9. Introduction to probability

> *[God] has afforded us only the twilight ... of Probability.*
> – John Locke

Up to this point in the book, we've discussed some of the key ideas in experimental design, and we've talked a little about how you can summarise a data set. To a lot of people, this is all there is to statistics: it's about calculating averages, collecting all the numbers, drawing pictures, and putting them all in a report somewhere. Kind of like stamp collecting, but with numbers. However, statistics covers much more than that. In fact, descriptive statistics is one of the smallest parts of statistics, and one of the least powerful. The bigger and more useful part of statistics is that it provides that let you make inferences about data.

Once you start thinking about statistics in these terms – that statistics is there to help us draw inferences from data – you start seeing examples of it everywhere. For instance, here's a tiny extract from a newspaper article in the Sydney Morning Herald (30 Oct 2010):

> "I have a tough job," the Premier said in response to a poll which found her government is now the most unpopular Labor administration in polling history, with a primary vote of just 23 per cent.

This kind of remark is entirely unremarkable in the papers or in everyday life, but let's have a think about what it entails. A polling company has conducted a survey, usually a pretty big one because they can afford it. I'm too lazy to track down the original survey, so let's just imagine that they called 1000 NSW voters at random, and 230 (23%) of those claimed that they intended to vote for the ALP. For the 2010 Federal election, the Australian Electoral Commission reported 4,610,795 enrolled voters in NSW; so the opinions of the remaining 4,609,795 voters (about 99.98% of voters) remain unknown to us. Even assuming that no-one lied to the polling company the only thing we can say with 100% confidence is that the true ALP primary vote is somewhere between 230/4610795 (about 0.005%) and 4610025/4610795 (about 99.83%). So, on what basis is it legitimate for the polling company, the newspaper, and the readership to conclude that the ALP primary vote is only about 23%?

The answer to the question is pretty obvious: if I call 1000 people at random, and 230 of them say they intend to vote for the ALP, then it seems very unlikely that these are the *only* 230 people out of the entire voting public who actually intend to do so. In other words, we assume that the data collected by the polling company is pretty representative of the population at large. But how representative? Would we be surprised to discover that the true ALP primary vote is actually 24%? 29%? 37%? At this point everyday intuition starts to break down a bit. No-one would be surprised by 24%, and everybody would be surprised by 37%, but it's a bit hard to say whether 29% is plausible. We need some more powerful tools than just looking at the numbers and guessing.

Inferential statistics provides the tools that we need to answer these sorts of questions, and since these kinds of questions lie at the heart of the scientific enterprise, they take up the lions share of every introductory course on statistics and research methods. However, the theory of statistical inference is built on top of **probability theory**. And it is to probability theory that we must now turn. This

discussion of probability theory is basically background: there's not a lot of statistics per se in this chapter, and you don't need to understand this material in as much depth as the other chapters in this part of the book. Nevertheless, because probability theory does underpin so much of statistics, it's worth covering some of the basics.

9.1 How are probability and statistics different?

Before we start talking about probability theory, it's helpful to spend a moment thinking about the relationship between probability and statistics. The two disciplines are closely related but they're not identical. Probability theory is "the doctrine of chances". It's a branch of mathematics that tells you how often different kinds of events will happen. For example, all of these questions are things you can answer using probability theory:

- What are the chances of a fair coin coming up heads 10 times in a row?
- If I roll two six sided dice, how likely is it that I'll roll two sixes?
- How likely is it that five cards drawn from a perfectly shuffled deck will all be hearts?
- What are the chances that I'll win the lottery?

Notice that all of these questions have something in common. In each case the "truth of the world" is known, and my question relates to the "what kind of events" will happen. In the first question I *know* that the coin is fair, so there's a 50% chance that any individual coin flip will come up heads. In the second question, I *know* that the chance of rolling a 6 on a single die is 1 in 6. In the third question I *know* that the deck is shuffled properly. And in the fourth question, I *know* that the lottery follows specific rules. You get the idea. The critical point is that probabilistic questions start with a known **model** of the world, and we use that model to do some calculations. The underlying model can be quite simple. For instance, in the coin flipping example, we can write down the model like this:

$$P(\text{heads}) = 0.5$$

which you can read as "the probability of heads is 0.5". As we'll see later, in the same way that percentages are numbers that range from 0% to 100%, probabilities are just numbers that range from 0 to 1. When using this probability model to answer the first question, I don't actually know exactly what's going to happen. Maybe I'll get 10 heads, like the question says. But maybe I'll get three heads. That's the key thing: in probability theory, the *model* is known, but the *data* are not.

So that's probability. What about statistics? Statistical questions work the other way around. In statistics, we do not know the truth about the world. All we have is the data, and it is from the data that we want to *learn* the truth about the world. Statistical questions tend to look more like these:

- If my friend flips a coin 10 times and gets 10 heads, are they playing a trick on me?
- If five cards off the top of the deck are all hearts, how likely is it that the deck was shuffled?
- If the lottery commissioner's spouse wins the lottery, how likely is it that the lottery was rigged?

This time around, the only thing we have are data. What I *know* is that I saw my friend flip the coin 10 times and it came up heads every time. And what I want to **infer** is whether or not I should conclude that what I just saw was actually a fair coin being flipped 10 times in a row, or whether I should suspect that my friend is playing a trick on me. The data I have look like this:

```
H H H H H H H H H H
```

and what I'm trying to do is work out which "model of the world" I should put my trust in. If the coin is fair, then the model I should adopt is one that says that the probability of heads is 0.5; that is, $P(\text{heads}) = 0.5$. If the coin is not fair, then I should conclude that the probability of heads is *not* 0.5, which we would write as $P(\text{heads}) \neq 0.5$. In other words, the statistical inference problem is to figure out which of these probability models is right. Clearly, the statistical question isn't the same as the probability question, but they're deeply connected to one another. Because of this, a good introduction to statistical theory will start with a discussion of what probability is and how it works.

9.2 What does probability mean?

Let's start with the first of these questions. What is "probability"? It might seem surprising to you, but while statisticians and mathematicians (mostly) agree on what the *rules* of probability are, there's much less of a consensus on what the word really *means*. It seems weird because we're all very comfortable using words like "chance", "likely", "possible" and "probable", and it doesn't seem like it should be a very difficult question to answer. If you had to explain "probability" to a five year old, you could do a pretty good job. But if you've ever had that experience in real life, you might walk away from the conversation feeling like you didn't quite get it right, and that (like many everyday concepts) it turns out that you don't *really* know what it's all about.

So I'll have a go at it. Let's suppose I want to bet on a soccer game between two teams of robots, *Arduino Arsenal* and *C Milan*. After thinking about it, I decide that there is an 80% probability that *Arduino Arsenal* winning. What do I mean by that? Here are three possibilities...

- They're robot teams, so I can make them play over and over again, and if I did that, *Arduino Arsenal* would win 8 out of every 10 games on average.
- For any given game, I would only agree that betting on this game is only "fair" if a \$1 bet on *C Milan* gives a \$5 payoff (i.e. I get my \$1 back plus a \$4 reward for being correct), as would a \$4 bet on *Arduino Arsenal* (i.e., my \$4 bet plus a \$1 reward).
- My subjective "belief" or "confidence" in an *Arduino Arsenal* victory is four times as strong as my belief in a *C Milan* victory.

Each of these seems sensible. However they're not identical, and not every statistician would endorse all of them. The reason is that there are different statistical ideologies (yes, really!) and depending on which one you subscribe to, you might say that some of those statements are meaningless or irrelevant. In this section, I give a brief introduction the two main approaches that exist in the literature. These are by no means the only approaches, but they're the two big ones.

9.2.1 The frequentist view

The first of the two major approaches to probability, and the more dominant one in statistics, is referred to as the **frequentist view**, and it defines probability as a **long-run frequency**. Suppose we were to try flipping a fair coin, over and over again. By definition, this is a coin that has $P(H) = 0.5$. What might we observe? One possibility is that the first 20 flips might look like this:

```
T,H,H,H,H,T,T,H,H,H,H,T,H,H,T,T,T,T,T,H
```

In this case 11 of these 20 coin flips (55%) came up heads. Now suppose that I'd been keeping a running tally of the number of heads (which I'll call N_H) that I've seen, across the first N flips, and calculate the proportion of heads N_H/N every time. Here's what I'd get (I did literally flip coins to produce this!):

number of flips	1	2	3	4	5	6	7	8	9	10
number of heads	0	1	2	3	4	4	4	5	6	7
proportion	.00	.50	.67	.75	.80	.67	.57	.63	.67	.70

number of flips	11	12	13	14	15	16	17	18	19	20
number of heads	8	8	9	10	10	10	10	10	10	11
proportion	.73	.67	.69	.71	.67	.63	.59	.56	.53	.55

Notice that at the start of the sequence, the *proportion* of heads fluctuates wildly, starting at .00 and rising as high as .80. Later on, one gets the impression that it dampens out a bit, with more and more of the values actually being pretty close to the "right" answer of .50. This is the frequentist definition of probability in a nutshell: flip a fair coin over and over again, and as N grows large (approaches infinity, denoted $N \rightarrow \infty$), the proportion of heads will converge to 50%. There are some subtle technicalities that the mathematicians care about, but qualitatively speaking, that's how the frequentists define probability. Unfortunately, I don't have an infinite number of coins, or the infinite patience required to flip a coin an infinite number of times. However, I do have a computer, and computers excel at mindless repetitive tasks. So I asked my computer to simulate flipping a coin 1000 times, and then drew a picture of what happens to the proportion N_H/N as N increases. Actually, I did it four times, just to make sure it wasn't a fluke. The results are shown in Figure 9.1. As you can see, the *proportion of observed heads* eventually stops fluctuating, and settles down; when it does, the number at which it finally settles is the true probability of heads.

The frequentist definition of probability has some desirable characteristics. Firstly, it is objective: the probability of an event is *necessarily* grounded in the world. The only way that probability statements can make sense is if they refer to (a sequence of) events that occur in the physical universe.[1] Secondly, it is unambiguous: any two people watching the same sequence of events unfold, trying to calculate the probability of an event, must inevitably come up with the same answer. However, it also has undesirable characteristics. Firstly, infinite sequences don't exist in the physical world. Suppose you picked up a coin from your pocket and started to flip it. Every time it lands, it impacts on the ground. Each impact wears the coin down a bit; eventually, the coin will be destroyed. So, one might ask whether it really makes sense to pretend that an "infinite" sequence of coin flips is even a meaningful concept, or an objective one. We can't say that an "infinite sequence" of events is a real thing in the physical universe, because the physical universe doesn't allow infinite anything. More seriously, the frequentist definition has a narrow scope. There are lots of things out there that human beings are happy to assign probability to in everyday language, but cannot (even in theory) be mapped onto a hypothetical sequence of events. For instance, if a meteorologist comes on TV and says, "the probability of rain in Adelaide on 2 November 2048 is 60%" we humans are happy to accept this. But it's not clear how to define this in frequentist terms. There's only one city of Adelaide, and only 2 November 2048. There's no infinite sequence of events here, just a once-off thing. Frequentist probability genuinely *forbids* us from making probability statements about a single event. From the frequentist perspective, it will either rain tomorrow or it will not; there is no "probability" that attaches to a single non-repeatable event. Now, it should be said that there are some very clever tricks that frequentists can use to get around this. One possibility is that what the meteorologist means is something like this: "There is a category of days for which I predict a 60% chance of rain; if we look only across those days for which I make this prediction, then on 60% of those days it will actually rain". It's very weird and counterintuitive to think of it this way, but you do see

[1] This doesn't mean that frequentists can't make hypothetical statements, of course; it's just that if you want to make a statement about probability, then it must be possible to redescribe that statement in terms of a sequence of potentially observable events, and the relative frequencies of different outcomes that appear within that sequence.

