coin flips with a success probability represented by . However, the challenge lies in not knowing the exact value of . Therefore, we will utilize our data to estimate this proportion within the population.

In contrast to the probability mass function, which assigns probabilities to specific values for discrete random variables, the probability density function (PDF) is associated with continuous random variables. Similar to the rules that the probability mass function follows, a valid probability density function must satisfy two specific rules: it must be greater than or equal to zero everywhere, and the total area under the function must be equal to one. The key concept of a probability density function is that areas under the curve correspond to probabilities for the random variable. For instance, if we state that intelligence quotients (IQ) are normally distributed with a mean of 100 and a standard deviation of 15, we are implying that the population follows a bell-shaped curve. In this case, the probability that a randomly selected individual from that population has an IQ between 100 and 115 is represented by the area under the curve within that range. It is important to note that the probability density function represents a statement about the population of IQs and not the data itself. The data will be used to assess and evaluate the assumptions made about the population’s probability distribution. It is worth emphasizing that whenever the term “probability” is used, it refers to a population quantity.



Figure : Figure 1.3: Area between 100-115 IQ under normal distribution

It is interesting to note that when we model continuous probabilities using probability density functions (PDFs) for continuous random variables, the probability of the variable taking any specific value is actually *zero*. This is due to the fact that the area under a line, which represents a single point, is zero. However, this does not pose a problem and is simply a quirk arising from modeling random variables with infinite precision. It does not affect the functioning of probability calculations.

The bell-shaped curve, which represents a normal distribution, can be quite challenging to work with until you learn the appropriate techniques, which will be covered in a separate lecture. For now, let’s consider a simpler density function that resembles a right triangle. We’ll use the function for x between 0 and 1, and 0 otherwise, as an example. Let’s provide some context for this function: imagine it represents the proportion of help calls that are addressed in a random day by a helpline.



Figure : Figure 1.4: Shape of the density function for f(x)=2x

What does this density function imply? It means that the probability of the number of calls being addressed falling between 20% and 60% of the total calls for that day is given by the area under the curve in that range. Now, let’s evaluate whether this function is a mathematically valid probability density function.

Looking at the plot of the PDF, which resembles a right triangle, we can see that it is always greater than or equal to zero. Next, let’s calculate the area under the curve. Since it is a right triangle, the area is equal to half the base (which is 1) multiplied by the height (which is 2). Thus, the area is 1. Therefore, this function satisfies the requirements of a valid probability density function, as it is always non-negative and the total area under the curve is equal to 1.

Example: we want to find the probability that 75% or fewer calls get addressed in a randomly sampled day from this population. At the point (0.75, 1.5) on the density function, the height is 1.5 because the function is defined as 2 times x. The base value is 0.75. To calculate the probability, we divide the area, which is half the base times the height, by 2. So the probability turns out to be 56%, as shown in the example.



Figure : Figure 1.5: Shape of the density function for f(x)=2x

Interestingly, this density function is a special case of a well-known distribution called the distribution. I have provided the R code here for obtaining the probability directly from the distribution. Although in this simple case we don’t need it because we are working with triangles, in more complex scenarios, we will require these functions. It’s worth mentioning that in R language we can right this as pbeta(0.75,2,1) the p prefix before a function denotes the calculation of probabilities, 1 define the specific triangle we are using in this example, and you can test and see that it yields the same result of 56%. Certain areas of the density are so commonly used that they are given specific names. For instance, the cumulative distribution function (CDF) of a random variable X gives the probability that X is less than or equal to a given value x.

This definition holds for both discrete and continuous random variables. In the case of the beta distribution we just examined, the pbeta function in R always returns the probability of being less than or equal to the first argument provided.

Alternatively, the survival function is another useful concept. It is defined as 1 minus the cumulative distribution function and represents the probability of a random variable being greater than a given value.

Suppose we wanted to determine the cumulative distribution function for the previously mentioned density. For instance, we might want to find the probability that 40% or fewer, 50% or fewer, or 60% or fewer of the calls get answered in a given day based on this specific right triangle population density function. In each case, the calculation will resemble what we did earlier for 0.75. Since the density function is a right triangle, the probability is half the area of the base times the height. This simplifies to one-half times x times 2x, which equals . Therefore, the function provides the probability of that percentage or fewer calls being answered on a randomly sampled day.

To examine the results when we use the pbeta function, which corresponds to the cumulative distribution function in R, for the three values mentioned earlier, we can write the followings.

pbeta(c(0.4,0.5,0.6),2,1) where parameters 2 and 1 are utilized to evaluate the specific density, yielding probabilities of 16%, 25%, and 36%. Therefore, the probability that 40% or fewer of the calls get answered on a given day is 16%, the probability that 50% or fewer get answered is 25%, and the probability that 60% or fewer get answered is 36%. In terms of the survival function, it is simply 1 minus the cumulative distribution function, which can be expressed as 1 minus .

As we progress, we will encounter more complex density functions. However, the process will be simpler since we can rely on existing functions such as pnorm and pbeta instead of calculating them directly.

### 1.2.2 Quantiles

You’re already familiar with sample quantiles, such as the 95th percentile, which represents the 0.95 quantile of a dataset. If you score at the 95th percentile on an exam, it means that 95% of the students scored worse than you while 5% scored better. Now, let’s introduce the concept of population analogs for quantiles. In the case of the 95th percentile or the 0.95 quantile, you would order the observations from least to greatest and locate the point or exam score below which 95% of the observations lie. This point is denoted as , where alpha corresponds to the quantile. In other words, it satisfies the condition , where F is the distribution function. To better understand this concept, let’s try to visualize it.

Let’s consider the distribution function , which represents the area below point x on a density plot. This area corresponds to the probability that a random variable from the population is less than or equal to x. As an example let’s imagine a population of test scores, an infinite population of students. The distribution function gives us the probability of obtaining a score equal to or lower than x for a randomly selected student from this population.

Now, let’s introduce the concept of the quantile. We move a line along the distribution until we find the point , where exactly proportion of the probability lies below it. This is similar to what we do with our data when finding an empirical quantile, where we locate the data point such that, for example, 95% of the test scores lie below it, which corresponds to the sample percentile. In the population distribution, we move the x point until we find the point where the probability of being below it is 95%. Percentiles are essentially quantiles with alpha expressed as a percentage rather than a proportion. The median, often the most well-known quantile, represents the 50th percentile.



Figure : Figure 1.6: 95 percentile of a distribution

Quantiles are frequently used, particularly with the normal distribution. However, we rarely need to directly work with densities to calculate quantiles, as the distributions we commonly encounter have well-defined quantiles. In R, we can easily find quantiles using the q prefix before the density function name. For example, for the density we discussed earlier, the function qbeta gives us the relevant quantile. We can input 0.5 (qbeta(0.5,2,1))to find the median, considering that R expects the quantile argument as a proportion rather than a percentage, i.e. 0.5 is acceptable and 50 for 50% is not acceptable. The parameters 2 and 1 are specific to the density we’re working with, which you’ll have to trust me on for now. When we calculate the quantile using qbeta with 0.5 as the argument, we obtain the same result as before, 0.7 or 0.71.

At this point, you might be wondering why the concept of the median seemed simpler before, when you would order observations and select the middle value or averaging the two middle values for an even number of observations.

The answer is there you had an estimator. However, in this class, we aim to go beyond just estimators and focus on the targets of estimation, known as estimands. In the case of the sample median, it estimates the population median.

To understand this, let’s consider an example where we sample a few days and calculate the percentage of calls answered on those days. If we line up these percentages in ascending order, the middle value represents the *sample median*. We can think of this sample median as an estimator for the true median percentage of calls answered in the population. However, to establish a connection between the sample and the population, we need to make certain assumptions, which we will thoroughly explore and formalize in this class.

In essence, for every estimator, there exists an estimand in this class. The sample mean estimates the population mean, the sample median estimates the population median, and the sample standard deviation estimates the population standard deviation, and so on. This process is known as *statistical inference*, where we link our sample data to the underlying population.

## 1.3 Conditional probability

Conditional probability is a very intuitive idea, “What is the probability given partial information about what has occurred?”. To illustrate the concept of conditioning, let’s consider [XKCD comic](https://xkcd.com/795/). The comic portrays two individuals standing in a field during a lightning storm near a tree. One person suggests going inside, but the other dismisses the idea, citing the low chance of getting struck by lightning, approximately one in seven million. However, the comic humorously points out that the death rate among people who know this statistic is one in six. The underlying message is that the second person has failed to consider the additional information available to them, leading to an incorrect assessment of risk.

Consider another example to better understand conditional probabilities. Suppose we have a standard die, and the probability of rolling a one is assumed to be . However, if we are given the extra information that the roll resulted in an odd number (one, three, or five), our perspective changes. Now, conditioned on this new information, we would no longer say that the probability of rolling a one is . Instead, we would consider the one, three, and five to be equally likely outcomes, so the probability of rolling a one becomes . This demonstrates how conditional probabilities adjust our understanding based on additional information.

To define conditional probability, suppose we have an event B with a nonzero probability. Then, the conditional probability of event A given that B has occurred is denoted as and is defined as:

In the case where A and B are statistically independent events (*we will define this later*), the conditional probability simplifies to the probability of A. This means that if the occurrence of event B provides no new information about event A, the probability of A remains unchanged.

Let’s verify that the concept of conditional probability aligns with our intuition in the example of rolling a die. Event B represents the occurrence of an odd number (one, three, or five), and event A represents rolling a one. We want to find the . In other words, we are interested in the probability of rolling a one when we know that the outcome is an odd number. Using the definition of conditional probability,

. Since A is entirely contained within B, the probability of A ∩ B is simply the probability of A, which is . The probability of B, in this case, is that is for each of the three mutually exclusive possibilities. Thus, the conditional probability equals divided by , which simplifies to , confirming our previous understanding.

Conditional probability allows us to update our probabilities based on new information, and it plays a **crucial** role in statistical inference. ### Bayes’ rule One of the well-known applications of conditional probability is Bayes’ rule, named after Thomas Bayes, a Presbyterian minister whose work was published posthumously. Bayes’ rule allows us to reverse the conditioning set and the set we are interested in finding the probability of. Suppose we want to calculate the probability of event B given event A, and we already know or can easily calculate the probability of event A given event B. Bayes’ rule enables us to evaluate the probability of B given A in terms of the probability of A given B.

However, to apply Bayes’ rule, we also need the marginal probability of event B, which is valuable in various contexts such as diagnostic tests.

Conditional probability in the context of a diagnostic test, exemplifies one of the significant applications of conditional probability and Bayes’ rule. Consider a test for a disease, where we define plus(+) and minus(-) as events representing a positive or negative test result, respectively. D and represent the events of having or not having the disease, respectively. The sensitivity of the test is the probability that the test is positive given that the subject actually has the disease. A high sensitivity indicates a good test. The specificity, on the other hand, is the probability that the test is negative given that the subject does not have the disease. A high specificity is desirable for a good test. While obtaining accurate estimates of sensitivity and specificity can be challenging, in certain cases, like an HIV blood test, it is possible to test individuals known to have or not have the disease to estimate these probabilities.

When a diagnostic test is positive, the probability of having the disease given the positive test result (positive predictive value) is of particular interest. Similarly, when the test is negative, the probability of not having the disease given the negative test result (negative predictive value) becomes relevant. In the absence of a test, the probability of having the disease is known as the prevalence of the disease.

Here is an example to illustrate the calculation of positive predictive value using Bayes’ rule. Suppose a study comparing the efficacy of an HIV test reports sensitivity as 99.7% and specificity as 98.5%. These numbers are for illustrative purposes and do not reflect actual HIV test statistics. Now, consider a subject from a population with a 0.1% prevalence of HIV who receives a positive test result. We want to calculate the associated positive predictive value.

Applying Bayes’ rule, we have the probability of disease given a positive test result equal to the probability of a positive test result given disease multiplied by the probability of disease , divided by the denominator. To simplify, we express the probability of a positive test result given no disease as and the probability of no disease as . Substituting known values, we find the positive predictive value to be 6% for this test in the given population. The low positive predictive value is primarily due to the low prevalence of the disease. However, in a counseling scenario, if the counselor discovers that the subject is an intravenous drug user who regularly has intercourse with an HIV-infected partner, the counselor would consider a much higher prevalence for this particular individual, leading to a higher positive predictive value.

Bayes’ rule provides a powerful framework for incorporating new information and adjusting probabilities based on conditional events, making it valuable in various fields, including diagnostics and decision-making. We want to distinguish between two components: the component that is dependent on the prevalence and the component that is objective evidence of the positive test result. This is where diagnostic likelihood ratios(DLR) come into play, and we’ll explore them further. First, let’s revisit the formula for positive predictive value in Bayes’ rule, which depends on sensitivity, specificity, and disease prevalence.

We can apply a similar approach to calculate the probability of not having the disease given a positive test result.

By dividing these two equations, we arrive at the odds of disease given a positive test result divided by the odds of not having the disease given a positive test result.

post test odds of = \* pre test odds of D Dividing a probability by 1 minus that probability gives us the **odds**. Therefore, on the left side, we have the odds of disease given a positive test result, while on the right side, we have the odds of disease without the test result. The factor in the middle represents the diagnostic likelihood ratio for a positive test result. The equation can be expressed as follows: the pretest odds of disease multiplied by the diagnostic likelihood ratio equals the post-test odds of disease. In other words, the diagnostic likelihood ratio of a positive test result indicates how much the odds change when multiplied by it, transitioning from pretest to post-test odds.

Returning to our example, assume a subject has a positive HIV test. Using the sensitivity and specificity values mentioned earlier, the diagnostic likelihood ratio is calculated as divided by , resulting in . Regardless of the pretest odds, multiplying them by 66 gives the post-test odds. Thus, the hypothesis of disease is 66 times more supported by the data compared to the hypothesis of no disease. Even if the pretest odds are initially small, multiplying them by 66 will still yield a larger but still small number.

Now, consider the scenario when a subject receives a negative test result using the . In this case, the , derived from the sensitivity and specificity values mentioned earlier, is 0.003.

Consequently, the post-test odds of disease in light of a negative test result become 0.3% of the pretest odds of disease. Stated differently, the hypothesis of disease is supported 0.003 times the hypothesis of no disease given the negative test result. By incorporating diagnostic likelihood ratios, we can assess the impact of a test result on the odds of disease and gain insights into the strength of evidence provided by the test.

### 1.3.1 Independence

As mentioned earlier, event A is considered independent of event B if the probability of A given B is equal to the probability of A, given that event B has a positive probability. Another definition of independence states that events A and B are independent if the probability of their intersection equals the product of their individual probabilities. This leads us to an important lesson: we cannot simply multiply probabilities without considering the independence of the events involved. Multiplication of probabilities is valid only for independent events.

Example: What is the probability of getting two consecutive heads when flipping a fair coin? We define event A as the probability of getting a head on the first flip and event B as the probability of getting a head on the second flip. Both probabilities are 0.5 since we assume a fair coin. In this case, because the events are independent, the probability of (getting heads on both flips) is the product of their probabilities, which is 0.25. This calculation is straightforward and correct. However, problems arise when people multiply probabilities in situations where they shouldn’t. A notable example of incorrectly multiplying probabilities was reported in volume 309 of Science. It involved a physician who gave expert testimony in a criminal trial. The trial concerned a mother whose two children had died from sudden infant death syndrome (SIDS). The expert testimony multiplied the prevalence of SIDS (1 out of 8,500) by itself to calculate the probability of two children from the same mother having SIDS. Based on this evidence, among other factors, the mother was convicted of murder. The fundamental mistake in this case was multiplying probabilities for events that were not necessarily independent. It is reasonable to assume that events within families, such as the occurrence of SIDS, are dependent due to genetic or familial environmental factors.

In our class, we will primarily use the concept of independence by assuming that a collection of random variables are independent and identically distributed (IID). This means that the random variables are independent from each other and follow the same probability distribution. For example, several coin flips can be considered IID because each flip is independent of the others, and they all follow the same distribution with a 0.5 probability for heads and 0.5 for tails. IID sampling serves as our default model for a random sample. Even if we do not have an actual random sample, we often use the conceptual model of random sampling or IID to analyze our data. It will be the principal mode of analysis in this class.

## 1.4 Expected values

The empirical average is a very intuitive idea; it’s the middle of our data in a sense. But, what is it estimating? We can formally define the middle of a population distribution. This is the expected value. Expected values are very useful for characterizing populations and usually represent the first thing that we’re interested in estimating.

Now, we will discuss the process of drawing conclusions about populations based on noisy data obtained from them. We will assume that the populations and the randomness governing our samples are described by probability density functions and probability mass functions. Instead of focusing on the entire function, we will examine characteristics of these distributions that are reflected in the random variables drawn from them. The most valuable such characteristics are expected values, particularly the mean. The mean represents the center of a distribution. As the mean shifts, the distribution moves either to the left or right.



Figure : Figure 1.7: Mean of a distribution

Another important characteristic is variance, which measures the spread of a distribution.  Similar to how sample quantiles estimate population quantiles, sample expected values estimate population expected values. Therefore, the sample mean serves as an estimate of the population mean, the sample variance estimates the population variance, and the sample standard deviation approximates the population standard deviation.

The expected value, or mean, of a random variable represents the center of its distribution. For a discrete random variable x with a probability mass function , the expected value is calculated by summing the possible values that x can take multiplied by their respective probabilities.

Conceptually, the expected value draws inspiration from the idea of the physical center of mass, where the probabilities act as weights and x represents the location along an axis. To illustrate this notion of center of mass, consider the sample mean. Even though we are focusing on the population mean in this discussion, it is interesting to note that the sample mean can be seen as the center of mass if we treat each data point as equally likely. In other words, each data point is assigned a probability of , where N is the sample size. Intuitively, we employ this center of mass idea when using the sample mean.

To demonstrate this concept, I have provided some code that calculates the sample mean of a dataset and depicts it as the center of mass by generating a histogram. The example employs a dataset from R called “Galton,” which consists of paired data representing the heights of parents and their children.

library(reshape2)  
library(UsingR)  
library(ggplot2)  
data(galton)  
longGalton <- melt(galton, measure.vars = c("child", "parent"))  
g <- ggplot(longGalton, aes(x = value)) + geom\_histogram(aes(y = ..density.., fill = variable), binwidth=1, colour = "black") + geom\_density(size = 2)  
g <- g + facet\_grid(. ~ variable)  
g

The histogram displays the child’s height distribution, and a continuous density estimate is superimposed.



Figure : Figure 1.9: Height distribution for Childran and Parents

To further explore this concept, we can use the “manipulate” function available in RStudio. By manipulating the mean value, we can observe how it balances out the histogram.

library(manipulate)  
library(UsingR)  
library(ggplot2)  
data(galton)  
  
myHist <- function(mu){  
 g <- ggplot(galton, aes(x = child))  
 g <- g + geom\_histogram(fill = "salmon",   
 binwidth=1, aes(y = ..density..), colour = "black")  
 g <- g + geom\_density(size = 2)  
 g <- g + geom\_vline(xintercept = mu, size = 2)  
 mse <- round(mean((galton$child - mu)^2), 3)   
 g <- g + labs(title = paste('mu = ', mu, ' MSE = ', mse))  
 g  
}  
manipulate(myHist(mu), mu = slider(62, 74, step = 0.5))

You can use the slider to move the mean value and observe how it affects the mean squared error. 

The mean squared error is a measure of imbalance, indicating how stable or unsteady the histogram appears. As we move the mean closer to the center of the distribution, the mean value increases, while the mean squared error decreases, signifying a better balance. However, if we move the mean too far from the center, the mean squared error increases again, indicating increased imbalance. This demonstration illustrates that the empirical mean serves as the balancing point for the empirical distribution, and we will utilize this concept when discussing the population mean, which serves as the balancing point for the population distribution.

Example: Suppose we flip a fair coin, and we assign the value 0 to tails and the value 1 to heads. What is the expected value of X? Again, the expected value represents a property of the population. By plugging the values into our formula, we calculate the expected value of X as follows:

When we compute this expression, we find that the expected value of X is 0.5. It’s interesting to note that the expected value is a value that the coin itself cannot actually take. However, from a geometric perspective, the answer becomes quite obvious. If we visualize the coin’s values as two bars of equal height, one at 0 and the other at 1, we can easily determine the balancing point by placing our finger exactly at 0.5.



Figure : Figure 1.11: Expected value of a coin flip

Example: A random variable X represents the outcome of a biased coin flip. The probability of obtaining heads is denoted as , while the probability of obtaining tails is . What is the expected value of X in this case? By directly applying the formula, we multiply the value 0 by the probability and add it to the value 1 multiplied by the probability . The result simplifies to . Therefore, the expected value of a coin flip, even when the coin is biased, corresponds to the true long-run proportion of obtaining heads in an infinite number of coin flips.

Example: Suppose we roll a fair six-sided die, and X represents the number that appears face up. What is the expected value of X? Here, we take the values 1, 2, 3, 4, 5, and 6 and multiply each by the corresponding probability of the random variable X taking those values (each value has a probability of ). When we perform this calculation, we find that the expected value of X is 3.5. Once again, this is a value that the die itself cannot actually show.



Figure : Figure 1.12: Expected value of a die roll

Similar to the coin example, the geometric argument makes it evident. We have six bars, each with a height of , representing the possible outcomes of the die. If we were to balance them, it becomes clear that the balancing point would be at 3.5. ### Expected values for PDFs When dealing with continuous random variables, it can be helpful to imagine cutting out the shape of probability density on a piece of wood and determining where you would place your finger to balance it out. This concept aligns with the notion of the center of mass of a continuous body. In the case of probability mass functions, as the bars representing the probabilities become narrower and smaller, we can visualize their balancing point.