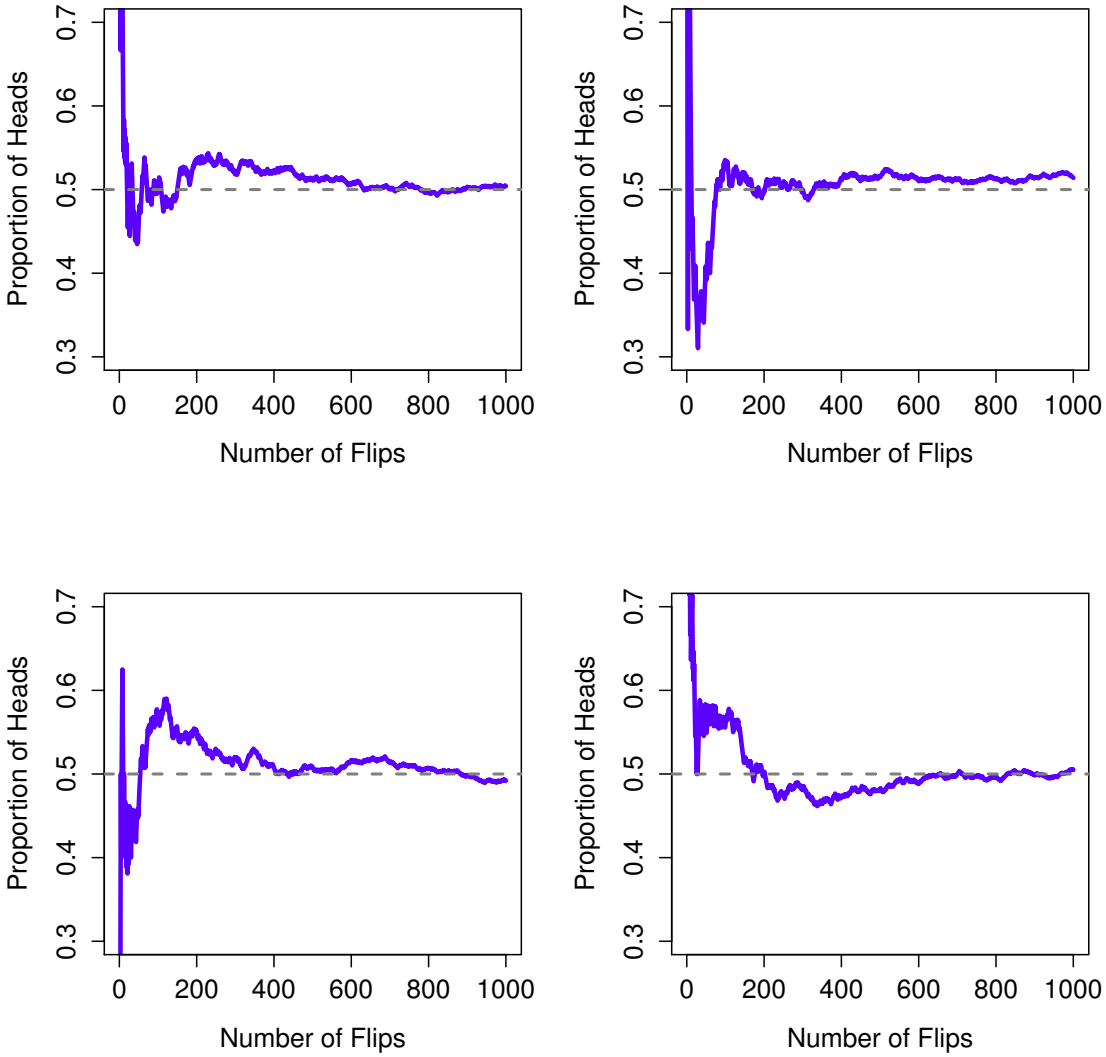


Figure 9.1: An illustration of how frequentist probability works. If you flip a fair coin over and over again, the proportion of heads that you've seen eventually settles down, and converges to the true probability of 0.5. Each panel shows four different simulated experiments: in each case, we pretend we flipped a coin 1000 times, and kept track of the proportion of flips that were heads as we went along. Although none of these sequences actually ended up with an exact value of .5, if we'd extended the experiment for an infinite number of coin flips they would have.

frequentists do this sometimes. And it *will* come up later in this book (see Section 10.5).

9.2.2 The Bayesian view

The **Bayesian view** of probability is often called the subjectivist view, and it is a minority view among statisticians, but one that has been steadily gaining traction for the last several decades. There are many flavours of Bayesianism, making hard to say exactly what "the" Bayesian view is. The most common way of thinking about subjective probability is to define the probability of an event as the **degree of belief** that an intelligent and rational agent assigns to that truth of that event. From that perspective, probabilities don't exist in the world, but rather in the thoughts and assumptions of people and other intelligent beings. However, in order for this approach to work, we need some way of operationalising "degree of belief". One way that you can do this is to formalise it in terms of "rational gambling", though there are many other ways. Suppose that I believe that there's a 60% probability of rain tomorrow. If someone offers me a bet: if it rains tomorrow, then I win $5, but if it doesn't rain then I lose $5. Clearly, from my perspective, this is a pretty good bet. On the other hand, if I think that the probability of rain is only 40%, then it's a bad bet to take. Thus, we can operationalise the notion of a "subjective probability" in terms of what bets I'm willing to accept.

What are the advantages and disadvantages to the Bayesian approach? The main advantage is that it allows you to assign probabilities to any event you want to. You don't need to be limited to those events that are repeatable. The main disadvantage (to many people) is that we can't be purely objective – specifying a probability requires us to specify an entity that has the relevant degree of belief. This entity might be a human, an alien, a robot, or even a statistician, but there has to be an intelligent agent out there that believes in things. To many people this is uncomfortable: it seems to make probability arbitrary. While the Bayesian approach does require that the agent in question be rational (i.e., obey the rules of probability), it does allow everyone to have their own beliefs; I can believe the coin is fair and you don't have to, even though we're both rational. The frequentist view doesn't allow any two observers to attribute different probabilities to the same event: when that happens, then at least one of them must be wrong. The Bayesian view does not prevent this from occurring. Two observers with different background knowledge can legitimately hold different beliefs about the same event. In short, where the frequentist view is sometimes considered to be too narrow (forbids lots of things that that we want to assign probabilities to), the Bayesian view is sometimes thought to be too broad (allows too many differences between observers).

9.2.3 What's the difference? And who is right?

Now that you've seen each of these two views independently, it's useful to make sure you can compare the two. Go back to the hypothetical robot soccer game at the start of the section. What do you think a frequentist and a Bayesian would say about these three statements? Which statement would a frequentist say is the correct definition of probability? Which one would a Bayesian do? Would some of these statements be meaningless to a frequentist or a Bayesian? If you've understood the two perspectives, you should have some sense of how to answer those questions.

Okay, assuming you understand the different, you might be wondering which of them is *right*? Honestly, I don't know that there is a right answer. As far as I can tell there's nothing mathematically incorrect about the way frequentists think about sequences of events, and there's nothing mathematically incorrect about the way that Bayesians define the beliefs of a rational agent. In fact, when you dig down into the details, Bayesians and frequentists actually agree about a lot of things. Many frequentist methods lead to decisions that Bayesians agree a rational agent would make. Many Bayesian methods have very good frequentist properties.

For the most part, I'm a pragmatist so I'll use any statistical method that I trust. As it turns out, that makes me prefer Bayesian methods, for reasons I'll explain towards the end of the book, but I'm not fundamentally opposed to frequentist methods. Not everyone is quite so relaxed. For instance, consider Sir Ronald Fisher, one of the towering figures of 20th century statistics and a vehement opponent to all things Bayesian, whose paper on the mathematical foundations of statistics referred to Bayesian probability as "an impenetrable jungle [that] arrests progress towards precision of statistical concepts" (Fisher, 1922b, p. 311). Or the psychologist Paul Meehl, who suggests that relying on frequentist methods could turn you into "a potent but sterile intellectual rake who leaves in his merry path a long train of ravished maidens but no viable scientific offspring" (Meehl, 1967, p. 114). The history of statistics, as you might gather, is not devoid of entertainment.

In any case, while I personally prefer the Bayesian view, the majority of statistical analyses are based on the frequentist approach. My reasoning is pragmatic: the goal of this book is to cover roughly the same territory as a typical undergraduate stats class in psychology, and if you want to understand the statistical tools used by most psychologists, you'll need a good grasp of frequentist methods. I promise you that this isn't wasted effort. Even if you end up wanting to switch to the Bayesian perspective, you really should read through at least one book on the "orthodox" frequentist view. And since R is the most widely used statistical language for Bayesians, you might as well read a book that uses R. Besides, I won't completely ignore the Bayesian perspective. Every now and then I'll add some commentary from a Bayesian point of view, and I'll revisit the topic in more depth in Chapter 17.

9.3 Basic probability theory

Ideological arguments between Bayesians and frequentists notwithstanding, it turns out that people mostly agree on the rules that probabilities should obey. There are lots of different ways of arriving at these rules. The most commonly used approach is based on the work of Andrey Kolmogorov, one of the great Soviet mathematicians of the 20th century. I won't go into a lot of detail, but I'll try to give you a bit of a sense of how it works. And in order to do so, I'm going to have to talk about my pants.

9.3.1 Introducing probability distributions

One of the disturbing truths about my life is that I only own 5 pairs of pants: three pairs of jeans, the bottom half of a suit, and a pair of tracksuit pants. Even sadder, I've given them names: I call them X_1, X_2, X_3, X_4 and X_5. I really do: that's why they call me Mister Imaginative. Now, on any given day, I pick out exactly one of pair of pants to wear. Not even I'm so stupid as to try to wear two pairs of pants, and thanks to years of training I never go outside without wearing pants anymore. If I were to describe this situation using the language of probability theory, I would refer to each pair of pants (i.e., each X) as an **elementary event**. The key characteristic of elementary events is that every time we make an observation (e.g., every time I put on a pair of pants), then the outcome will be one and only one of these events. Like I said, these days I always wear exactly one pair of pants, so my pants satisfy this constraint. Similarly, the set of all possible events is called a **sample space**. Granted, some people would call it a "wardrobe", but that's because they're refusing to think about my pants in probabilistic terms. Sad.

Okay, now that we have a sample space (a wardrobe), which is built from lots of possible elementary events (pants), what we want to do is assign a **probability** of one of these elementary events. For an event X, the probability of that event $P(X)$ is a number that lies between 0 and 1. The bigger the value of $P(X)$, the more likely the event is to occur. So, for example, if $P(X) = 0$, it means the event X is impossible (i.e., I never wear those pants). On the other hand, if $P(X) = 1$ it means that event X is

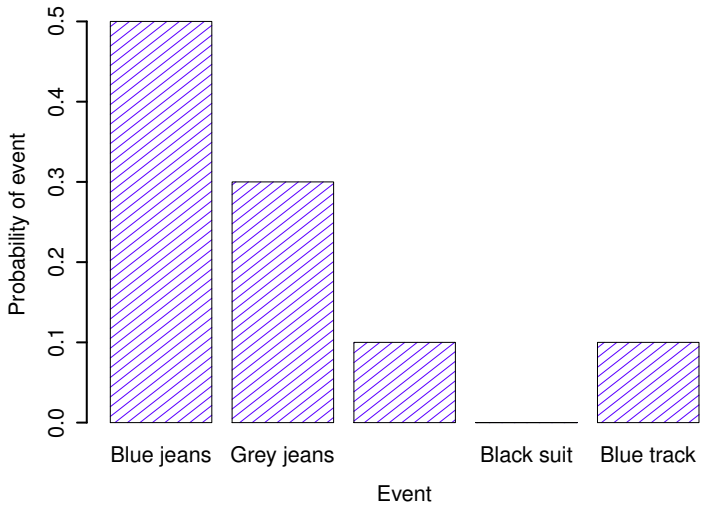


Figure 9.2: A visual depiction of the "pants" probability distribution. There are five "elementary events", corresponding to the five pairs of pants that I own. Each event has some probability of occurring: this probability is a number between 0 to 1. The sum of these probabilities is 1.

certain to occur (i.e., I always wear those pants). For probability values in the middle, it means that I sometimes wear those pants. For instance, if $P(X) = 0.5$ it means that I wear those pants half of the time.

At this point, we're almost done. The last thing we need to recognise is that "something always happens". Every time I put on pants, I really do end up wearing pants (crazy, right?). What this somewhat trite statement means, in probabilistic terms, is that the probabilities of the elementary events need to add up to 1. This is known as the **law of total probability**, not that any of us really care. More importantly, if these requirements are satisfied, then what we have is a **probability distribution**. For example, this is an example of a probability distribution

Which pants?	Label	Probability
Blue jeans	X_1	$P(X_1) = .5$
Grey jeans	X_2	$P(X_2) = .3$
Black jeans	X_3	$P(X_3) = .1$
Black suit	X_4	$P(X_4) = 0$
Blue tracksuit	X_5	$P(X_5) = .1$

Each of the events has a probability that lies between 0 and 1, and if we add up the probability of all events, they sum to 1. Awesome. We can even draw a nice bar graph (see Section 6.7) to visualise this distribution, as shown in Figure 9.2. And at this point, we've all achieved something. You've learned what a probability distribution is, and I've finally managed to find a way to create a graph that focuses entirely on my pants. Everyone wins!

The only other thing that I need to point out is that probability theory allows you to talk about **non elementary events** as well as elementary ones. The easiest way to illustrate the concept is with an example. In the pants example, it's perfectly legitimate to refer to the probability that I wear jeans. In

Table 9.1: Some basic rules that probabilities must satisfy. You don't really need to know these rules in order to understand the analyses that we'll talk about later in the book, but they are important if you want to understand probability theory a bit more deeply.

English	Notation		Formula
not A	$P(\neg A)$	=	$1 - P(A)$
A or B	$P(A \cup B)$	=	$P(A) + P(B) - P(A \cap B)$
A and B	$P(A \cap B)$	=	$P(A\|B)P(B)$

this scenario, the "Dan wears jeans" event said to have happened as long as the elementary event that actually did occur is one of the appropriate ones; in this case "blue jeans", "black jeans" or "grey jeans". In mathematical terms, we defined the "jeans" event E to correspond to the set of elementary events (X_1, X_2, X_3). If any of these elementary events occurs, then E is also said to have occurred. Having decided to write down the definition of the E this way, it's pretty straightforward to state what the probability $P(E)$ is: we just add everything up. In this particular case

$$P(E) = P(X_1) + P(X_2) + P(X_3)$$

and, since the probabilities of blue, grey and black jeans respectively are .5, .3 and .1, the probability that I wear jeans is equal to .9.

At this point you might be thinking that this is all terribly obvious and simple and you'd be right. All we've really done is wrap some basic mathematics around a few common sense intuitions. However, from these simple beginnings it's possible to construct some extremely powerful mathematical tools. I'm definitely not going to go into the details in this book, but what I will do is list – in Table 9.1 – some of the other rules that probabilities satisfy. These rules can be derived from the simple assumptions that I've outlined above, but since we don't actually use these rules for anything in this book, I won't do so here.

9.4 The binomial distribution

As you might imagine, probability distributions vary enormously, and there's an enormous range of distributions out there. However, they aren't all equally important. In fact, the vast majority of the content in this book relies on one of five distributions: the binomial distribution, the normal distribution, the t distribution, the χ^2 ("chi-square") distribution and the F distribution. Given this, what I'll do over the next few sections is provide a brief introduction to all five of these, paying special attention to the binomial and the normal. I'll start with the binomial distribution, since it's the simplest of the five.

9.4.1 Introducing the binomial

The theory of probability originated in the attempt to describe how games of chance work, so it seems fitting that our discussion of the **binomial distribution** should involve a discussion of rolling dice and flipping coins. Let's imagine a simple "experiment": in my hot little hand I'm holding 20 identical six-sided dice. On one face of each die there's a picture of a skull; the other five faces are all blank. If I

proceed to roll all 20 dice, what's the probability that I'll get exactly 4 skulls? Assuming that the dice are fair, we know that the chance of any one die coming up skulls is 1 in 6; to say this another way, the skull probability for a single die is approximately .167. This is enough information to answer our question, so let's have a look at how it's done.

As usual, we'll want to introduce some names and some notation. We'll let N denote the number of dice rolls in our experiment; which is often referred to as the **size parameter** of our binomial distribution. We'll also use θ to refer to the the probability that a single die comes up skulls, a quantity that is usually called the **success probability** of the binomial.[2] Finally, we'll use X to refer to the results of our experiment, namely the number of skulls I get when I roll the dice. Since the actual value of X is due to chance, we refer to it as a **random variable**. In any case, now that we have all this terminology and notation, we can use it to state the problem a little more precisely. The quantity that we want to calculate is the probability that $X = 4$ given that we know that $\theta = .167$ and $N = 20$. The general "form" of the thing I'm interested in calculating could be written as

$$P(X \mid \theta, N)$$

and we're interested in the special case where $X = 4$, $\theta = .167$ and $N = 20$. There's only one more piece of notation I want to refer to before moving on to discuss the solution to the problem. If I want to say that X is generated randomly from a binomial distribution with parameters θ and N, the notation I would use is as follows:

$$X \sim \text{Binomial}(\theta, N)$$

Yeah, yeah. I know what you're thinking: notation, notation, notation. Really, who cares? Very few readers of this book are here for the notation, so I should probably move on and talk about how to use the binomial distribution. I've included the formula for the binomial distribution in Table 9.2, since some readers may want to play with it themselves, but since most people probably don't care that much and because we don't need the formula in this book, I won't talk about it in any detail. Instead, I just want to show you what the binomial distribution looks like. To that end, Figure 9.3 plots the binomial probabilities for all possible values of X for our dice rolling experiment, from $X = 0$ (no skulls) all the way up to $X = 20$ (all skulls). Note that this is basically a bar chart, and is no different to the "pants probability" plot I drew in Figure 9.2. On the horizontal axis we have all the possible events, and on the vertical axis we can read off the probability of each of those events. So, the probability of rolling 4 skulls out of 20 times is about 0.20 (the actual answer is 0.2022036, as we'll see in a moment). In other words, you'd expect that to happen about 20% of the times you repeated this experiment.

9.4.2 Working with the binomial distribution in R

Although some people find it handy to know the formulas in Table 9.2, most people just want to know how to use the distributions without worrying too much about the maths. To that end, R has a function called `dbinom()` that calculates binomial probabilities for us. The main arguments to the function are

- `x`. This is a number, or vector of numbers, specifying the outcomes whose probability you're trying to calculate.
- `size`. This is a number telling R the size of the experiment.
- `prob`. This is the success probability for any one trial in the experiment.

[2] Note that the term "success" is pretty arbitrary, and doesn't actually imply that the outcome is something to be desired. If θ referred to the probability that any one passenger gets injured in a bus crash, I'd still call it the success probability, but that doesn't mean I want people to get hurt in bus crashes!

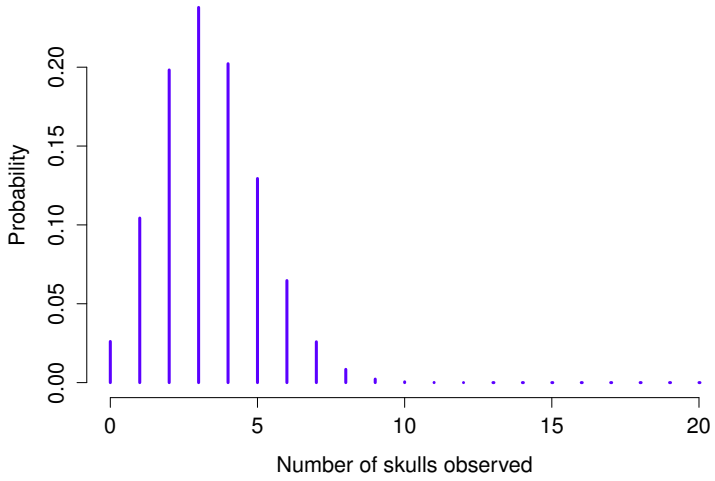


Figure 9.3: The binomial distribution with size parameter of $N = 20$ and an underlying success probability of $\theta = 1/6$. Each vertical bar depicts the probability of one specific outcome (i.e., one possible value of X). Because this is a probability distribution, each of the probabilities must be a number between 0 and 1, and the heights of the bars must sum to 1 as well.

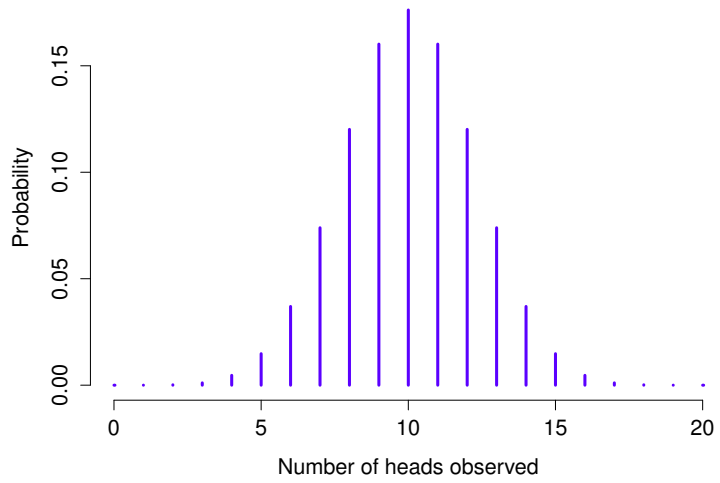
So, in order to calculate the probability of getting `x = 4` skulls, from an experiment of `size = 20` trials, in which the probability of getting a skull on any one trial is `prob = 1/6` ... well, the command I would use is simply this:

```
> dbinom( x = 4, size = 20, prob = 1/6 )
[1] 0.2022036
```

To give you a feel for how the binomial distribution changes when we alter the values of θ and N, let's suppose that instead of rolling dice, I'm actually flipping coins. This time around, my experiment involves flipping a fair coin repeatedly, and the outcome that I'm interested in is the number of heads that I observe. In this scenario, the success probability is now $\theta = 1/2$. Suppose I were to flip the coin $N = 20$ times. In this example, I've changed the success probability, but kept the size of the experiment the same. What does this do to our binomial distribution? Well, as Figure 9.4a shows, the main effect of this is to shift the whole distribution, as you'd expect. Okay, what if we flipped a coin $N = 100$ times? Well, in that case, we get Figure 9.4b. The distribution stays roughly in the middle, but there's a bit more variability in the possible outcomes.

At this point, I should probably explain the name of the `dbinom()` function. Obviously, the "binom" part comes from the fact that we're working with the binomial distribution, but the "d" prefix is probably a bit of a mystery. In this section I'll give a partial explanation: specifically, I'll explain why there is a prefix. As for why it's a "d" specifically, you'll have to wait until the next section. What's going on here is that R actually provides *four* functions in relation to the binomial distribution. These four functions are `dbinom()`, `pbinom()`, `rbinom()` and `qbinom()`, and each one calculates a different quantity of interest. Not only that, R does the same thing for *every* probability distribution that it implements. No matter what distribution you're talking about, there's a `d` function, a `p` function, a `q` function and a `r` function. This is illustrated in Table 9.3, using the binomial distribution and the normal distribution as examples.

(a)



(b)

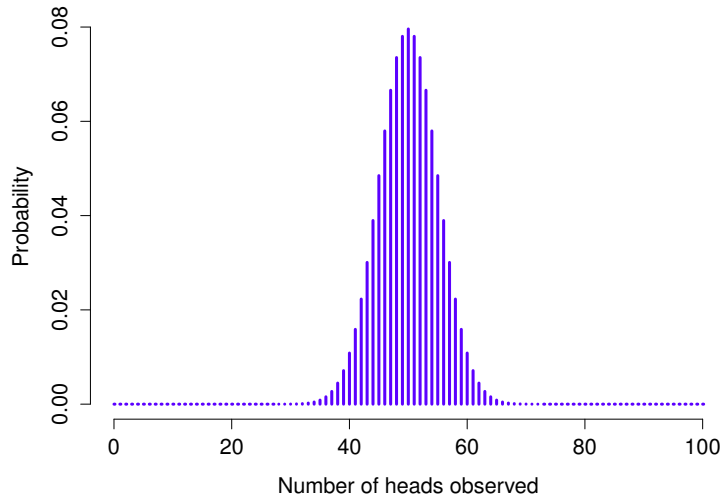


Figure 9.4: Two binomial distributions, involving a scenario in which I'm flipping a fair coin, so the underlying success probability is $\theta = 1/2$. In panel (a), we assume I'm flipping the coin $N = 20$ times. In panel (b) we assume that the coin is flipped $N = 100$ times.

. . . . . .

Table 9.2: Formulas for the binomial and normal distributions. We don't really use these formulas for anything in this book, but they're pretty important for more advanced work, so I thought it might be best to put them here in a table, where they can't get in the way of the text. In the equation for the binomial, $X!$ is the factorial function (i.e., multiply all whole numbers from 1 to X), and for the normal distribution "exp" refers to the exponential function, which we discussed in Chapter 7. If these equations don't make a lot of sense to you, don't worry too much about them.

Binomial	Normal
$P(X \mid \theta, N) = \frac{N!}{X!(N-X)!}\theta^X(1-\theta)^{N-X}$	$p(X \mid \mu, \sigma) = \frac{1}{\sqrt{2\pi}\sigma}\exp\left(-\frac{(X-\mu)^2}{2\sigma^2}\right)$

Table 9.3: The naming system for R probability distribution functions. Every probability distribution implemented in R is actually associated with four separate functions, and there is a pretty standardised way for naming these functions.

what it does	prefix	**norm**al distribution	**binom**ial distribution
probability (**d**ensity) of	`d`	`dnorm()`	`dbinom()`
cumulative **p**robability of	`p`	`pnorm()`	`pbinom()`
generate **r**andom number from	`r`	`rnorm()`	`rbinom()`
quantile of	`q`	`qnorm()`	`qbinom()`

Let's have a look at what all four functions do. Firstly, all four versions of the function require you to specify the `size` and `prob` arguments: no matter what you're trying to get R to calculate, it needs to know what the parameters are. However, they differ in terms of what the other argument is, and what the output is. So let's look at them one at a time.

- The `d` form we've already seen: you specify a particular outcome `x`, and the output is the probability of obtaining exactly that outcome. (the "d" is short for **density**, but ignore that for now).
- The `p` form calculates the **cumulative probability**. You specify a particular quantile `q`, and it tells you the probability of obtaining an outcome *smaller than or equal to* `q`.
- The `q` form calculates the **quantiles** of the distribution. You specify a probability value `p`, and gives you the corresponding percentile. That is, the value of the variable for which there's a probability `p` of obtaining an outcome lower than that value.
- The `r` form is a **random number generator**: specifically, it generates `n` random outcomes from the distribution.