Example: Suppose we have a density that ranges from zero to one, and the question arises: Is this a valid density? The answer is yes; it corresponds to a well-known density called the **Uniform density**. Now, what is its expected value? If we were to cut this density out of a piece of wood and balance it, the position where we would place our finger to achieve balance is precisely at 0.5. This aligns perfectly with the expected value of the uniform density.



Figure : Figure 1.13: Uniform density

It’s crucial to understand that expected values represent properties of the distribution. They serve as the center of mass of a distribution. Additionally, it’s important to note that the average of random variables is, in itself, a random variable. For example, if we roll six dice and calculate their average, the resulting value is a random variable. By repeatedly sampling from this average through multiple dice rolls, we generate a distribution that also possesses an expected value. The center of mass of this distribution coincides with the center of mass of the original distribution.

This topic becomes highly relevant to the field of inference, so let’s explore some simulation examples to gain a better understanding.



Figure : Figure 1.14: Simulation example

In the first example, the blue density represents the outcome of numerous simulations based on a standard normal distribution. Due to the large number of simulations, this density provides a reliable approximation of the true distribution. It shows that collecting ample data from a population allows us to approximate its originating distribution effectively. The center of mass of this distribution, which would achieve balance, is located at zero.

Now, let’s shift our focus to simulating the average of ten standard normals. By repeatedly performing this process and plotting the resulting histogram or density estimate, we obtain a different distribution. It no longer represents the distribution of standard normals; rather, it illustrates the distribution of averages of ten standard normals. This new distribution, represented by the salmon-colored plot, exhibits interesting properties. Notably, it is concentrated around zero, and this aligns with our previous point. The distribution of averages from a population tends to be centered at the same location as the distribution of the original population itself.

Although calculations and simulations can help us grasp these concepts conceptually, we can observe this phenomenon without explicitly performing them. Imagine rolling a die thousands of times and plotting a histogram of the results. In this case, approximately of the rolls would occur for each number from one to six. As we increase the number of rolls, these bars would eventually balance out. The center of mass for this distribution, which would achieve balance, is 3.5 (not exactly, given the finite number of rolls, but in theory, it would converge to 3.5 with an infinite number of rolls).



Figure : Figure 1.15: Die roll simulation

Consider the scenario where we roll the die twice and calculate the average of the numbers obtained. If we repeat this process multiple times and create a distribution of these averages, we see a different pattern in the second panel. It appears more Gaussian in shape (we’ll discuss this further later), and importantly, it is centered at the same location as before.



Figure : Figure 1.16: Coin toss average

The population mean of averages of two die rolls is identical to the population mean of individual die rolls. This concept applies to other scenarios as well. For instance, if we were to flip a coin numerous times, we would expect approximately 50% of the outcomes to be zero (tails) and 50% to be one (heads). These proportions would converge to balance at around 0.5. When flipping the coin only a few times, the observed sample proportion may deviate from 0.5. However, as we increase the number of flips, the simulation variability becomes insignificant, and the proportion approaches 0.5.

If we flip the coin ten times, calculate the average, and repeat this process multiple times. This simulation provides insights into the distribution of averages of ten coin flips. We can extend this analysis to averages of 20 coin flips and averages of 30 coin flips. In each case, we observe that as the average incorporates more coin flips, the distribution becomes more concentrated around the mean. Nevertheless, regardless of the number of coin flips involved, the distribution of averages is consistently centered at 0.5.

To summarize the key points covered thus far:

* Expected values are inherent properties of distributions. The population mean represents the center of mass of that population, and any movement in the mean would correspondingly shift the distribution.
* The sample mean represents the center of mass of the observed data. It serves as an estimate of the population mean and is considered unbiased.
* The population mean of the distribution of sample means precisely matches the population mean it aims to estimate. This understanding is vital as it allows us to estimate the population distribution accurately when collecting substantial amounts of data.
* We must recognize that while we obtain only one sample mean from our data, knowing the properties associated with sample means is immensely valuable.
* As more data contributes to the sample mean, the density mass function becomes more concentrated around the population mean. We also observe that, even in cases such as coin flipping and dice rolling, the distribution tends to exhibit Gaussian-like characteristics. We’ll explore these concepts further in subsequent lectures.

## 1.5 Practical R Exercises in swirl

During this course we’ll be using the [swirl](http://swirlstats.com/) software package for R in order to illustrate some key concepts. The swirl package turns the R console into an interactive learning environment. Using swirl will also give you the opportunity to construct and explore your own regression models. In this programming assignment, you’ll have the opportunity to practice some key concepts from this course.

Since swirl is an R package, you can easily install it by entering a single command from the R console:

install.packages("swirl")

If you’ve installed swirl in the past make sure you have version 2.2.21 or later. You can check this with:

packageVersion("swirl")

Every time you want to use swirl, you need to first load the package. From the R console:

library(swirl)

Install the Statistical Inference course swirl offers a variety of interactive courses, but for our purposes, you want the one called Statistical Inference. Type the following from the R prompt to install this course:

install\_from\_swirl("Statistical Inference")

Start swirl and complete the lessons Type the following from the R console to start swirl:

swirl()

Then, follow the menus and select the Statistical Inference course when given the option. For the first part of this course you should complete the following lessons:

* Introduction
* Probability1
* Probability2
* ConditionalProbability
* Expectations

If you need help…

* Visit the [Frequently Asked Questions](https://github.com/swirldev/swirl/wiki/Coursera-FAQ) (FAQ) page to see if you can answer your own question immediately.
* Search the Discussion Forums this course.
* If you still can’t find an answer to your question, then create a new thread under the swirl Programming Assignment sub-forum and provide the following information:
  + A descriptive title
  + Any input/output from the console (copy & paste) or a screenshot
  + The output from sessionInfo()

Good luck and have fun!

For more information on swirl, visit Swirlstats(<https://swirlstats.com>).

# 2 Variability, Distribution, & Asymptotics

## 2.1 Variability

An important characterization of a population is how spread out it is. One of the key measures of spread is variability. We measure population variability with the sample variance, or more often we consider the square root of it, called the standard deviation. The reason for taking the standard deviation is because that measure has the same units as the population. So if our population is a length measurement in meters, the standard deviation is in meters (whereas the variance is in meters squared). Variability has many important uses in statistics. First, the population variance is itself an intrinsically interesting quantity that we want to estimate. Secondly, variability in our estimates is what makes them not imprecise. An important aspect of statistics is quantifying the variability in our estimates.

In the previous lecture, we discussed the population mean as a measure of the center of a distribution. Now, let’s explore another important property called variance, which describes the spread or concentration of the density around the mean. If we imagine a bell curve, the probability density function will shift to the left or right as the mean changes. Variance quantifies how widely or narrowly the density is distributed around the mean. 

library(ggplot2)  
x <- seq(-4, 4, length.out = 1000)  
mean <- 0  
  
# Standard deviations  
sds <- c(0.5, 1, 1.5, 2)  
  
# Create the plot  
plot(x, dnorm(x, mean = mean, sd = sds[1]), type = "l", lwd = 3, xlab = "x", ylab = "",yaxt="n")  
  
# Add lines for the other distributions with different colors  
colors <- c("blue", "green", "orange", "purple")  
for (i in 1:length(sds)) {  
 lines(x, dnorm(x, mean = mean, sd = sds[i]), col = colors[i], lwd = 3)  
}  
  
# Add legend  
legend("topright", legend = paste("sd=", sds), col = colors, lwd = 2,box.lwd = 0, box.col = "white")

The blue-colored density represents a standard normal distribution with a standard deviation of 0.5. As the standard deviation increases, the density becomes flatter and spreads more into the tails. Consequently, if a variable is from a normal distribution with a standard deviation of 1.5, they are more likely to have a value beyond 2 compared to a variable from a normal distribution with a standard deviation of 1.

For a random variable X with a mean μ, the variance is precisely the expected squared distance between the random variable and the mean.

There’s also a useful shortcut:

Densities with higher variance are more spread out compared to those with lower variances. The square root of variance is known as the standard deviation, which is expressed in the same units as X.

Example: In the previous lecture, we found that the expected value of X, when rolling a die, is 3.5.

To calculate the expected value of X squared, we square each number (1, 2, 3, 4, 5) and multiply them by their associated probabilities. Summing these values gives us 15.17.

Example: Consider tossing a coin with a probability of heads, . From the previous lecture, we know that the expected value of a coin toss is . When calculating the expected value of X squared, 0 squared is 0, and 1 squared is 1. Thus, the expected value of X squared is . Plugging these values into our formula, we get , which simplifies to . This formula is widely recognized and we suggest you memorize it.

Similar to the relationship between population mean and sample mean, the population variance and sample variance are directly analogous. The population mean represents the center of mass of the population, while the sample mean represents the center of mass of the observed data. Similarly, the population variance quantifies the expected squared distance of a random variable from the population mean, while the sample variance measures the average squared distance of the observed data points from the sample mean.

Note that in the denominator of the sample variance formula, we divide by instead of .

Recall that the sample variance is a function of the data, making it a random variable with its own population distribution. The expected value of this distribution corresponds to the population variance being estimated by the sample variance. As we gather more data, the distribution of the sample variance becomes increasingly concentrated around the population variance it seeks to estimate.

### 2.1.1 Variance simulation examples

Suppose we simulate ten standard normal random variables and calculate their sample variance. If we repeat this process many times, we will obtain a distribution of sample variances. This distribution, represented by the salmon-colored density, emerges from repeating the process thousands of times. If we sample enough data points, the center of mass of this distribution will precisely match the variance of the original population we were sampling from—the standard normal distribution with a variance of one.



Figure : Figure 1.3: Variance of a distribution of die roll

library(ggplot2)  
nosim <- 10000;   
dat <- data.frame(  
 x = c(apply(matrix(rnorm(nosim \* 10), nosim), 1, var),  
 apply(matrix(rnorm(nosim \* 20), nosim), 1, var),  
 apply(matrix(rnorm(nosim \* 30), nosim), 1, var)),  
 n = factor(rep(c("10", "20", "30"), c(nosim, nosim, nosim)))   
 )  
ggplot(dat, aes(x = x, fill = n)) + geom\_density(size = 2, alpha = .2) + geom\_vline(xintercept = 1, size = 2)

The same holds true when we consider sample variances based on 20 observations from the standard normal distribution. we repeat the process of sampling 20 standard normals, calculating the sample variance, and obtaining a distribution of sample variances. This distribution, depicted in a more aqua color, is also centered at one. The pattern continues when we examine sample variances based on 30 observations. However, what’s interesting to note is that as the sample size increases, the variance of the population distribution of the sample variances becomes more concentrated. In simpler terms, collecting more data leads to a better and more tightly focused estimate of what the sample variance is trying to estimate. In this case, all the sample variances are estimating a population variance of one because they are sampled from a population with a variance of one.