This is a little abstract, so let's look at some concrete examples. Again, we've already covered `dbinom()` so let's focus on the other three versions. We'll start with `pbinom()`, and we'll go back to the skull-dice example. Again, I'm rolling 20 dice, and each die has a 1 in 6 chance of coming up skulls. Suppose, however, that I want to know the probability of rolling 4 *or fewer* skulls. If I wanted to, I could use the `dbinom()` function to calculate the exact probability of rolling 0 skulls, 1 skull, 2 skulls, 3 skulls and 4 skulls and then add these up, but there's a faster way. Instead, I can calculate this using the `pbinom()` function. Here's the command:

```
> pbinom( q= 4, size = 20, prob = 1/6)
[1] 0.7687492
```

In other words, there is a 76.9% chance that I will roll 4 or fewer skulls. Or, to put it another way, R is telling us that a value of 4 is actually the 76.9th percentile of this binomial distribution.

Next, let's consider the `qbinom()` function. Let's say I want to calculate the 75th percentile of the binomial distribution. If we're sticking with our skulls example, I would use the following command to do this:

```
> qbinom( p = 0.75, size = 20, prob = 1/6 )
[1] 4
```

Hm. There's something odd going on here. Let's think this through. What the `qbinom()` function appears to be telling us is that the 75th percentile of the binomial distribution is 4, even though we saw from the `pbinom()` function that 4 is *actually* the 76.9th percentile. And it's definitely the `pbinom()` function that is correct. I promise. The weirdness here comes from the fact that our binomial distribution doesn't really *have* a 75th percentile. Not really. Why not? Well, there's a 56.7% chance of rolling 3 or fewer skulls (you can type `pbinom(3, 20, 1/6)` to confirm this if you want), and a 76.9% chance of rolling 4 or fewer skulls. So there's a sense in which the 75th percentile should lie "in between" 3 and 4 skulls. But that makes no sense at all! You can't roll 20 dice and get 3.9 of them come up skulls. This issue can be handled in different ways: you could report an in between value (or *interpolated* value, to use the technical name) like 3.9, you could round down (to 3) or you could round up (to 4). The `qbinom()` function rounds upwards: if you ask for a percentile that doesn't actually exist (like the 75th in this example), R finds the smallest value for which the the percentile rank is *at least* what you asked for. In this case, since the "true" 75th percentile (whatever that would mean) lies somewhere between 3 and 4 skulls, R rounds up and gives you an answer of 4. This subtlety is tedious, I admit, but thankfully it's only an issue for discrete distributions like the binomial (see Section 2.2.5 for a discussion of continuous versus discrete). The other distributions that I'll talk about (normal, t, χ^2 and F) are all continuous, and so R can always return an exact quantile whenever you ask for it.

Finally, we have the random number generator. To use the `rbinom()` function, you specify how many times R should "simulate" the experiment using the `n` argument, and it will generate random outcomes from the binomial distribution. So, for instance, suppose I were to repeat my die rolling experiment 100 times. I could get R to simulate the results of these experiments by using the following command:

```
> rbinom( n = 100, size = 20, prob = 1/6 )
  [1] 3 4 8 4 4 3 1 4 4 1 3 0 3 3 4 3 1 2 2 3 4 2
 [23] 2 1 2 4 4 3 5 4 2 3 1 2 7 4 2 5 2 3 0 2 3 3
 [45] 2 2 2 3 4 4 2 0 2 4 4 3 4 1 2 3 5 3 7 5 0 5
 [67] 1 5 4 3 4 4 1 5 4 4 3 2 3 3 4 5 0 5 1 4 7 2
 [89] 5 1 1 2 4 5 5 3 3 3 3 3
```

As you can see, these numbers are pretty much what you'd expect given the distribution shown in Figure 9.3. Most of the time I roll somewhere between 1 to 5 skulls. There are a lot of subtleties associated with random number generation using a computer,[3] but for the purposes of this book we don't need to worry too much about them.

[3] Since computers are deterministic machines, they can't actually produce truly random behaviour. Instead, what they do is take advantage of various mathematical functions that share a lot of similarities with true randomness. What this means is that any random numbers generated on a computer are *pseudorandom*, and the quality of those numbers depends on the specific method used. By default R uses the "Mersenne twister" method. In any case, you can find out more by typing `?Random`, but as usual the R help files are fairly dense.

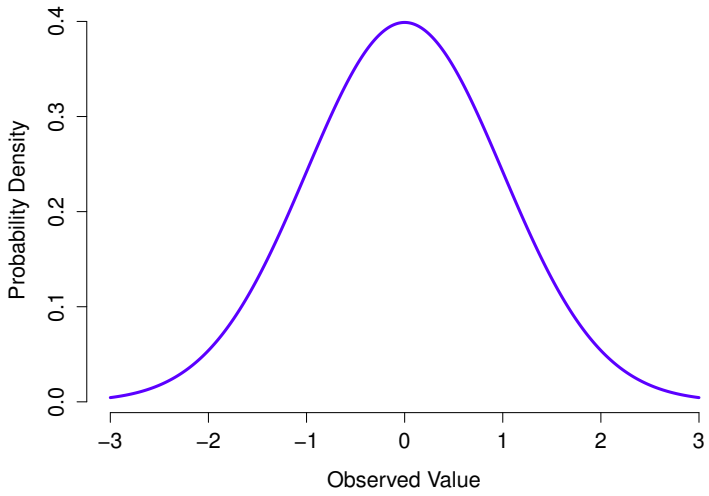


Figure 9.5: The normal distribution with mean $\mu = 0$ and standard deviation $\sigma = 1$. The x-axis corresponds to the value of some variable, and the y-axis tells us something about how likely we are to observe that value. However, notice that the y-axis is labelled "Probability Density" and not "Probability". There is a subtle and somewhat frustrating characteristic of continuous distributions that makes the y axis behave a bit oddly: the height of the curve here isn't actually the probability of observing a particular x value. On the other hand, it *is* true that the heights of the curve tells you which x values are more likely (the higher ones!). (see Section 9.5.1 for all the annoying details)

9.5 The normal distribution

While the binomial distribution is conceptually the simplest distribution to understand, it's not the most important one. That particular honour goes to the **normal distribution**, which is also referred to as "the bell curve" or a "Gaussian distribution". A normal distribution is described using two parameters, the mean of the distribution μ and the standard deviation of the distribution σ. The notation that we sometimes use to say that a variable X is normally distributed is as follows:

$$X \sim \text{Normal}(\mu, \sigma)$$

Of course, that's just notation. It doesn't tell us anything interesting about the normal distribution itself. As was the case with the binomial distribution, I have included the formula for the normal distribution in this book, because I think it's important enough that everyone who learns statistics should at least look at it, but since this is an introductory text I don't want to focus on it, so I've tucked it away in Table 9.2. Similarly, the R functions for the normal distribution are `dnorm()`, `pnorm()`, `qnorm()` and `rnorm()`. However, they behave in pretty much exactly the same way as the corresponding functions for the binomial distribution, so there's not a lot that you need to know. The only thing that I should point out is that the argument names for the parameters are `mean` and `sd`. In pretty much every other respect, there's nothing else to add.

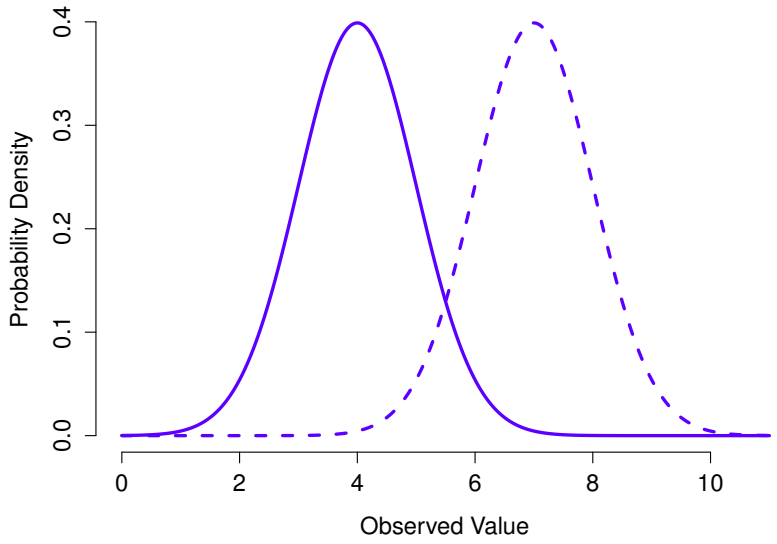


Figure 9.6: An illustration of what happens when you change the mean of a normal distribution. The solid line depicts a normal distribution with a mean of $\mu = 4$. The dashed line shows a normal distribution with a mean of $\mu = 7$. In both cases, the standard deviation is $\sigma = 1$. Not surprisingly, the two distributions have the same shape, but the dashed line is shifted to the right.

Instead of focusing on the maths, let's try to get a sense for what it means for a variable to be normally distributed. To that end, have a look at Figure 9.5, which plots a normal distribution with mean $\mu = 0$ and standard deviation $\sigma = 1$. You can see where the name "bell curve" comes from: it looks a bit like a bell. Notice that, unlike the plots that I drew to illustrate the binomial distribution, the picture of the normal distribution in Figure 9.5 shows a smooth curve instead of "histogram-like" bars. This isn't an arbitrary choice: the normal distribution is continuous, whereas the binomial is discrete. For instance, in the die rolling example from the last section, it was possible to get 3 skulls or 4 skulls, but impossible to get 3.9 skulls. The figures that I drew in the previous section reflected this fact: in Figure 9.3, for instance, there's a bar located at $X = 3$ and another one at $X = 4$, but there's nothing in between. Continuous quantities don't have this constraint. For instance, suppose we're talking about the weather. The temperature on a pleasant Spring day could be 23 degrees, 24 degrees, 23.9 degrees, or anything in between since temperature is a continuous variable, and so a normal distribution might be quite appropriate for describing Spring temperatures.[4]

With this in mind, let's see if we can't get an intuition for how the normal distribution works. Firstly, let's have a look at what happens when we play around with the parameters of the distribution. To that end, Figure 9.6 plots normal distributions that have different means, but have the same standard deviation. As you might expect, all of these distributions have the same "width". The only difference between them is that they've been shifted to the left or to the right. In every other respect they're identical. In contrast, if we increase the standard deviation while keeping the mean constant, the peak

[4] In practice, the normal distribution is so handy that people tend to use it even when the variable isn't actually continuous. As long as there are enough categories (e.g., Likert scale responses to a questionnaire), it's pretty standard practice to use the normal distribution as an approximation. This works out much better in practice than you'd think.

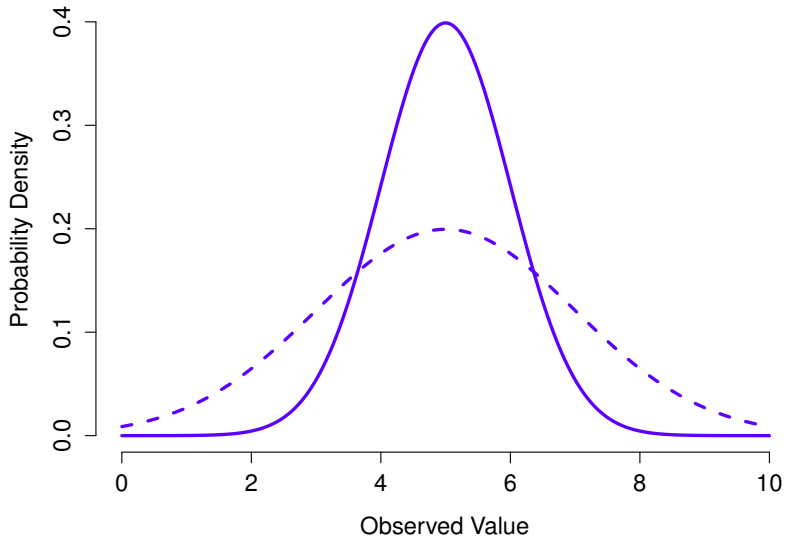


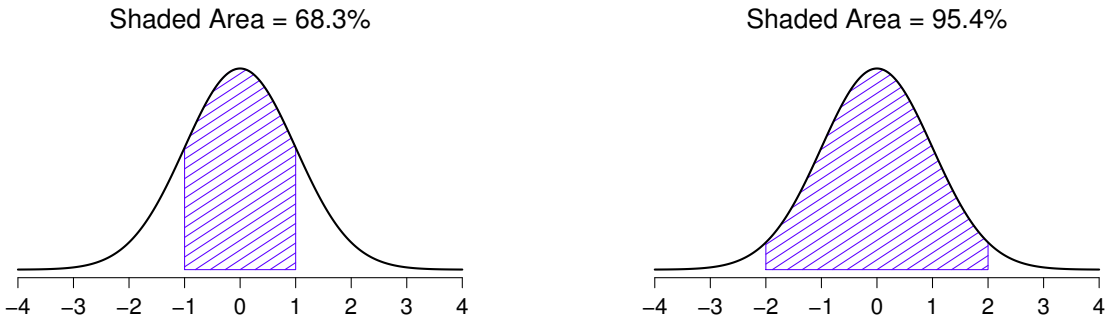
Figure 9.7: An illustration of what happens when you change the the standard deviation of a normal distribution. Both distributions plotted in this figure have a mean of $\mu = 5$, but they have different standard deviations. The solid line plots a distribution with standard deviation $\sigma = 1$, and the dashed line shows a distribution with standard deviation $\sigma = 2$. As a consequence, both distributions are "centred" on the same spot, but the dashed line is wider than the solid one.

of the distribution stays in the same place, but the distribution gets wider, as you can see in Figure 9.7. Notice, though, that when we widen the distribution, the height of the peak shrinks. This has to happen: in the same way that the heights of the bars that we used to draw a discrete binomial distribution have to *sum* to 1, the total *area under the curve* for the normal distribution must equal 1. Before moving on, I want to point out one important characteristic of the normal distribution. Irrespective of what the actual mean and standard deviation are, 68.3% of the area falls within 1 standard deviation of the mean. Similarly, 95.4% of the distribution falls within 2 standard deviations of the mean, and 99.7% of the distribution is within 3 standard deviations. This idea is illustrated in Figure 9.8.

9.5.1 Probability density

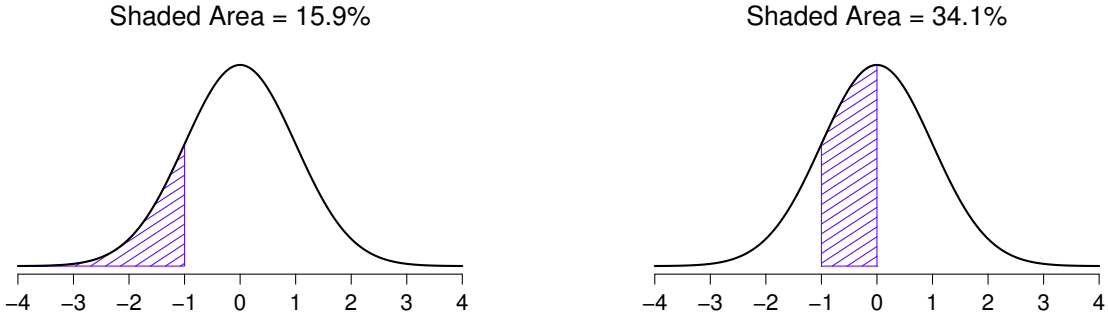
There's something I've been trying to hide throughout my discussion of the normal distribution, something that some introductory textbooks omit completely. They might be right to do so: this "thing" that I'm hiding is weird and counterintuitive even by the admittedly distorted standards that apply in statistics. Fortunately, it's not something that you need to understand at a deep level in order to do basic statistics: rather, it's something that starts to become important later on when you move beyond the basics. So, if it doesn't make complete sense, don't worry: try to make sure that you follow the gist of it.

Throughout my discussion of the normal distribution, there's been one or two things that don't quite make sense. Perhaps you noticed that the y-axis in these figures is labelled "Probability Density" rather



(a) (b)

Figure 9.8: The area under the curve tells you the probability that an observation falls within a particular range. The solid lines plot normal distributions with mean $\mu = 0$ and standard deviation $\sigma = 1$. The shaded areas illustrate "areas under the curve" for two important cases. In panel a, we can see that there is a 68.3% chance that an observation will fall within one standard deviation of the mean. In panel b, we see that there is a 95.4% chance that an observation will fall within two standard deviations of the mean.



(a) (b)

Figure 9.9: Two more examples of the "area under the curve idea". There is a 15.9% chance that an observation is one standard deviation below the mean or smaller (panel a), and a 34.1% chance that the observation is greater than one standard deviation below the mean but still below the mean (panel b). Notice that if you add these two numbers together you get 15.9% + 34.1% = 50%. For normally distributed data, there is a 50% chance that an observation falls below the mean. And of course that also implies that there is a 50% chance that it falls above the mean.

than density. Maybe you noticed that I used $p(X)$ instead of $P(X)$ when giving the formula for the normal distribution. Maybe you're wondering why R uses the "d" prefix for functions like `dnorm()`. And maybe, just maybe, you've been playing around with the `dnorm()` function, and you accidentally typed in a command like this:

```
> dnorm( x = 1, mean = 1, sd = 0.1 )
[1] 3.989423
```

And if you've done the last part, you're probably very confused. I've asked R to calculate the probability that `x = 1`, for a normally distributed variable with `mean = 1` and standard deviation `sd = 0.1`; and it tells me that the probability is 3.99. But, as we discussed earlier, probabilities *can't* be larger than 1. So either I've made a mistake, or that's not a probability.

As it turns out, the second answer is correct. What we've calculated here isn't actually a probability: it's something else. To understand what that something is, you have to spend a little time thinking about what it really *means* to say that X is a continuous variable. Let's say we're talking about the temperature outside. The thermometer tells me it's 23 degrees, but I know that's not really true. It's not *exactly* 23 degrees. Maybe it's 23.1 degrees, I think to myself. But I know that that's not really true either, because it might actually be 23.09 degrees. But, I know that... well, you get the idea. The tricky thing with genuinely continuous quantities is that you never really know exactly what they are.

Now think about what this implies when we talk about probabilities. Suppose that tomorrow's maximum temperature is sampled from a normal distribution with mean 23 and standard deviation 1. What's the probability that the temperature will be *exactly* 23 degrees? The answer is "zero", or possibly, "a number so close to zero that it might as well be zero". Why is this? It's like trying to throw a dart at an infinitely small dart board: no matter how good your aim, you'll never hit it. In real life you'll never get a value of exactly 23. It'll always be something like 23.1 or 22.99998 or something. In other words, it's completely meaningless to talk about the probability that the temperature is exactly 23 degrees. However, in everyday language, if I told you that it was 23 degrees outside and it turned out to be 22.9998 degrees, you probably wouldn't call me a liar. Because in everyday language, "23 degrees" usually means something like "somewhere between 22.5 and 23.5 degrees". And while it doesn't feel very meaningful to ask about the probability that the temperature is exactly 23 degrees, it does seem sensible to ask about the probability that the temperature lies between 22.5 and 23.5, or between 20 and 30, or any other range of temperatures.

The point of this discussion is to make clear that, when we're talking about continuous distributions, it's not meaningful to talk about the probability of a specific value. However, what we *can* talk about is the probability that the value lies within a particular range of values. To find out the probability associated with a particular range, what you need to do is calculate the "area under the curve". We've seen this concept already: in Figure 9.8, the shaded areas shown depict genuine probabilities (e.g., in Figure 9.8a it shows the probability of observing a value that falls within 1 standard deviation of the mean).

Okay, so that explains part of the story. I've explained a little bit about how continuous probability distributions should be interpreted (i.e., area under the curve is the key thing), but I haven't actually explained what the `dnorm()` function actually calculates. Equivalently, what does the formula for $p(x)$ that I described earlier actually mean? Obviously, $p(x)$ doesn't describe a probability, but what is it? The name for this quantity $p(x)$ is a **probability density**, and in terms of the plots we've been drawing, it corresponds to the *height* of the curve. The densities themselves aren't meaningful in and of themselves: but they're "rigged" to ensure that the *area* under the curve is always interpretable as

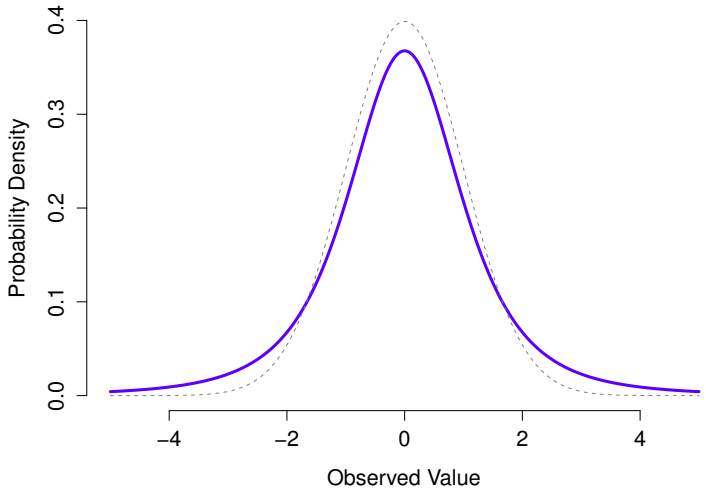


Figure 9.10: A t distribution with 3 degrees of freedom (solid line). It looks similar to a normal distribution, but it's not quite the same. For comparison purposes, I've plotted a standard normal distribution as the dashed line. Note that the "tails" of the t distribution are "heavier" (i.e., extend further outwards) than the tails of the normal distribution? That's the important difference between the two.

genuine probabilities. To be honest, that's about as much as you really need to know for now.[5]

9.6 Other useful distributions

The normal distribution is the distribution that statistics makes most use of (for reasons to be discussed shortly), and the binomial distribution is a very useful one for lots of purposes. But the world of statistics is filled with probability distributions, some of which we'll run into in passing. In particular, the three that will appear in this book are the t distribution, the χ^2 distribution and the F distribution. I won't give formulas for any of these, or talk about them in too much detail, but I will show you some pictures.

- The *t* **distribution** is a continuous distribution that looks very similar to a normal distribution, but has heavier tails: see Figure 9.10. This distribution tends to arise in situations where you think that the data actually follow a normal distribution, but you don't know the mean or standard deviation. As you might expect, the relevant R functions are `dt()`, `pt()`, `qt()` and `rt()`, and we'll run into this distribution again in Chapter 13.

[5] For those readers who know a little calculus, I'll give a slightly more precise explanation. In the same way that probabilities are non-negative numbers that must sum to 1, probability densities are non-negative numbers that must integrate to 1 (where the integral is taken across all possible values of X). To calculate the probability that X falls between a and b we calculate the definite integral of the density function over the corresponding range, $\int_a^b p(x)\ dx$. If you don't remember or never learned calculus, don't worry about this. It's not needed for this book.

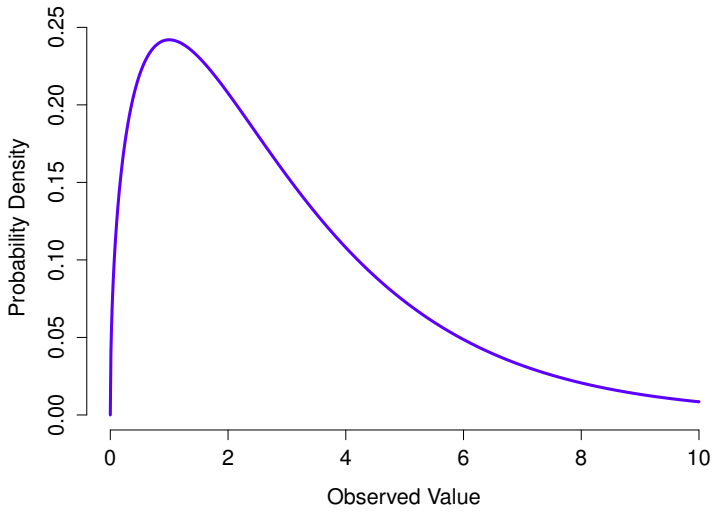


Figure 9.11: A χ^2 distribution with 3 degrees of freedom. Notice that the observed values must always be greater than zero, and that the distribution is pretty skewed. These are the key features of a chi-square distribution.

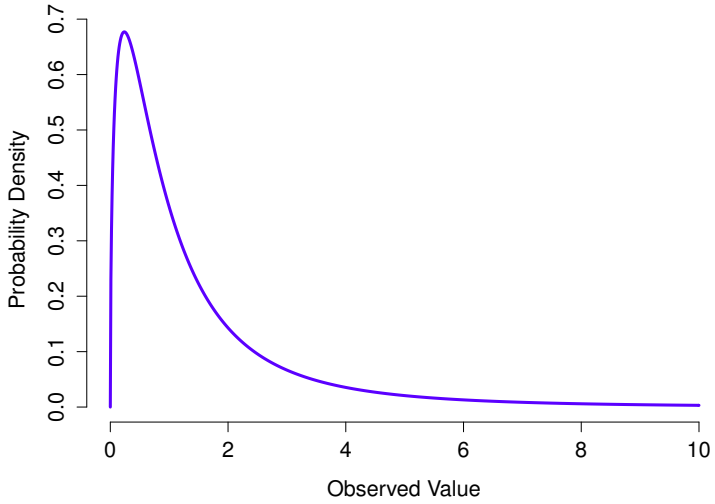


Figure 9.12: An F distribution with 3 and 5 degrees of freedom. Qualitatively speaking, it looks pretty similar to a chi-square distribution, but they're not quite the same in general.