Before we found that the variance of a die roll was . Now, imagine if we were to roll ten dice and calculate the sample variance of the numbers on the sides facing up. By repeating this process numerous times, we can obtain a reliable understanding of the population distribution of the variance of ten die rolls. Although it requires a large number of repetitions, with the help of a computer, we can simulate this process thousands of times, as demonstrated here. 

dat <- data.frame(  
 x = c(apply(matrix(sample(1 : 6, nosim \* 10, replace = TRUE),   
 nosim), 1, var),  
 apply(matrix(sample(1 : 6, nosim \* 20, replace = TRUE),   
 nosim), 1, var),  
 apply(matrix(sample(1 : 6, nosim \* 30, replace = TRUE),   
 nosim), 1, var)  
 ),  
 size = factor(rep(c(10, 20, 30), rep(nosim, 3))))  
g <- ggplot(dat, aes(x = x, fill = size)) + geom\_histogram(alpha = .20, binwidth=.3, colour = "black")   
g <- g + geom\_vline(xintercept = 2.92, size = 2)  
g + facet\_grid(. ~ size)

Notice that the distribution of the variance of ten die rolls is precisely centered around 2.92, which is the variance of a single die roll. As I increase the number of dice to 20 and 30, the center of the distribution remains the same, but it becomes more concentrated around the true population variance. This indicates that the sample variance provides a good estimate of the population variance. As we collect more data, the distribution of the sample variance becomes increasingly concentrated around the true value it aims to estimate, demonstrating its unbiasedness.

The reason we divide by instead of in the denominator of the sample variance formula is to ensure its unbiasedness. ### Standard error of the mean Now that we have extensively discussed variances and briefly touched upon the distribution of sample variances, let’s revisit the distribution of sample means. It is important to remember that the average of numbers sampled from a population is a random variable with its own population mean and population variance. The population mean remains the same as the original population, while the variance of the sample mean can be related to the variance of the original population. Specifically, the variance of the sample mean decreases to zero as more data is accumulated.

This means that the sample mean becomes more concentrated around the population mean it is trying to estimate, which is a valuable characteristic since we usually only have one sample mean in a given dataset.

Although we do not have multiple repeated sample means to investigate their variability like we do in simulation experiments, we can still estimate the population variance, denoted as , using the available data. With knowledge of and the sample size (denoted as n), we can gather valuable information about the distribution of the sample mean. The square root of the statistic, sigma over square root n, is referred to as the standard error of the mean, denoted as the standard deviation of the distribution of a statistic. The term “standard error” is used to represent the variability of means, while the standard error of a regression coefficient describes the variability in regression coefficients.

In summary, considering a population with a mean and variance , when we draw a random sample from that population and calculate the variance , it serves as an estimate of . Similarly, when we calculate the mean, it estimates (population mean). However, (sample variance) is also a random variable with its own distribution centered around , becoming more concentrated around it as more observations contribute to the squared value. Additionally, the distribution of sample means from that population is centered at and becomes more concentrated around as more observations are included. Moreover, we precisely know the variance of the distribution of sample means, which is divided by n.

Since we lack repeated sample means in a given dataset, we estimate the sample variance of the mean as divided by n and the logical estimate of the standard error as . The standard error of the mean (or the sample standard error of the mean) is defined as . The standard deviation (S) is an estimate of the variability of the population, while the standard error () represents the variability of averages of random samples of size n from the population.

Example: If we take standard normals (with a variance of one), the standard deviation of means of n standard normals is expected to be one over . By simulating multiple draws of ten standard normals and calculating their mean, followed by taking the standard deviation of these averages, we should obtain an approximate value of .

You can explore this using the following code snippet in R:

nosim <- 1000  
n <- 10  
sd(apply(matrix(rnorm(nosim \* n), nosim), 1, mean))

## [1] 0.326209

1 / sqrt(n)

## [1] 0.3162278

Similar simulations can be performed for standard uniforms (variance of ), Poisson(4) distributions (variance of 4), and coin flips (variance of , assuming p=0.5 then ). The results of these simulations should align with the theoretical values predicted by our rule.

Understanding the standard error of the mean is crucial in determining the variability of sample means. Simulation experiments can help illustrate these concepts, especially when investigating the distribution of sample means and estimating their standard error.

Example: Consider the father-son data from UsingR library. We will focus on the height of the sons, with “n” representing the number of observations as usual. If we plot a histogram of the son’s height and overlay it with a continuous density estimate, we observe a distribution that closely resembles a Gaussian curve. 

library(UsingR); data(father.son);   
x <- father.son$sheight  
n<-length(x)  
g <- ggplot(data = father.son, aes(x = sheight))   
g <- g + geom\_histogram(aes(y = ..density..), fill = "lightblue", binwidth=1, colour = "black")  
g <- g + geom\_density(size = 2, colour = "black")  
g

This density estimate provides an approximation of the population density, given the finite amount of data we have collected. The histogram’s variability, which the sample variance calculates, serves as an estimate of the variability in son’s height from the population this data was drawn from, assuming it was a random sample.

By calculating the variance of x, variance of x divided by n, standard deviation of x, and standard deviation of , and rounding them to two decimal places, we obtain 7.92 and 2.81 as the variance of x and the standard deviation of x, respectively.

library(UsingR); data(father.son);   
x <- father.son$sheight  
n<-length(x)  
round(c(var(x), var(x) / n, sd(x), sd(x) / sqrt(n)),2)

These numbers represent the variability in son’s heights from the dataset and act as estimates of the population variability of son’s heights if we assume these sons are a random sample from a meaningful population. In this case, we prefer the value 2.81 over 7.92 since 7.92 is expressed in inches squared, while 2.81 is expressed in inches. Working with the actual units is more intuitive. Moving on to 0.01 and 0.09, these values no longer reflect the variability in children’s heights. Instead, they represent the variability in averages of ten children’s heights. The value 0.09 is particularly meaningful as it represents the standard error or the standard deviation in the distribution of averages of n children’s heights. While it’s an estimate based on the available data, it’s the best estimate we can derive from the dataset.

In this section we covered several complex topics, but at its core, understanding variability is the key to understanding statistics. In fact, grasping the concept of variability might be the most crucial aspect of statistics. Here’s a summary of our findings: the sample variance provides an estimate of the population variance, and the distribution of the sample variance is centered around the value it is estimating, indicating an unbiased estimation. Moreover, as more data is collected, the distribution becomes more concentrated around the estimated value, leading to a better estimate. We have also gained insights into the distribution of sample means. In addition to knowing its center, as discussed in the previous lecture, we now understand that the variance of the sample mean is the population variance divided by n, and its square root, is known as the standard error. These quantities capture the variability of averages drawn from the population, and surprisingly, even though we only have access to one sample mean in a given dataset, we can make substantial inferences about the distribution of averages from random samples. This knowledge provides us with a solid foundation for various statistical analyses and methodologies. ## Distributions Some probability distributions are so important that we need to internalize their characteristics. Here we will cover the most important probability distributions. ### Binomial distribution Perhaps the simplest distribution is known as the Bernoulli distribution, named after Jacob Bernoulli, a renowned mathematician from a distinguished family of mathematicians. If you’re interested, you can explore the Bernoulli family further through their Wikipedia pages. The Bernoulli distribution originates from a coin flip, where a “0” represents tails and a “1” represents heads. We can consider a potentially biased coin with a probability “p” for heads and “1 - p” for tails. The Bernoulli probability mass function is typically denoted as:

As we have seen before, the mean of a Bernoulli random variable is , and the variance is . In the context of a Bernoulli random variable, we often refer to “x = 1” as a success, irrespective of the specific definition of success in a given scenario, and “x = 0” as a failure.

A binomial random variable is obtained by summing up a series of independent and identically distributed (iid) Bernoulli random variables. Essentially, a binomial random variable represents the total number of heads obtained in a series of coin flips with a potentially biased coin. Mathematically, if we let to be iid Bernoulli variables with parameter , then the sum of these variables, denoted as , is a binomial random variable.

The binomial probability mass function closely resembles the Bernoulli mass function, but with the inclusion of “n choose x” in front. The notation “n choose x” represents the binomial coefficient, calculated as . It is worth noting that “n choose 0” and “n choose n” both equal 1. This coefficient helps solve a common combinatorial problem, counting the number of ways to select “x” items out of “n” without replacement while disregarding the ordering of the items.

Example: Suppose your friend has eight children, with seven of them being girls (and no twins). Assuming each gender has an independent 50% probability for each birth, what is the probability of having seven or more girls out of eight births? We can apply the binomial formula to calculate this probability:

In the provided R code, you can find the implementation of this calculation. Furthermore, for most common distributions, including the binomial distribution, there are built-in functions in R. For example, the pbinom function can be used to obtain these probabilities conveniently.

choose(8, 7) \* .5 ^ 8 + choose(8, 8) \* .5 ^ 8   
pbinom(6, size = 8, prob = .5, lower.tail = FALSE)

### 2.1.2 Normal distribution

Probabilities play a crucial role in statistics, and among all the distributions, the normal distribution stands out as the most important one. In the upcoming lecture, we will explore why it holds such significance. In fact, if all distributions were to gather and elect a leader, the normal distribution would undoubtedly take the crown.

A random variable that follows a normal (Gaussian) distribution with a mean of and a variance of . This distribution is characterized by a density function that resembles a bell curve. If we have a random variable X with this density, its expected value is μ, and its variance is . We can express this concisely as , denoting a normal distribution with mean μ and variance . When μ=0 and σ=1, the resulting distribution is known as the **standard normal distribution**. Standard normal random variables are often denoted by the letter . Here, we depict the standard normal density function, which represents the famous bell curve you have likely encountered before.

x <- seq(-3, 3, length = 1000)  
library(ggplot2)  
g <- ggplot(data.frame(x = x, y = dnorm(x)),   
 aes(x = x, y = y)) + geom\_line(size = 2)  
g <- g + geom\_vline(xintercept = -3 : 3, size = 2)  
g



Figure : Figure 1.12: Standard normal distribution

It is important to note that for the standard normal distribution, the mean is 0, and the standard deviation (and variance) is 1. In the diagram, we illustrate one standard deviation above and below the mean, two standard deviations above and below the mean, and three standard deviations above and below the mean. The units on the standard normal distribution can be interpreted as standard deviation units. Additionally, it is worth mentioning that statisticians often find it convenient to revert to the standard normal distribution when discussing normal probabilities, even when dealing with non-standard normal distributions. Therefore, if you want to calculate the probability that a non-standard normal lies between and (where μ and σ are specific to its distribution), the probability area is equivalent to that between -1 and +1 on the standard normal distribution. In essence, all normal distributions have the same underlying shape, with the only difference being the units along the axis. By reverting to standard deviations from the mean, all probabilities and calculations can be transformed back to those associated with the standard normal distribution.

Some fundamental reference probabilities related to the standard normal distribution can be easily explained using the graph above as visual aids. First, consider one standard deviation from the mean in the standard normal distribution (or any normal distribution). Approximately 34% of the distribution lies on each side, resulting in a total area of 68% within one standard deviation. Moving on to two standard deviations, denoted by the magenta area in the diagram, around 95% of the distribution falls within this range for any normal distribution. This leaves 2.5% in each tail, and we often utilize this information when calculating confidence intervals. Lastly, when considering three standard deviations from the mean, the area encompasses approximately 99% of the distribution’s mass, although it may be difficult to discern from the diagram. *These reference probabilities are essential to commit to memory.*

Probabilities are a fundamental concept, and the normal distribution holds a special place in statistics. Understanding its properties and the relationship to the standard normal distribution allows us to solve problems effectively. All normal distributions share the same essential shape, differing only in their units along the axis. By leveraging the standard normal distribution and converting the non standard normals to standard normals, we can simplify calculations and derive consistent results. The primary difference between different normal distributions lies in the units along the axis. When discussing normal probabilities and converting to standard deviations from the mean, all probabilities and calculations revert back to those associated with the standard normal distribution.