- The χ^2 **distribution** is another distribution that turns up in lots of different places. The situation in which we'll see it is when doing categorical data analysis (Chapter 12), but it's one of those things that actually pops up all over the place. When you dig into the maths (and who doesn't love doing that?), it turns out that the main reason why the χ^2 distribution turns up all over the place is that, if you have a bunch of variables that are normally distributed, square their values and then add them up (a procedure referred to as taking a "sum of squares"), this sum has a χ^2 distribution. You'd be amazed how often this fact turns out to be useful. Anyway, here's what a χ^2 distribution looks like: Figure 9.11. Once again, the R commands for this one are pretty predictable: `dchisq()`, `pchisq()`, `qchisq()`, `rchisq()`.

- The F **distribution** looks a bit like a χ^2 distribution, and it arises whenever you need to compare two χ^2 distributions to one another. Admittedly, this doesn't exactly sound like something that any sane person would want to do, but it turns out to be very important in real world data analysis. Remember when I said that χ^2 turns out to be the key distribution when we're taking a "sum of squares"? Well, what that means is if you want to compare two different "sums of squares", you're probably talking about something that has an F distribution. Of course, as yet I still haven't given you an example of anything that involves a sum of squares, but I will... in Chapter 14. And that's where we'll run into the F distribution. Oh, and here's a picture: Figure 9.12. And of course we can get R to do things with F distributions just by using the commands `df()`, `pf()`, `qf()` and `rf()`.

Because these distributions are all tightly related to the normal distribution and to each other, and because they are will turn out to be the important distributions when doing inferential statistics later in this book, I think it's useful to do a little demonstration using R, just to "convince ourselves" that these distributions really are related to each other in the way that they're supposed to be. First, we'll use the `rnorm()` function to generate 1000 normally-distributed observations:

```
> normal.a <- rnorm( n=1000, mean=0, sd=1 )
> print(normal.a)
   [1]  0.2913131706 -0.4156161554  0.1482611948  0.8516858463 -0.6658081840
   [6]  0.8827940964  1.3757851963  0.2497812249 -0.1926513775  0.2160192605
  [11] -0.7982884040 -1.4027212056  0.0281455244 -0.1266362460  0.8645205990

        BLAH BLAH BLAH
```

So the `normal.a` variable contains 1000 numbers that are normally distributed, and have mean 0 and standard deviation 1, and the actual print out of these numbers goes on for rather a long time. Note that, because the default parameters of the `rnorm()` function are `mean=0` and `sd=1`, I could have shortened the command to `rnorm( n=1000 )`. In any case, what we can do is use the `hist()` function to draw a histogram of the data, like so:

```
> hist( normal.a )
```

If you do this, you should see something similar to Figure 9.13a. Your plot won't look quite as pretty as the one in the figure, of course, because I've played around with all the formatting (see Chapter 6), and I've also plotted the true distribution of the data as a solid black line (i.e., a normal distribution with mean 0 and standard deviation 1) so that you can compare the data that we just generated to the true distribution.

In the previous example all I did was generate lots of normally distributed observations using `rnorm()` and then compared those to the true probability distribution in the figure (using `dnorm()` to generate the black line in the figure, but I didn't show the commmands for that). Now let's try something trickier. We'll try to generate some observations that follow a chi-square distribution with 3 degrees of freedom, but instead of using `rchisq()`, we'll start with variables that are normally distributed, and see if we

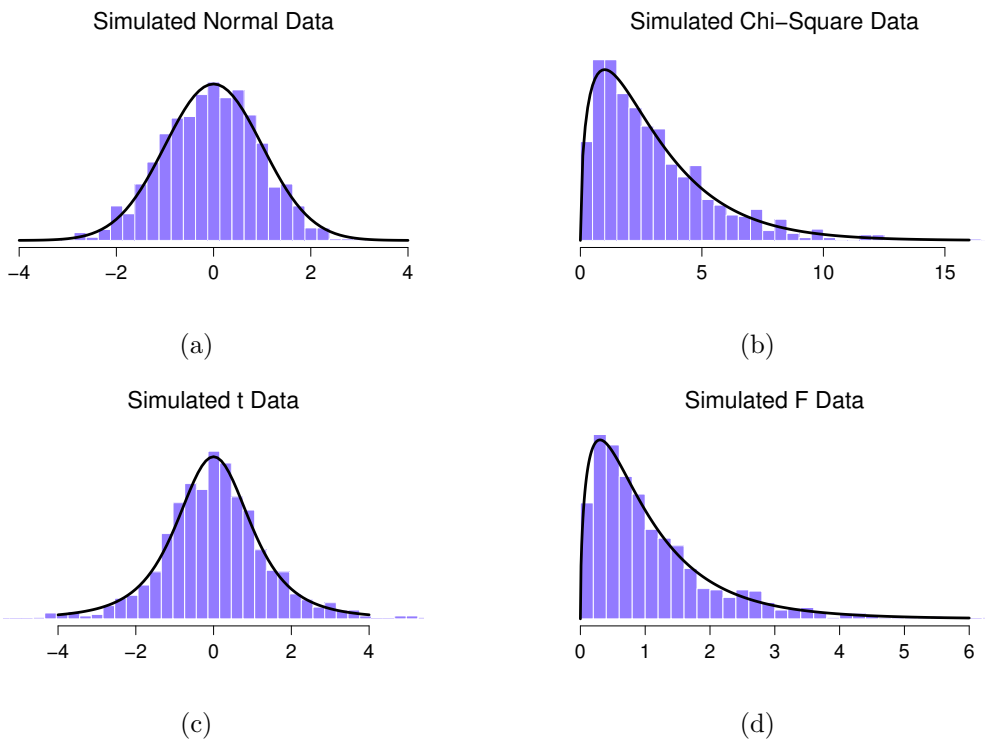


Figure 9.13: Data sampled from different distributions. See the main text for details.

can exploit the known relationships between normal and chi-square distributions to do the work. As I mentioned earlier, a chi-square distribution with k degrees of freedom is what you get when you take k normally-distributed variables (with mean 0 and standard deviation 1), square them, and add them up. Since we want a chi-square distribution with 3 degrees of freedom, we'll need to supplement our `normal.a` data with two more sets of normally-distributed observations, imaginatively named `normal.b` and `normal.c`:

```
> normal.b <- rnorm( n=1000 )  # another set of normally distributed data
> normal.c <- rnorm( n=1000 )  # and another!
```

Now that we've done that, the theory says we should square these and add them together, like this

```
> chi.sq.3 <- (normal.a)^2 + (normal.b)^2 + (normal.c)^2
```

and the resulting `chi.sq.3` variable should contain 1000 observations that follow a chi-square distribution with 3 degrees of freedom. You can use the `hist()` function to have a look at these observations yourself, using a command like this,

```
> hist( chi.sq.3 )
```

and you should obtain a result that looks pretty similar to the plot in Figure 9.13b. Once again, the plot that I've drawn is a little fancier: in addition to the histogram of `chi.sq.3`, I've also plotted a chi-square distribution with 3 degrees of freedom. It's pretty clear that – even though I used `rnorm()` to do all the

work rather than `rchisq()` – the observations stored in the `chi.sq.3` variable really do follow a chi-square distribution. Admittedly, this probably doesn't seem all that interesting right now, but later on when we start encountering the chi-square distribution in Chapter 12, it will be useful to understand the fact that these distributions are related to one another.

We can extend this demonstration to the t distribution and the F distribution. Earlier, I implied that the t distribution is related to the normal distribution when the standard deviation is unknown. That's certainly true, and that's the what we'll see later on in Chapter 13, but there's a somewhat more precise relationship between the normal, chi-square and t distributions. Suppose we "scale" our chi-square data by dividing it by the degrees of freedom, like so

```
> scaled.chi.sq.3 <- chi.sq.3 / 3
```

We then take a set of normally distributed variables and divide them by (the square root of) our scaled chi-square variable which had $df = 3$, and the result is a t distribution with 3 degrees of freedom:

```
> normal.d <- rnorm( n=1000 )  # yet another set of normally distributed data
> t.3 <- normal.d / sqrt( scaled.chi.sq.3 )  # divide by square root of scaled chi-square to get t
```

If we plot the histogram of `t.3`, we end up with something that looks very similar to Figure 9.13c. Similarly, we can obtain an F distribution by taking the ratio between two scaled chi-square distributions. Suppose, for instance, we wanted to generate data from an F distribution with 3 and 20 degrees of freedom. We could do this using `df()`, but we could also do the same thing by generating two chi-square variables, one with 3 degrees of freedom, and the other with 20 degrees of freedom. As the example with `chi.sq.3` illustrates, we can actually do this using `rnorm()` if we really want to, but this time I'll take a short cut:

```
> chi.sq.20 <- rchisq( 1000, 20)  # generate chi square data with df = 20...
> scaled.chi.sq.20 <- chi.sq.20 / 20  # scale the chi square variable...
> F.3.20 <-  scaled.chi.sq.3  / scaled.chi.sq.20 # take the ratio of the two chi squares...
> hist( F.3.20 ) # ... and draw a picture
```

The resulting `F.3.20` variable does in fact store variables that follow an F distribution with 3 and 20 degrees of freedom. This is illustrated in Figure 9.13d, which plots the histgram of the observations stored in `F.3.20` against the true F distribution with $df_1 = 3$ and $df_2 = 20$. Again, they match.

Okay, time to wrap this section up. We've seen three new distributions: χ^2, t and F. They're all continuous distributions, and they're all closely related to the normal distribution. I've talked a little bit about the precise nature of this relationship, and shown you some R commands that illustrate this relationship. The key thing for our purposes, however, is not that you have a deep understanding of all these different distributions, nor that you remember the precise relationships between them. The main thing is that you grasp the basic idea that these distributions are all deeply related to one another, and to the normal distribution. Later on in this book, we're going to run into data that are normally distributed, or at least assumed to be normally distributed. What I want you to understand right now is that, if you make the assumption that your data are normally distributed, you shouldn't be surprised to see χ^2, t and F distributions popping up all over the place when you start trying to do your data analysis.

9.7 Summary

In this chapter we've talked about probability. We've talked what probability means, and why statisticians can't agree on what it means. We talked about the rules that probabilities have to obey. And we

introduced the idea of a probability distribution, and spent a good chunk of the chapter talking about some of the more important probability distributions that statisticians work with. The section by section breakdown looks like this:

- Probability theory versus statistics (Section 9.1)
- Frequentist versus Bayesian views of probability (Section 9.2)
- Basics of probability theory (Section 9.3)
- Binomial distribution (Section 9.4), normal distribution (Section 9.5), and others (Section 9.6)

As you'd expect, my coverage is by no means exhaustive. Probability theory is a large branch of mathematics in its own right, entirely separate from its application to statistics and data analysis. As such, there are thousands of books written on the subject and universities generally offer multiple classes devoted entirely to probability theory. Even the "simpler" task of documenting standard probability distributions is a big topic. I've described five standard probability distributions in this chapter, but sitting on my bookshelf I have a 45-chapter book called "Statistical Distributions" (M. Evans, Hastings, & Peacock, 2011) that lists a *lot* more than that. Fortunately for you, very little of this is necessary. You're unlikely to need to know dozens of statistical distributions when you go out and do real world data analysis, and you definitely won't need them for this book, but it never hurts to know that there's other possibilities out there.

Picking up on that last point, there's a sense in which this whole chapter is something of a digression. Many undergraduate psychology classes on statistics skim over this content very quickly (I know mine did), and even the more advanced classes will often "forget" to revisit the basic foundations of the field. Most academic psychologists would not know the difference between probability and density, and until recently very few would have been aware of the difference between Bayesian and frequentist probability. However, I think it's important to understand these things before moving onto the applications. For example, there are a lot of rules about what you're "allowed" to say when doing statistical inference, and many of these can seem arbitrary and weird. However, they start to make sense if you understand that there is this Bayesian/frequentist distinction. Similarly, in Chapter 13 we're going to talk about something called the t-test, and if you really want to have a grasp of the mechanics of the t-test it really helps to have a sense of what a t-distribution actually looks like. You get the idea, I hope.

10. Estimating unknown quantities from a sample

At the start of the last chapter I highlighted the critical distinction between *descriptive statistics* and *inferential statistics*. As discussed in Chapter 5, the role of descriptive statistics is to concisely summarise what we *do* know. In contrast, the purpose of inferential statistics is to "learn what we do not know from what we do". Now that we have a foundation in probability theory, we are in a good position to think about the problem of statistical inference. What kinds of things would we like to learn about? And how do we learn them? These are the questions that lie at the heart of inferential statistics, and they are traditionally divided into two "big ideas": estimation and hypothesis testing. The goal in this chapter is to introduce the first of these big ideas, estimation theory, but I'm going to witter on about sampling theory first because estimation theory doesn't make sense until you understand sampling. As a consequence, this chapter divides naturally into two parts Sections 10.1 through 10.3 are focused on sampling theory, and Sections 10.4 and 10.5 make use of sampling theory to discuss how statisticians think about estimation.