Rules for converting between standard and non-standard normal distributions. If we have a random variable X that follows a normal distribution with a mean of μ and variance of σ squared, we can convert the units of X to standard deviations from the mean by subtracting the mean μ and dividing by the standard deviation σ. If then:

The resulting random variable Z will follow a standard normal distribution. Conversely, if we start with a standard normal random variable Z and want to convert back to the units of the original data, we multiply Z by σ and add μ. If is standard normal

The resulting random variable X will then follow a non-standard normal distribution with a mean of μ and variance of .

Standard normal quantiles that are important to remember -1.28 is a quantile such that 10% of the density lies below it, and 90% lies above it. By symmetry, 1.28 on the standard normal distribution represents the quantile at which 10% lies above it. For a potentially non-standard normal distribution, this point would be . Another crucial quantile is 1.96 (often approximated as 2), where -1.96 represents the point below which 2.5% of the mass of the normal distribution lies, and +1.96 represents the point above which 2.5% of the mass lies. This implies that 95% of the distribution lies between these two points. For a potentially non-standard normal distribution, these points would be and , respectively. It is worth noting that when μ equals 0 and σ equals 1 for the standard normal distribution, the calculation of 1.96 directly yields the correct value.

Example: Determine the percentile of a normal distribution with mean μ and variance σ squared. In other words, we seek the value such that 95% of the distribution lies below it. This value represents the threshold if we were to draw samples from this population.

We can find the point , which represents the percentile of a normal distribution, by utilizing the q qualifier for the density in R. In this case, we can use the function qnorm with the desired quantile 0.95.

qnorm(0.95, mean = mu, sd = sd)

It’s crucial to input the mean μ and the standard deviation σ (not the variance) into the function. By using qnorm with the specified parameters, we can directly obtain the desired value. Another approach to solving this is by leveraging our memorized standard normal quartiles. Since we know that 1.645 standard deviations from the mean corresponds to a quantile with 95% lying below it and 5% lying above it for the standard normal distribution (centered at 0 with standard deviation units from the mean), we can apply this concept to a non-standard normal distribution as well. To calculate the desired point, we can simply compute .

Example: What is the probability that a non-standard normal distribution is larger than x? To answer this question in R, we can use the pnorm function with the specified values of , , and standard deviation (). It’s important to remember to input the sigma value rather than the value to avoid incorrect results. Additionally, we set the argument lower.tail = FALSE to indicate that we are interested in the upper tail of the distribution. Alternatively, we can omit this argument and calculate to achieve the same result.

A conceptually easy way to estimate this probability, which allows us to quickly assess probabilities mentally, is to convert the value x into the number of standard deviations it is from the mean. To achieve this, we compute . The resulting number represents x expressed in terms of how many standard deviations it is from the mean. For example, if the calculated value is approximately two standard deviations from the mean, we can estimate that the probability associated with it is around 2.5%.

Example: The number of daily ad clicks for companies follows an approximately normal distribution with a mean of 1020 clicks per day and a standard deviation of 50 clicks per day. We want to determine the probability of getting more than 1160 clicks on a given day.

Since which means 2.8 standard deviation away from the mean, we can infer that this probability will be relatively low. This is because it is nearly 3 standard deviations away from the mean, and we know that such values are located in the tail of the normal distribution. To calculate this probability, we can use the pnorm function with the input values of 1,160 for the clicks, a mean of 1,020, and a standard deviation of 50.

pnorm(1160, mean = 1020, sd = 50, lower.tail = FALSE)  
pnorm(2.8, lower.tail = FALSE)

By setting the argument lower.tail = FALSE, we ensure that we obtain the probability of the value being larger than 1,060. The result we obtain is approximately 0.003.

Alternatively, we can directly calculate this probability using the standard normal distribution. By expressing 1,160 as the number of standard deviations it is away from the mean, which is 2.8, we can plug this value into the pnorm function with lower.tail = FALSE and obtain the same result.

pnorm(2.8, lower.tail = FALSE)

Example: Assuming the number of daily ad clicks for the company follows an approximately normal distribution with a mean of 1020 and a standard deviation of 50, we want to find the number of daily ad clicks that represents the point where 75% of the days have fewer clicks.

Since 1020 is both the mean and the median of the specific normal distribution, we know that about 50% of the days lie below this point. Therefore, the desired number of clicks should be greater than 1020. Additionally, one standard deviation above the mean, which corresponds to 1,070. Within this range, we know that 68% of the days lie, leaving 32% outside of it, and 16% in each tail due to the symmetry of the normal distribution. Hence, the desired number of clicks should be around 84% of the distribution, lying between 1,020 and 1,070.

To calculate this quantile, we can use the qnorm function with the input value of 0.75, representing the 75th percentile. The mean is set to 1020, and the standard deviation is 50. When we execute this command, qnorm(0.75, mean = 1020, sd = 50), we obtain a number between the previously mentioned range, approximately 1054.

### 2.1.3 Poisson distribution

If there were a competition to determine the most useful distribution, the normal distribution would unquestionably win by a wide margin. However, selecting the second most useful distribution would spark a lively debate, with the Poisson distribution being a strong contender. The Poisson distribution is commonly employed to model counts, and its probability mass function is given by

where x represents non-negative integers (0, 1, 2, and so on). The mean of a Poisson random variable is equal to , and the variance also equals . When modeling with Poisson data, the mean and variance must be equal a condition that can be verified if one has repeated Poisson data. fig xxx poisson distribution

The Poisson distribution finds utility in various instances. Whenever count data needs to be modeled, especially when the counts are unbounded, the Poisson distribution is a suitable choice. Another prevalent application arises in the field of biostatistics, where event time or survival data is common. For example, in cancer trials, the time until the recurrence of symptoms is modeled using statistical techniques that account for censoring, and these techniques have a strong association with the Poisson distribution. Additionally, when classifying a sample of people based on certain characteristics, creating a contingency table—such as tabulating hair color by race—the Poisson distribution is the default choice for modeling such data. The Poisson distribution is deeply connected to other models, including multinomials and binomials, which might be considered as alternatives.

Another prominent application of the Poisson distribution, though often overlooked due to its commonplace usage, is in cases where a binomial distribution is approximated by the Poisson distribution. This occurs when the sample size (n) is large, and the probability of success (p) is small. Epidemiology, for instance, frequently employs this approximation when dealing with situations where n is large (representing a population) and p is small (indicating the occurrence of rare events). By assuming a Poisson distribution, researchers can effectively model the occurrence rates of events, such as the number of new cases of respiratory diseases in a city as air pollution levels fluctuate. This practice is so prevalent that it is commonly understood within the field without explicit mention.

Example: The number of people showing up at a bus stop follows a Poisson distribution with a mean of 2.5 people per hour. If we observe the bus stop for four hours, we can calculate the probability of three or fewer people showing up during that entire duration. To do this, we apply the Poisson probability formula to the values of three, two, one, and zero, using a rate of 2.5 events per hour multiplied by four hours. The resulting probability is approximately 1%.

ppois(3, lambda = 2.5 \* 4)

Furthermore, we can discuss the Poisson approximation to the binomial distribution, specifically when the sample size (n) is large, and the probability of success (p) is small. In this scenario, the Poisson distribution can serve as a reasonably accurate approximation for the binomial distribution. To establish notation, let x represent a binomial distribution with parameters n and p, and define . When n is large and p is small, it is proposed that the probability distribution governing x can be well approximated using Poisson probabilities, where the rate parameter λ is determined as n times p.

Example: In flipping a coin with a success probability of 0.01 for a total of 500 times, we want to calculate the probability of obtaining two or fewer successes. Using the binomial distribution with size 500 and probability 0.01, we obtain approximately 12%. By employing the Poisson approximation with a rate of λ = 500 \* 0.01, the result is around 12.5%, which is reasonably close to the binomial calculation.

pbinom(2, size = 500, prob = .01)  
ppois(2, lambda=500 \* .01)

## 2.2 Asymptotics

Asymptotics are an important topics in statistics. Asymptotics refers to the behavior of estimators as the sample size goes to infinity. Our very notion of probability depends on the idea of asymptotics. For example, many people define probability as the proportion of times an event would occur in infinite repetitions. That is, the probability of a head on a coin is 50% because we believe that if we were to flip it infinitely many times, we would get exactly 50% heads.

We can use asymptotics to help is figure out things about distributions without knowing much about them to begin with. A profound idea along these lines is the **Central Limit Theorem**. It states that the distribution of averages is often normal, even if the distribution that the data is being sampled from is very non-normal. This helps us create robust strategies for creating statistical inferences when we’re not willing to assume much about the generating mechanism of our data. ### Asymptotics and LLN Here we will explore the behavior of statistics as the sample size or some other relevant quantity approaches infinity, which is known as asymptotics. Specifically, we will discuss the case where the sample size tends to infinity.

In the land of asymptopia, everything works out well because there is an infinite amount of data available. Asymptotics play a crucial role in simple statistical inference and approximations. They serve as a versatile tool, akin to a Swiss army knife, allowing us to investigate the statistical properties of various statistics without requiring extensive computations. Asymptotics form the foundation for the frequency interpretation of probabilities. For instance, intuitively, we know that if we flip a coin and calculate the proportion of heads, it should approach 0.5 for a fair coin.

Fortunately, we don’t have to delve into the mathematical intricacies of the limits of random variables. Instead, we can rely on a set of powerful tools that enable us to discuss the behavior of sample means from a collection of independently and identically distributed (iid) observations in large samples. One of these tools is the law of large numbers, which states that the average of the observations converges to the population mean it is estimating. For example, if we repeatedly flip a fair coin, the sample proportion of heads will eventually converge to the true probability of a head.

Example: We’ll generate a large number of random normal variables and calculate their cumulative means. Initially, there is considerable variability in the means, but as the number of simulations increases, the cumulative means converge towards the true population mean of zero.



Figure : Figure 2.2: Cumulative means of random normal variables

n <- 10000; means <- cumsum(rnorm(n)) / (1 : n); library(ggplot2)  
g <- ggplot(data.frame(x = 1 : n, y = means), aes(x = x, y = y))   
g <- g + geom\_hline(yintercept = 0) + geom\_line(size = 2)   
g <- g + labs(x = "Number of obs", y = "Cumulative mean")  
g

Similarly, we can apply the law of large numbers to the case of coin flipping. By repeatedly flipping a coin and calculating the cumulative means, we observe that the sample proportion of heads converges to the true value of 0.5 as the number of coin flips increases. 

means <- cumsum(sample(0 : 1, n , replace = TRUE)) / (1 : n)  
g <- ggplot(data.frame(x = 1 : n, y = means), aes(x = x, y = y))   
g <- g + geom\_hline(yintercept = 0.5) + geom\_line(size = 2)   
g <- g + labs(x = "Number of obs", y = "Cumulative mean")  
g

Note: An estimator is considered **consistent** if it converges to the parameter it aims to estimate. For instance, the sample proportion from iid coin flips is consistent for estimating the true success probability of a coin. As we collect more and more coin flip data, the sample proportion of heads approaches the actual probability of obtaining a head. Moreover, not only are sample means consistent estimators, but the sample variance and sample standard deviation of iid random variables are also consistent estimators.

The law of large numbers guarantees the consistency of sample means, but it also applies to sample variances and standard deviations of iid random variables. In other words, these estimators also converge to their respective population counterparts as the sample size increases.

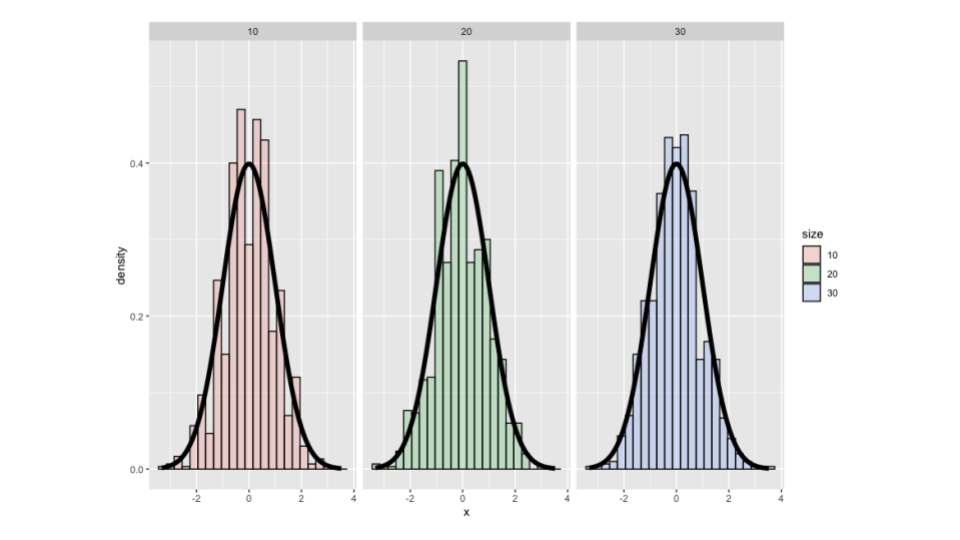
### 2.2.1 Asymptotics and the CLT

The Central Limit Theorem (CLT) is perhaps the most important theorem in statistics. It states that the distribution of averages of iid random variables becomes approximately standard normal as the sample size grows. The Central Limit Theorem is remarkably versatile, applying to a wide range of populations. Its loose requirements make it applicable in numerous settings.

To understand the Central Limit Theorem, let’s consider an estimate like the sample average . If we subtract its population mean and divide by its standard error the resulting random variable approaches a standard normal distribution as the sample size increases.

Importantly, replacing the unknown population standard deviation with the known sample standard deviation does not affect the Central Limit Theorem.

The most useful interpretation of the Central Limit Theorem is that the sample average is approximately normally distributed, with a mean equal to the population mean and a variance given by the standard error of the mean.

Example: Using standard die with the mean of 3.5, and variance of 2.92. We simulate the die roll n times, calculate the sample mean, subtract the population mean, and dividing by the standard error. 

nosim <- 1000  
cfunc <- function(x, n) sqrt(n) \* (mean(x) - 3.5) / 1.71  
dat <- data.frame(  
 x = c(apply(matrix(sample(1 : 6, nosim \* 10, replace = TRUE),   
 nosim), 1, cfunc, 10),  
 apply(matrix(sample(1 : 6, nosim \* 20, replace = TRUE),   
 nosim), 1, cfunc, 20),  
 apply(matrix(sample(1 : 6, nosim \* 30, replace = TRUE),   
 nosim), 1, cfunc, 30)  
 ),  
 size = factor(rep(c(10, 20, 30), rep(nosim, 3))))  
g <- ggplot(dat, aes(x = x, fill = size)) + geom\_histogram(alpha = .20, binwidth=.3, colour = "black", aes(y = ..density..))   
g <- g + stat\_function(fun = dnorm, size = 2)  
g + facet\_grid(. ~ size)

The distribution approximates a bell curve. As we increase the number of rolls, the approximation improves.

Example: Let be the or result of the flip of a possibly unfair coin. The sample proportion, say , is the average of the coin flips. and Standard error of the mean is Then

will be approximately normally distributed

Flipping a fair coin times, taking the sample proportion of heads, subtracting off 0.5 and multiply the result by divide by is displayed below.

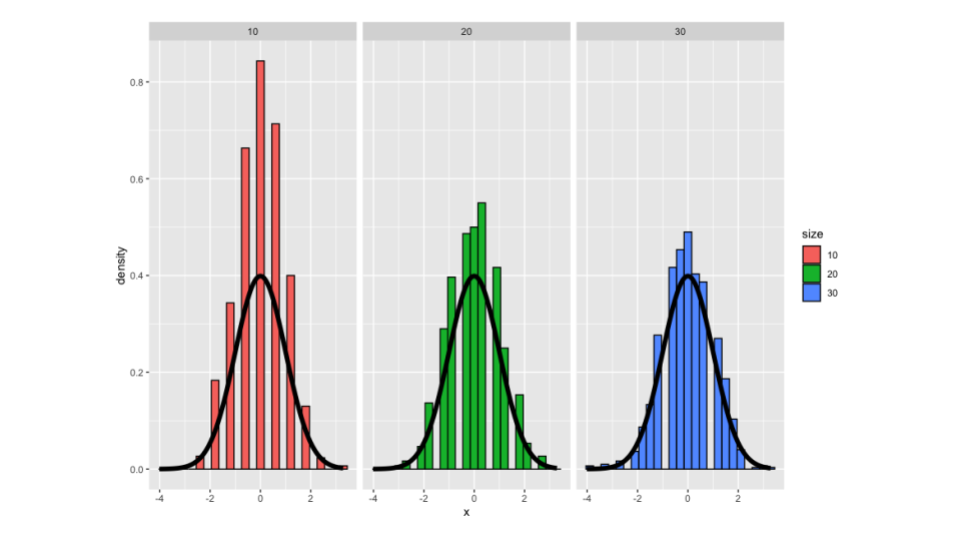


Figure : Figure 2.5: Distribution of averages of iid random variables in coin flip

nosim <- 1000  
cfunc <- function(x, n) 2 \* sqrt(n) \* (mean(x) - 0.5)   
dat <- data.frame(  
 x = c(apply(matrix(sample(0:1, nosim \* 10, replace = TRUE),   
 nosim), 1, cfunc, 10),  
 apply(matrix(sample(0:1, nosim \* 20, replace = TRUE),   
 nosim), 1, cfunc, 20),  
 apply(matrix(sample(0:1, nosim \* 30, replace = TRUE),   
 nosim), 1, cfunc, 30)  
 ),  
 size = factor(rep(c(10, 20, 30), rep(nosim, 3))))  
g <- ggplot(dat, aes(x = x, fill = size)) + geom\_histogram(binwidth=.3, colour = "black", aes(y = ..density..))   
g <- g + stat\_function(fun = dnorm, size = 2)  
g + facet\_grid(. ~ size)

Taking the result of each flip (0 or 1) as an iid random variable, we calculate the sample proportion of heads . We again obtain a distribution that approximates a bell curve. Similar to the previous example, the approximation improves as the number of coin flips increases.

It’s important to note that the speed at which the normalized coin flips converge to normality depends on the bias of the coin. If the coin is heavily biased, the approximation may not be perfect even with a large sample size. However, as the number of coin flips approaches infinity, the Central Limit Theorem guarantees an excellent approximation.

As a fun example, let’s discuss Galton’s quincunx. This machine, often found in science museums, visually demonstrates the Central Limit Theorem using a game resembling Pachinko. [An image from Wikipedia showing Galton’s quincunx](https://upload.wikimedia.org/wikipedia/commons/c/c1/Galton_box.jpg). In Galton’s quincunx, a ball falls through a series of pegs, bouncing left or right at each peg. Each bounce can be thought of as a coin flip or binomial experiment. The total number of successes (heads) follows an approximately normal distribution, as predicted by the Central Limit Theorem. At the museum, the balls collect in bins, forming a histogram that aligns with the expected normal distribution.

In summary, the Central Limit Theorem is a powerful tool that allows us to approximate the distribution of averages of iid random variables. It applies to various settings and provides valuable insights into statistical inference. The examples we explored, from dice rolls to coin flips to Galton’s quincunx, illustrate the practical applications of the Central Limit Theorem and the convergence to a standard normal distribution as the sample size increases.

### 2.2.2 Asymptotics and confidence intervals

The central limit theorem tells us that the sample mean follows an approximately normal distribution with a population mean of μ and a standard deviation of . This distribution allows us to make inferences about the population mean based on sample data. When considering the distribution, we observe that standard errors is quite far out in the tail, with only a 2.5% chance of a normal value being larger than two standard deviations in the tail. Similarly, standard errors is far in the left tail, with only a 2.5% chance of a normal value being smaller than two standard deviations in the left tail. Therefore, the probability that the sample mean is greater than standard errors or smaller than standard errors is 5%. Equivalently, the probability that μ is between these limits is 95%. By reversing the roles of and μ, we can conclude that the interval contains μ with a probability of 95%.

It’s important to note that in this interpretation, we treat the interval as random, while μ is fixed. This allows us to discuss the probability that the interval contains μ. In practice, if we repeatedly obtain samples of size n from the population and construct a confidence interval in each case, about 95% of the intervals will contain μ, the parameter we are trying to estimate. If we want a 90% confidence interval, we need 5% in each tail, so we would use a different multiplier instead of 2 (e.g., 1.645).

Example: Using the father-son data from the “Using R” package we want to estimate the average height of sons . We can calculate the mean of the sample plus or minus the 0.975th normal quantile times the standard error of the mean.

library(UsingR);data(father.son); x <- father.son$sheight  
(mean(x) + c(-1, 1) \* qnorm(.975) \* sd(x) / sqrt(length(x))) / 12

Dividing by 12 ensures that our confidence interval is in feet rather than inches. If we obtain a confidence interval of 5.710 to 5.738, we can say that if the sons’ height in this data are a random sample from the population of interest, the confidence interval for the average height of the sons would be 5.71 to 5.74.

Another application is when dealing with coin flips and estimating the success probability of the coin. Each observation in this case is either 0 or 1, with a common success probability . The variance of a coin flip is , where p is the true success probability of the coin. The standard error of the mean is then:

Since we don’t know the true value of , we replace it with the estimated value . This type of confidence interval is known as the **Wald confidence interval**, named after the statistician Wald. When p equals 0.5, the variance is maximized, resulting in a standard error of 0.5. Multiplying it by 2 in the 95% interval cancels out, leaving the following expression for a 95% confidence interval, which is a quick estimate for p:

Example: Imaging you are running for political office, and in a random sample of 100 likely voters, 56 intend to vote for you. To determine if you can relax or if you need to campaign more, you can use a quick calculation.