10.1 Samples, populations and sampling

In the prelude to Part IV I discussed the riddle of induction, and highlighted the fact that *all* learning requires you to make assumptions. Accepting that this is true, our first task to come up with some fairly general assumptions about data that make sense. This is where **sampling theory** comes in. If probability theory is the foundations upon which all statistical theory builds, sampling theory is the frame around which you can build the rest of the house. Sampling theory plays a huge role in specifying the assumptions upon which your statistical inferences rely. And in order to talk about "making inferences" the way statisticians think about it, we need to be a bit more explicit about what it is that we're drawing inferences *from* (the sample) and what it is that we're drawing inferences *about* (the population).

In almost every situation of interest, what we have available to us as researchers is a **sample** of data. We might have run experiment with some number of participants; a polling company might have phoned some number of people to ask questions about voting intentions; etc. Regardless: the data set available to us is finite, and incomplete. We can't possibly get every person in the world to do our experiment; a polling company doesn't have the time or the money to ring up every voter in the country etc. In our earlier discussion of descriptive statistics (Chapter 5), this sample was the only thing we were interested in. Our only goal was to find ways of describing, summarising and graphing that sample. This is about to change.

10.1.1 Defining a population

A sample is a concrete thing. You can open up a data file, and there's the data from your sample. A **population**, on the other hand, is a more abstract idea. It refers to the set of all possible people, or all possible observations, that you want to draw conclusions about, and is generally *much* bigger than the sample. In an ideal world, the researcher would begin the study with a clear idea of what the population of interest is, since the process of designing a study and testing hypotheses about the data that it produces does depend on the population about which you want to make statements. However, that doesn't always happen in practice: usually the researcher has a fairly vague idea of what the population is and designs the study as best he/she can on that basis.

Sometimes it's easy to state the population of interest. For instance, in the "polling company" example that opened the chapter, the population consisted of all voters enrolled at the a time of the study – millions of people. The sample was a set of 1000 people who all belong to that population. In most situations the situation is much less simple. In a typical a psychological experiment, determining the population of interest is a bit more complicated. Suppose I run an experiment using 100 undergraduate students as my participants. My goal, as a cognitive scientist, is to try to learn something about how the mind works. So, which of the following would count as "the population":

- All of the undergraduate psychology students at the University of Adelaide?
- Undergraduate psychology students in general, anywhere in the world?
- Australians currently living?
- Australians of similar ages to my sample?
- Anyone currently alive?
- Any human being, past, present or future?
- Any biological organism with a sufficient degree of intelligence operating in a terrestrial environment?
- Any intelligent being?

Each of these defines a real group of mind-possessing entities, all of which might be of interest to me as a cognitive scientist, and it's not at all clear which one ought to be the true population of interest. As another example, consider the Wellesley-Croker game that we discussed in the prelude. The sample here is a specific sequence of 12 wins and 0 losses for Wellesley. What is the population?

- All outcomes until Wellesley and Croker arrived at their destination?
- All outcomes if Wellesley and Croker had played the game for the rest of their lives?
- All outcomes if Wellseley and Croker lived forever and played the game until the world ran out of hills?
- All outcomes if we created an infinite set of parallel universes and the Wellesely/Croker pair made guesses about the same 12 hills in each universe?

Again, it's not obvious what the population is.

10.1.2 Simple random samples

Irrespective of how I define the population, the critical point is that the sample is a subset of the population, and our goal is to use our knowledge of the sample to draw inferences about the properties of the population. The relationship between the two depends on the *procedure* by which the sample was selected. This procedure is referred to as a **sampling method**, and it is important to understand why it matters.

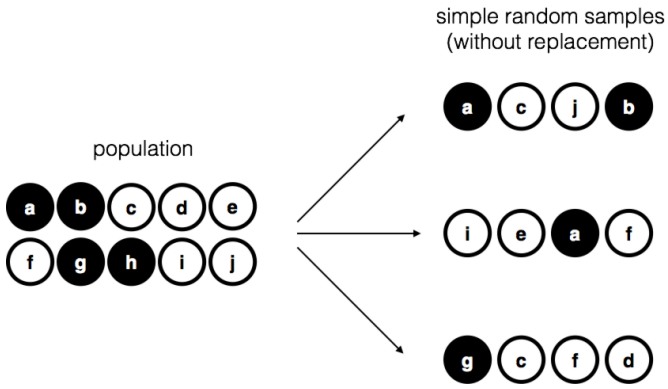


Figure 10.1: Simple random sampling without replacement from a finite population

To keep things simple, let's imagine that we have a bag containing 10 chips. Each chip has a unique letter printed on it, so we can distinguish between the 10 chips. The chips come in two colours, black and white. This set of chips is the population of interest, and it is depicted graphically on the left of Figure 10.1. As you can see from looking at the picture, there are 4 black chips and 6 white chips, but of course in real life we wouldn't know that unless we looked in the bag. Now imagine you run the following "experiment": you shake up the bag, close your eyes, and pull out 4 chips without putting any of them back into the bag. First out comes the a chip (black), then the c chip (white), then j (white) and then finally b (black). If you wanted, you could then put all the chips back in the bag and repeat the experiment, as depicted on the right hand side of Figure 10.1. Each time you get different results, but the procedure is identical in each case. The fact that the same procedure can lead to different results each time, we refer to it as a *random* process.[1] However, because we shook the bag before pulling any chips out, it seems reasonable to think that every chip has the same chance of being selected. A procedure in which every member of the population has the same chance of being selected is called a **simple random sample**. The fact that we did *not* put the chips back in the bag after pulling them out means that you can't observe the same thing twice, and in such cases the observations are said to have been sampled **without replacement**.

To help make sure you understand the importance of the sampling procedure, consider an alternative way in which the experiment could have been run. Suppose that my 5-year old son had opened the bag, and decided to pull out four black chips without putting any of them back in the bag. This *biased* sampling scheme is depicted in Figure 10.2. Now consider the evidentiary value of seeing 4 black chips and 0 white chips. Clearly, it depends on the sampling scheme, does it not? If you know that the sampling scheme is biased to select only black chips, then a sample that consists of only black chips doesn't tell you very much about the population! For this reason, statisticians really like it when a data set can be considered a simple random sample, because it makes the data analysis *much* easier.

A third procedure is worth mentioning. This time around we close our eyes, shake the bag, and pull out a chip. This time, however, we record the observation and then put the chip back in the bag. Again we close our eyes, shake the bag, and pull out a chip. We then repeat this procedure until we have 4 chips. Data sets generated in this way are still simple random samples, but because we put the chips back in the bag immediately after drawing them it is referred to as a sample **with replacement**. The difference between this situation and the first one is that it is possible to observe the same population

[1] The proper mathematical definition of randomness is extraordinarily technical, and way beyond the scope of this book. We'll be non-technical here and say that a process has an element of randomness to it whenever it is possible to repeat the process and get different answers each time.

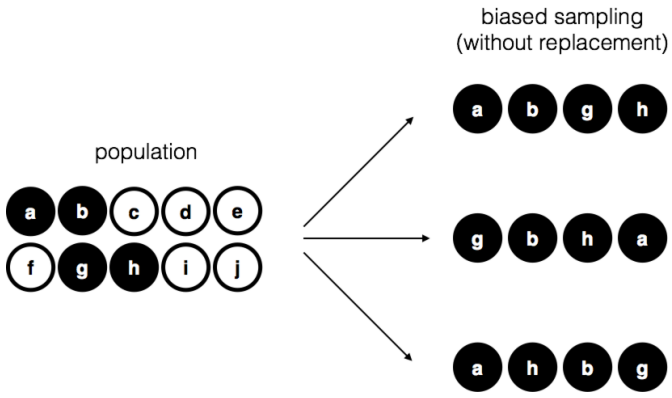


Figure 10.2: Biased sampling without replacement from a finite population

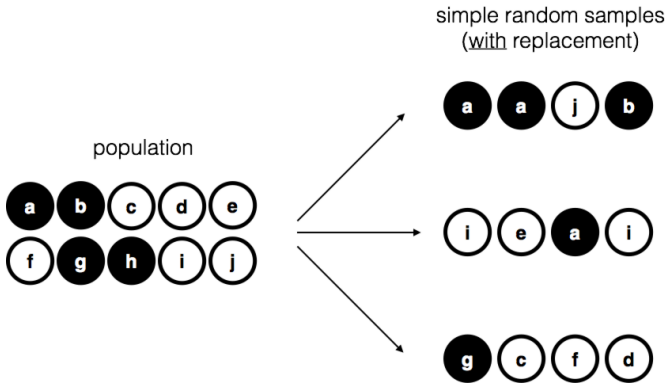


Figure 10.3: Simple random sampling *with* replacement from a finite population

member multiple times, as illustrated in Figure 10.3.

In my experience, most psychology experiments tend to be sampling without replacement, because the same person is not allowed to participate in the experiment twice. However, most statistical theory is based on the assumption that the data arise from a simple random sample *with* replacement. In real life, this very rarely matters. If the population of interest is large (e.g., has more than 10 entities!) the difference between sampling with- and without- replacement is too small to be concerned with. The difference between simple random samples and biased samples, on the other hand, is not such an easy thing to dismiss.

10.1.3 Most samples are not simple random samples

As you can see from looking at the list of possible populations that I showed above, it is almost impossible to obtain a simple random sample from most populations of interest. When I run experiments, I'd consider it a minor miracle if my participants turned out to be a random sampling of the undergraduate psychology students at Adelaide university, even though this is by far the narrowest population that I might want to generalise to. A thorough discussion of other types of sampling schemes is beyond the

scope of this book, but to give you a sense of what's out there I'll list a few of the more important ones:

- *Stratified sampling*. Suppose your population is (or can be) divided into several different subpopulations, or *strata*. Perhaps you're running a study at several different sites, for example. Instead of trying to sample randomly from the population as a whole, you instead try to collect a separate random sample from each of the strata. Stratified sampling is sometimes easier to do than simple random sampling, especially when the population is already divided into the distinct strata. It can also be more efficient that simple random sampling, especially when some of the subpopulations are rare. For instance, when studying schizophrenia it would be much better to divide the population into two[2] strata (schizophrenic and not-schizophrenic), and then sample an equal number of people from each group. If you selected people randomly, you would get so few schizophrenic people in the sample that your study would be useless. This specific kind of of stratified sampling is referred to as *oversampling* because it makes a deliberate attempt to over-represent rare groups.

- *Snowball sampling* is a technique that is especially useful when sampling from a "hidden" or hard to access population, and is especially common in social sciences. For instance, suppose the researchers want to conduct an opinion poll among transgender people. The research team might only have contact details for a few trans folks, so the survey starts by asking them to participate (stage 1). At the end of the survey, the participants are asked to provide contact details for other people who might want to participate. In stage 2, those new contacts are surveyed. The process continues until the researchers have sufficient data. The big advantage to snowball sampling is that it gets you data in situations that might otherwise be impossible to get any. On the statistical side, the main disadvantage is that the sample is highly non-random, and non-random in ways that are difficult to address. On the real life side, the disadvantage is that the procedure can be unethical if not handled well, because hidden populations are often hidden for a reason. I chose transgender people as an example here to highlight this: if you weren't careful you might end up outing people who don't want to be outed (very, very bad form), and even if you don't make that mistake it can still be intrusive to use people's social networks to study them. It's certainly very hard to get people's informed consent *before* contacting them, yet in many cases the simple act of contacting them and saying "hey we want to study you" can be hurtful. Social networks are complex things, and just because you can use them to get data doesn't always mean you should.

- *Convenience sampling* is more or less what it sounds like. The samples are chosen in a way that is convenient to the researcher, and not selected at random from the population of interest. Snowball sampling is one type of convenience sampling, but there are many others. A common example in psychology are studies that rely on undergraduate psychology students. These samples are generally non-random in two respects: firstly, reliance on undergraduate psychology students automatically means that your data are restricted to a single subpopulation. Secondly, the students usually get to pick which studies they participate in, so the sample is a self selected subset of psychology students not a randomly selected subset. In real life, most studies are convenience samples of one form or another. This is sometimes a severe limitation, but not always.

10.1.4 How much does it matter if you don't have a simple random sample?

Okay, so real world data collection tends not to involve nice simple random samples. Does that matter? A little thought should make it clear to you that it *can* matter if your data are not a simple random sample: just think about the difference between Figures 10.1 and 10.2. However, it's not quite as bad as it sounds. Some types of biased samples are entirely unproblematic. For instance, when using

[2] Nothing in life is that simple: there's not an obvious division of people into binary categories like "schizophrenic" and "not schizophrenic". But this isn't a clinical psychology text, so please forgive me a few simplifications here and there.

a stratified sampling technique you actually *know* what the bias is because you created it deliberately, often to *increase* the effectiveness of your study, and there are statistical techniques that you can use to adjust for the biases you've introduced (not covered in this book!). So in those situations it's not a problem.