With the information from the sample you can with with probability of 0.56 taking means the approximate 95% interval is 0.46 to 0.66. The confidence interval suggests that we cannot rule out possibilities below 0.5 with 95% confidence. Therefore, you shouldn’t relax and should continue campaigning.

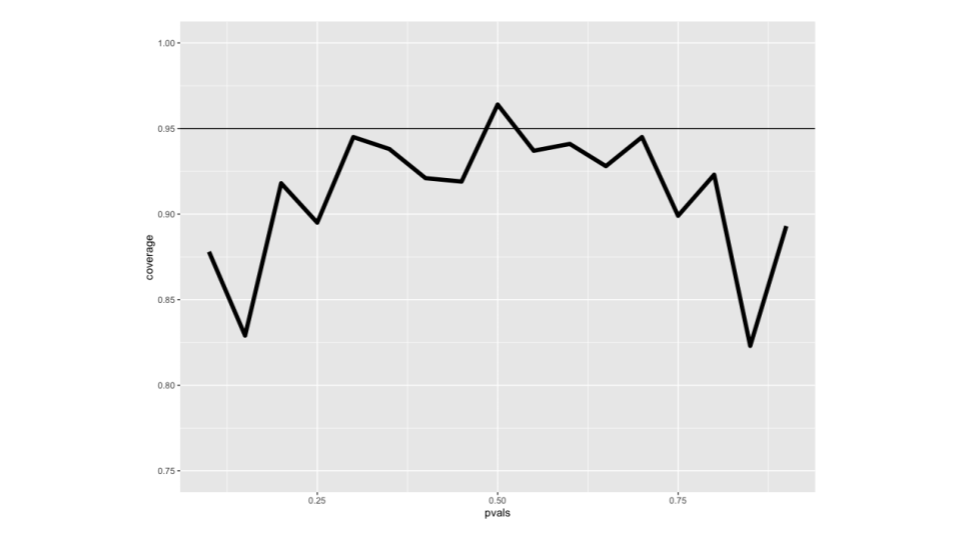
As a general guideline, you typically need at least 100 observations for one decimal place in a binomial experiment, 10,000 for two decimal places, and a million for three decimal places. These numbers reflect the approximate sample sizes needed for accurate estimation.

In summary, the central limit theorem provides us with a practical tool for constructing confidence intervals and making inferences about population parameters. It allows us to estimate the population mean using the sample mean and provides a measure of uncertainty through confidence intervals. The Wald confidence interval is a useful approximation for estimating the success probability in binomial experiments. Additionally, considering the sample size helps determine the level of precision and confidence in our estimates.

Consider a simulation where we repeatedly flip a coin with a known success probability. The goal is to calculate the percentage of times that the confidence interval covers the true probability. In each simulation, we flip the coin 20 times and vary the true success probability between 0.1 and 0.9 in steps of 0.05. We conduct 1,000 simulations for each true success probability.

n <- 20; pvals <- seq(.1, .9, by = .05); nosim <- 1000  
coverage <- sapply(pvals, function(p){  
 phats <- rbinom(nosim, prob = p, size = n) / n  
 ll <- phats - qnorm(.975) \* sqrt(phats \* (1 - phats) / n)  
 ul <- phats + qnorm(.975) \* sqrt(phats \* (1 - phats) / n)  
 mean(ll < p & ul > p)  
})

For each true success probability, we generate 1,000 sets of 20 coin flips and calculate the sample proportion. Then, we compute the lower and upper limits of the confidence interval for each set of coin flips. Finally, we determine the proportion of times that the confidence interval covers the true value of the success probability. we store these proportions in a variable called “coverage.”

To visualize the results, we can plot the coverage as a function of the true success probability used in the simulation. For example, if the true value of p is 0.5, we perform 1,000 simulations and calculate the coverage based on whether the confidence interval covers 0.5 or not. In this case, the coverage is over 95%, indicating that the confidence interval provides better than 95% coverage for a true success probability of 0.5. 

Although there is some Monte Carlo error due to the finite number of simulations, 1,000 simulations generally yield good accuracy. For a true success probability around 12%, the coverage falls well below the expected 95%. The reason behind this discrepancy is that the central limit theorem is not accurate enough for this specific value of n (the number of coin flips) and the true probability. To address this issue for smaller values of n, a quick fix is to add 2 to the number of successes and 2 to the number of failures. This adjustment modifies the sample proportion, making it . After applying this adjustment, the confidence interval procedure can be performed as usual. This modified interval is known as the **Agresti/Coull interval** and tends to perform better than the standard Wald interval. Before demonstrating the results for the adjusted intervals, it is important to note that larger values of n yield better performance. In a simulation where n is increased to 100, the coverage probability improves and remains close to the expected 95% across different values of p.

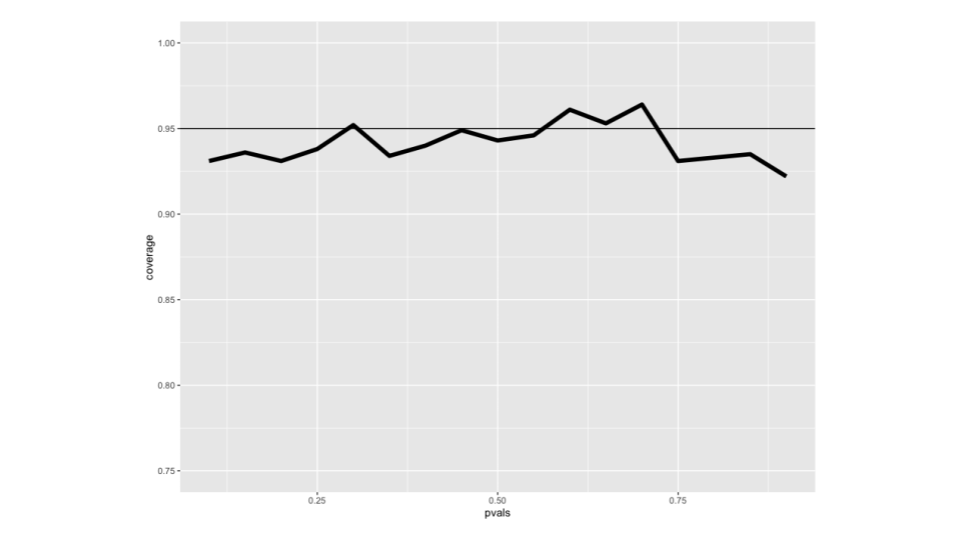


Figure : Figure 2.7: Coverage of confidence intervals for coin flips, n=100

Returning to the simulation with n=20, when using the add 2 successes and 2 failures interval, the coverage probability is higher than 95%, indicating an improvement compared to the poor coverage of the Wald interval for certain true probability values. However, it’s important to balance coverage and interval width, as being too conservative can lead to overly wide intervals. Based on these observations, we strongly recommend using the add 2 successes and 2 failures interval instead of the Wald interval in this specific scenario.

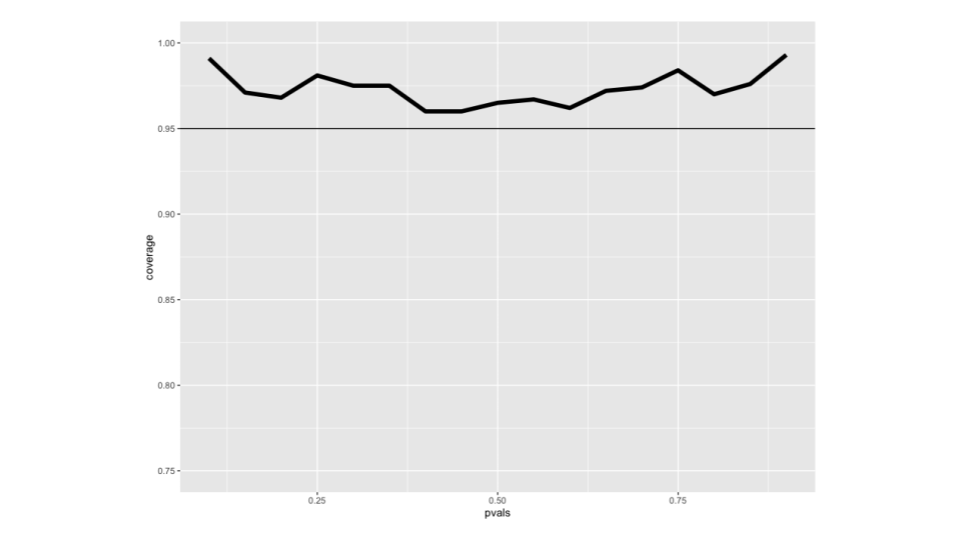


Figure : Figure 2.8: Coverage of confidence intervals for coin flips, n=20, add 2 successes and 2 failures

Example: Create a Poisson interval using the formula that involves the estimate plus or minus the normal quantile standard error. Although the application of the central limit theorem in this case may be less clear, we will discuss it shortly.Consider a nuclear pump that failed 5 times out of 94.32 days over a monitoring period. We want to calculate a 95% confidence interval for the failure rate per day. Assuming the number of failures follows a Poisson distribution with a failure rate of lambda and the monitoring period is denoted as t, the estimate of the failure rate is the number of failures divided by the total monitoring time. The variance of this estimate is .

x <- 5; t <- 94.32; lambda <- x / t  
round(lambda + c(-1, 1) \* qnorm(.975) \* sqrt(lambda / t), 3)  
poisson.test(x, T = 94.32)$conf

In the calculations performed in R, the number of events is set to 5, and the monitoring time is 94.32. The rate estimate is computed as , and the confidence interval estimate is obtained by adding or subtracting the relevant standard normal quantile multiplied by the standard error. The resulting interval is rounded to three decimal places. In addition to the large sample interval, we can also calculate an exact Poisson interval using the poisson.test function in R. This exact interval guarantees the specified coverage (e.g., 95%), but it may be conservative and result in wider intervals than necessary.

To examine how confidence intervals perform in repeated samplings, let’s conduct a simulation similar to the one for the coin example, but for the Poisson coverage rate. We select a range of values around those from our previous example and perform 1,000 simulations. The monitoring time is set to 100 for simplicity. We define coverage as the percentage of times the simulated interval contains the true value used in the simulation. The simulation is repeated for various values, and the resulting plot shows the values on the x-axis and the estimated coverage on the y-axis.

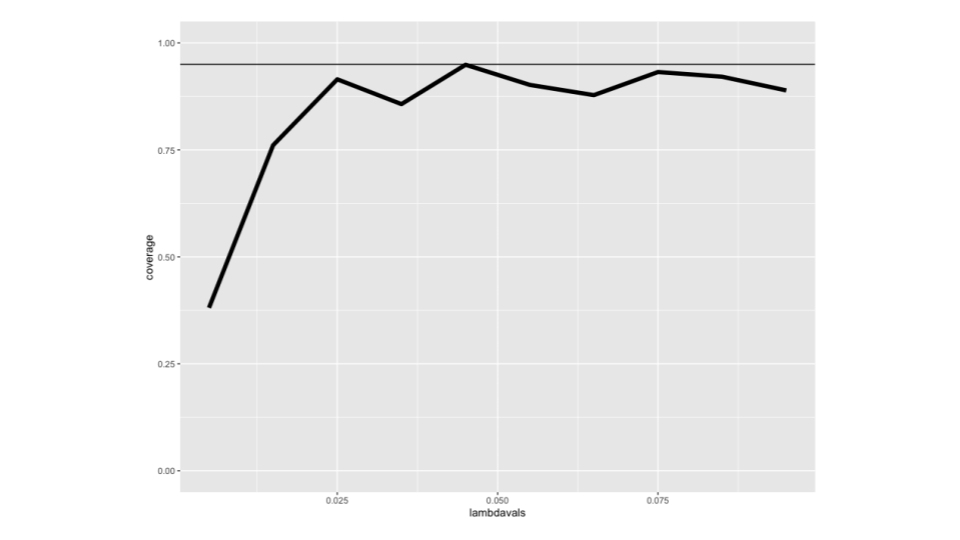


Figure : Figure 2.9: Coverage of confidence intervals for Poisson data

The plot reveals that as values increase, the coverage approaches 95%. However, there is some Monte Carlo error due to the finite number of simulations. On the other hand, as the true value becomes smaller, the coverage deteriorates significantly. For very small values, the purported 95% interval may only provide 50% actual coverage. To address this issue, it is recommended not to rely on the asymptotic interval for small values, especially when there are relatively few events during a large monitoring time. In such cases, the asymptotic interval does not align well with the Poisson distribution. Instead, an exact Poisson interval can be used as an alternative.

Although the central limit theorem’s application in the Poisson case may not be immediately clear, a simulation with a larger monitoring time (e.g., changing t from 100 to 1,000) demonstrates that as the monitoring time increases, the coverage improves and converges to 95% for most values. However, some poor coverage may still occur for small values, which we know the interval has trouble handling. In such cases, the exact Poisson interval remains a viable option.

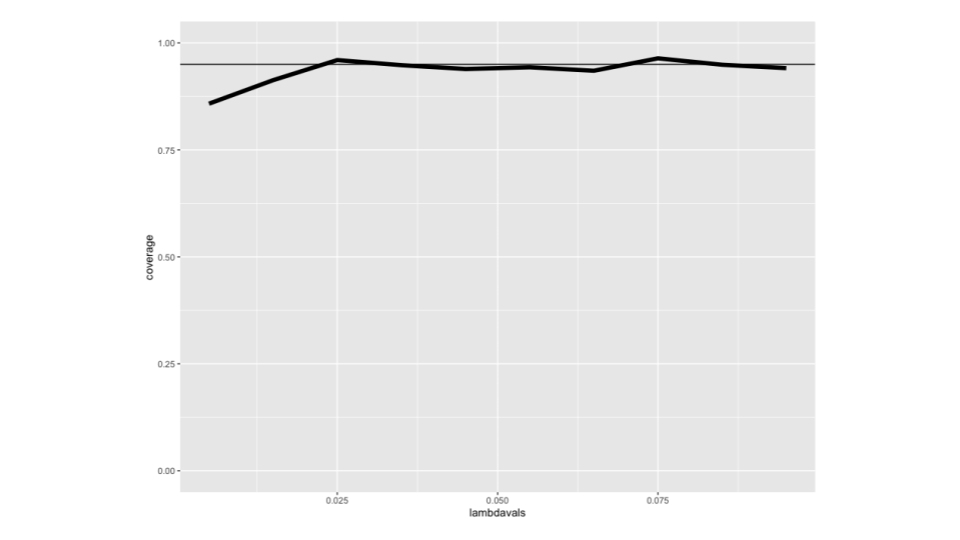


Figure : Figure 2.10: Coverage of confidence intervals for Poisson data, t=1000

To summarize briefly, we covered the Law of Large Numbers, which states that averages of independent and identically distributed (iid) random variables converge to the quantities they are estimating. This applies to Poisson rates as well, although the convergence process may be less clear. As the monitoring time tends to infinity, for example, Poisson rates converge to their estimated values. We also discussed the Central Limit Theorem, which states that averages are approximately normally distributed. These distributions are centered at the population mean, a concept we already knew without the theorem, with standard deviations equal to the standard error of the mean. However, the Central Limit Theorem does not guarantee that the sample size is large enough for this approximation to be accurate. We have observed instances where confidence intervals are very accurate and others where they are less accurate. Speaking of confidence intervals, our default approach for constructing them is to take the mean estimate and add or subtract the relevant normal quantile times the standard error. This method, known as “walled intervals,” is used not only in this context but also in regression analysis, general linear models, and other complex subjects. For a 95% confidence interval, the quantile value can be taken as 2 or, for more accuracy, 1.96. Confidence intervals become wider as the desired coverage increases within a specific technique. This is because wider intervals provide more certainty that the parameter lies within them. To illustrate, imagine an extreme scenario where your life depends on the confidence interval containing the true parameter. In this case, you would want to make the interval as wide as possible to ensure your safety. The mathematics behind confidence intervals follows the same principle. In the cases of Poisson and binomial distributions, which are discrete, the Central Limit Theorem may not accurately approximate their distributions. However, exact procedures exist for these cases. We also learned a simple fix for constructing confidence intervals in the binomial case by adding two successes and two failures, which provides a better interval without requiring complex computations. This method can be easily done by hand or mentally, even without access to a computer.

* The LLN states that averages of iid samples converge to the population means that they are estimating
* The CLT states that averages are approximately normal, with distributions
  + centered at the population mean
  + with standard deviation equal to the standard error of the mean
  + CLT gives no guarantee that is large enough
* Taking the mean and adding and subtracting the relevant normal quantile times the SE yields a confidence interval for the mean
  + Adding and subtracting 2 SEs works for 95% intervals
* Confidence intervals get wider as the coverage increases (why?)
* Confidence intervals get narrower with less variability or larger sample sizes
* The Poisson and binomial case have exact intervals that don’t require the CLT
  + But a quick fix for small sample size binomial calculations is to add 2 successes and failures

## 2.3 Practical R Exercises in swirl

# About the Authors

These credits are based on our [course contributors table guidelines](https://www.ottrproject.org/more_features.html#giving-credits-to-contributors).

| Credits | Names |
| --- | --- |
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| Lead Content Instructor(s) | [FirstName LastName](link%20to%20personal%20website) |
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| Content Contributor(s) (include section name/link in parentheses) - make new line if more than one section involved | Wrote less than a chapter |
| Content Editor(s)/Reviewer(s) | Checked your content |
| Content Director(s) | Helped guide the content direction |
| Content Consultants (include chapter name/link in parentheses or word “General”) - make new line if more than one chapter involved | Gave high level advice on content |
| Acknowledgments | Gave small assistance to content but not to the level of consulting |
| **Production** |  |
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| Figure Artist(s) | Created figures/plots for course |
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## ─ Session info ───────────────────────────────────────────────────────────────  
## setting value   
## version R version 4.0.2 (2020-06-22)  
## os Ubuntu 20.04.5 LTS   
## system x86\_64, linux-gnu   
## ui X11   
## language (EN)   
## collate en\_US.UTF-8   
## ctype en\_US.UTF-8   
## tz Etc/UTC   
## date 2023-07-12   
##   
## ─ Packages ───────────────────────────────────────────────────────────────────  
## package \* version date lib source   
## assertthat 0.2.1 2019-03-21 [1] RSPM (R 4.0.5)   
## bookdown 0.24 2023-03-28 [1] Github (rstudio/bookdown@88bc4ea)   
## cachem 1.0.7 2023-02-24 [1] CRAN (R 4.0.2)   
## callr 3.5.0 2020-10-08 [1] RSPM (R 4.0.2)   
## cli 3.6.1 2023-03-23 [1] CRAN (R 4.0.2)   
## crayon 1.3.4 2017-09-16 [1] RSPM (R 4.0.0)   
## desc 1.2.0 2018-05-01 [1] RSPM (R 4.0.3)   
## devtools 2.3.2 2020-09-18 [1] RSPM (R 4.0.3)   
## digest 0.6.25 2020-02-23 [1] RSPM (R 4.0.0)   
## ellipsis 0.3.1 2020-05-15 [1] RSPM (R 4.0.3)   
## evaluate 0.20 2023-01-17 [1] CRAN (R 4.0.2)   
## fastmap 1.1.1 2023-02-24 [1] CRAN (R 4.0.2)   
## fs 1.5.0 2020-07-31 [1] RSPM (R 4.0.3)   
## glue 1.4.2 2020-08-27 [1] RSPM (R 4.0.5)   
## htmltools 0.5.5 2023-03-23 [1] CRAN (R 4.0.2)   
## knitr 1.33 2023-03-28 [1] Github (yihui/knitr@a1052d1)   
## magrittr 2.0.3 2022-03-30 [1] CRAN (R 4.0.2)   
## memoise 2.0.1 2021-11-26 [1] CRAN (R 4.0.2)   
## pkgbuild 1.1.0 2020-07-13 [1] RSPM (R 4.0.2)   
## pkgload 1.1.0 2020-05-29 [1] RSPM (R 4.0.3)   
## prettyunits 1.1.1 2020-01-24 [1] RSPM (R 4.0.3)   
## processx 3.4.4 2020-09-03 [1] RSPM (R 4.0.2)   
## ps 1.4.0 2020-10-07 [1] RSPM (R 4.0.2)   
## R6 2.4.1 2019-11-12 [1] RSPM (R 4.0.0)   
## remotes 2.2.0 2020-07-21 [1] RSPM (R 4.0.3)   
## rlang 1.1.0 2023-03-14 [1] CRAN (R 4.0.2)   
## rmarkdown 2.10 2023-03-28 [1] Github (rstudio/rmarkdown@02d3c25)  
## rprojroot 2.0.3 2022-04-02 [1] CRAN (R 4.0.2)   
## sessioninfo 1.1.1 2018-11-05 [1] RSPM (R 4.0.3)   
## stringi 1.5.3 2020-09-09 [1] RSPM (R 4.0.3)   
## stringr 1.4.0 2019-02-10 [1] RSPM (R 4.0.3)   
## testthat 3.0.1 2023-03-28 [1] Github (R-lib/testthat@e99155a)   
## usethis 1.6.3 2020-09-17 [1] RSPM (R 4.0.2)   
## withr 2.3.0 2020-09-22 [1] RSPM (R 4.0.2)   
## xfun 0.26 2023-03-28 [1] Github (yihui/xfun@74c2a66)   
## yaml 2.2.1 2020-02-01 [1] RSPM (R 4.0.3)   
##   
## [1] /usr/local/lib/R/site-library  
## [2] /usr/local/lib/R/library

# 3 References