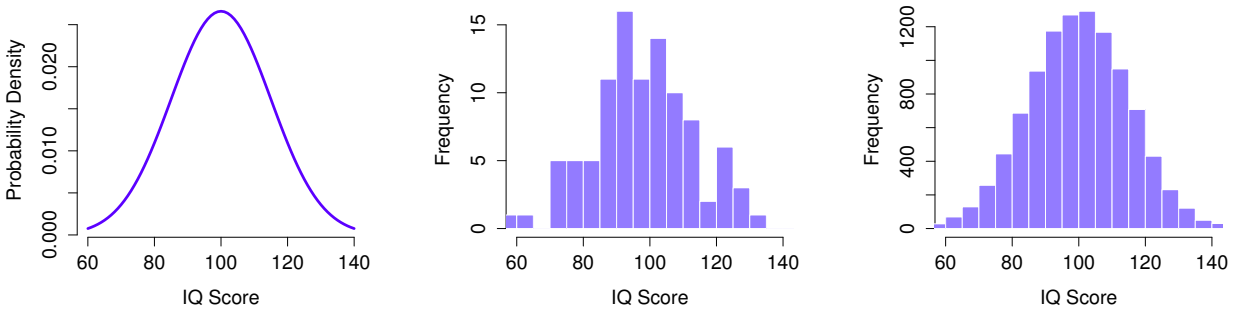
More generally though, it's important to remember that random sampling is a means to an end, not the end in itself. Let's assume you've relied on a convenience sample, and as such you can assume it's biased. A bias in your sampling method is only a problem if it causes you to draw the wrong conclusions. When viewed from that perspective, I'd argue that we don't need the sample to be randomly generated in *every* respect: we only need it to be random with respect to the psychologically-relevant phenomenon of interest. Suppose I'm doing a study looking at working memory capacity. In study 1, I actually have the ability to sample randomly from all human beings currently alive, with one exception: I can only sample people born on a Monday. In study 2, I am able to sample randomly from the Australian population. I want to generalise my results to the population of all living humans. Which study is better? The answer, obviously, is study 1. Why? Because we have no reason to think that being "born on a Monday" has any interesting relationship to working memory capacity. In contrast, I can think of several reasons why "being Australian" might matter. Australia is a wealthy, industrialised country with a very well-developed education system. People growing up in that system will have had life experiences much more similar to the experiences of the people who designed the tests for working memory capacity. This shared experience might easily translate into similar beliefs about how to "take a test", a shared assumption about how psychological experimentation works, and so on. These things might actually matter. For instance, "test taking" style might have taught the Australian participants how to direct their attention exclusively on fairly abstract test materials relative to people that haven't grown up in a similar environment; leading to a misleading picture of what working memory capacity is.

There are two points hidden in this discussion. Firstly, when designing your own studies, it's important to think about what population you care about, and try hard to sample in a way that is appropriate to that population. In practice, you're usually forced to put up with a "sample of convenience" (e.g., psychology lecturers sample psychology students because that's the least expensive way to collect data, and our coffers aren't exactly overflowing with gold), but if so you should at least spend some time thinking about what the dangers of this practice might be.

Secondly, if you're going to criticise someone else's study because they've used a sample of convenience rather than laboriously sampling randomly from the entire human population, at least have the courtesy to offer a specific theory as to *how* this might have distorted the results. Remember, everyone in science is aware of this issue, and does what they can to alleviate it. Merely pointing out that "the study only included people from group BLAH" is entirely unhelpful, and borders on being insulting to the researchers, who are of course aware of the issue. They just don't happen to be in possession of the infinite supply of time and money required to construct the perfect sample. In short, if you want to offer a responsible critique of the sampling process, then be *helpful*. Rehashing the blindingly obvious truisms that I've been rambling on about in this section isn't helpful.

10.1.5 Population parameters and sample statistics

Okay. Setting aside the thorny methodological issues associated with obtaining a random sample and my rather unfortunate tendency to rant about lazy methodological criticism, let's consider a slightly different issue. Up to this point we have been talking about populations the way a scientist might. To a psychologist, a population might be a group of people. To an ecologist, a population might be a group of bears. In most cases the populations that scientists care about are concrete things that actually exist in the real world. Statisticians, however, are a funny lot. On the one hand, they *are* interested in real world data and real science in the same way that scientists are. On the other hand, they also operate in the realm of pure abstraction in the way that mathematicians do. As a consequence, statistical theory tends to be a bit abstract in how a population is defined. In much the same way that psychological researchers



(a) (b) (c)

Figure 10.4: The population distribution of IQ scores (panel a) and two samples drawn randomly from it. In panel b we have a sample of 100 observations, and panel c we have a sample of 10,000 observations.

operationalise our abstract theoretical ideas in terms of concrete measurements (Section 2.1), statisticians operationalise the concept of a "population" in terms of mathematical objects that they know how to work with. You've already come across these objects in Chapter 9: they're called probability distributions.

The idea is quite simple. Let's say we're talking about IQ scores. To a psychologist, the population of interest is a group of actual humans who have IQ scores. A statistician "simplifies" this by operationally defining the population as the probability distribution depicted in Figure 10.4a. IQ tests are designed so that the average IQ is 100, the standard deviation of IQ scores is 15, and the distribution of IQ scores is normal. These values are referred to as the **population parameters** because they are characteristics of the entire population. That is, we say that the population mean μ is 100, and the population standard deviation σ is 15.

Now suppose I run an experiment. I select 100 people at random and administer an IQ test, giving me a simple random sample from the population. My sample would consist of a collection of numbers like this:

```
106 101 98 80 74 ... 107 72 100
```

Each of these IQ scores is sampled from a normal distribution with mean 100 and standard deviation 15. So if I plot a histogram of the sample, I get something like the one shown in Figure 10.4b. As you can see, the histogram is *roughly* the right shape, but it's a very crude approximation to the true population distribution shown in Figure 10.4a. When I calculate the mean of my sample, I get a number that is fairly close to the population mean 100 but not identical. In this case, it turns out that the people in my sample have a mean IQ of 98.5, and the standard deviation of their IQ scores is 15.9. These **sample statistics** are properties of my data set, and although they are fairly similar to the true population values, they are not the same. In general, sample statistics are the things you can calculate from your data set, and the population parameters are the things you want to learn about. Later on in this chapter I'll talk about how you can estimate population parameters using your sample statistics (Section 10.4) and how to work out how confident you are in your estimates (Section 10.5) but before we get to that there's a few more ideas in sampling theory that you need to know about.

10.2

The law of large numbers

In the previous section I showed you the results of one fictitious IQ experiment with a sample size of $N = 100$. The results were somewhat encouraging: the true population mean is 100, and the sample mean of 98.5 is a pretty reasonable approximation to it. In many scientific studies that level of precision is perfectly acceptable, but in other situations you need to be a lot more precise. If we want our sample statistics to be much closer to the population parameters, what can we do about it?

The obvious answer is to collect more data. Suppose that we ran a much larger experiment, this time measuring the IQs of 10,000 people. We can simulate the results of this experiment using R. In Section 9.5 I introduced the `rnorm()` function, which generates random numbers sampled from a normal distribution. For an experiment with a sample size of `n = 10000`, and a population with `mean = 100` and `sd = 15`, R produces our fake IQ data using these commands:

```
> IQ <- rnorm(n = 10000, mean = 100, sd = 15) # generate IQ scores
> IQ <- round(IQ) # IQs are whole numbers!
> print(IQ)
    [1]  74 104 100 104 102 106 122  87  92 101 104 119 109  92 114 121 133
   [18] 111 108 104 117 118 121  90  86  79 102 122  86  68  95 108  91  88
   [35]  89  81  89  76 124  79  76 100 135  94  91  88  84  92 104 113 108
   [52] 103  94 123 102 120  95 112 137  96  75 105 109  81 117 110 112 106

BLAH BLAH BLAH

 [9963] 106 124 108 108 117 121  94 114 106  98 103  84  93 102 104 121 106
 [9980]  87 106  95  92 100 104  94  98  95 124 114  86  83  94  95 116  89
 [9997]  49 126 112  97
```

I can compute the mean IQ using the command `mean(IQ)` and the standard deviation using the command `sd(IQ)`, and I can draw a histgram using `hist()`. The histogram of this much larger sample is shown in Figure 10.4c. Even a moment's inspections makes clear that the larger sample is a much better approximation to the true population distribution than the smaller one. This is reflected in the sample statistics: the mean IQ for the larger sample turns out to be 99.9, and the standard deviation is 15.1. These values are now very close to the true population.

I feel a bit silly saying this, but the thing I want you to take away from this is that large samples generally give you better information. I feel silly saying it because it's so bloody obvious that it shouldn't need to be said. In fact, it's such an obvious point that when Jacob Bernoulli – one of the founders of probability theory – formalised this idea back in 1713, he was kind of a jerk about it. Here's how he described the fact that we all share this intuition:

> *For even the most stupid of men, by some instinct of nature, by himself and without any instruction (which is a remarkable thing), is convinced that the more observations have been made, the less danger there is of wandering from one's goal* (see Stigler, 1986, p65)

Okay, so the passage comes across as a bit condescending (not to mention sexist), but his main point is correct: it really does feel obvious that more data will give you better answers. The question is, why is this so? Not surprisingly, this intuition that we all share turns out to be correct, and statisticians refer to it as the **law of large numbers**. The law of large numbers is a mathematical law that applies to many different sample statistics, but the simplest way to think about it is as a law about averages. The sample mean is the most obvious example of a statistic that relies on averaging (because that's what the mean

is... an average), so let's look at that. When applied to the sample mean, what the law of large numbers states is that as the sample gets larger, the sample mean tends to get closer to the true population mean. Or, to say it a little bit more precisely, as the sample size "approaches" infinity (written as $N \rightarrow \infty$) the sample mean approaches the population mean ($\bar{X} \rightarrow \mu$).[3]

I don't intend to subject you to a proof that the law of large numbers is true, but it's one of the most important tools for statistical theory. The law of large numbers is the thing we can use to justify our belief that collecting more and more data will eventually lead us to the truth. For any particular data set, the sample statistics that we calculate from it will be wrong, but the law of large numbers tells us that if we keep collecting more data those sample statistics will tend to get closer and closer to the true population parameters.

10.3 Sampling distributions and the central limit theorem

The law of large numbers is a very powerful tool, but it's not going to be good enough to answer all our questions. Among other things, all it gives us is a "long run guarantee". In the long run, if we were somehow able to collect an infinite amount of data, then the law of large numbers guarantees that our sample statistics will be correct. But as John Maynard Keynes famously argued in economics, a long run guarantee is of little use in real life:

> *[The] long run is a misleading guide to current affairs. In the long run we are all dead. Economists set themselves too easy, too useless a task, if in tempestuous seasons they can only tell us, that when the storm is long past, the ocean is flat again.* (Keynes, 1923, p. 80)

As in economics, so too in psychology and statistics. It is not enough to know that we will *eventually* arrive at the right answer when calculating the sample mean. Knowing that an infinitely large data set will tell me the exact value of the population mean is cold comfort when my *actual* data set has a sample size of $N = 100$. In real life, then, we must know something about the behaviour of the sample mean when it is calculated from a more modest data set!

10.3.1 Sampling distribution of the mean

With this in mind, let's abandon the idea that our studies will have sample sizes of 10000, and consider a very modest experiment indeed. This time around we'll sample $N = 5$ people and measure their IQ scores. As before, I can simulate this experiment in R using the `rnorm()` function:

```
> IQ.1 <- round( rnorm(n=5, mean=100, sd=15 ))
> IQ.1
[1]  90  82  94  99 110
```

The mean IQ in this sample turns out to be exactly 95. Not surprisingly, this is much less accurate than the previous experiment. Now imagine that I decided to **replicate** the experiment. That is, I repeat the procedure as closely as possible: I randomly sample 5 new people and measure their IQ. Again, R allows me to simulate the results of this procedure:

[3] Technically, the law of large numbers pertains to any sample statistic that can be described as an average of independent quantities. That's certainly true for the sample mean. However, it's also possible to write many other sample statistics as averages of one form or another. The variance of a sample, for instance, can be rewritten as a kind of average and so is subject to the law of large numbers. The minimum value of a sample, however, cannot be written as an average of anything and is therefore not governed by the law of large numbers.

Table 10.1: Ten replications of the IQ experiment, each with a sample size of $N = 5$.

	Person 1	Person 2	Person 3	Person 4	Person 5	Sample Mean
Replication 1	90	82	94	99	110	95.0
Replication 2	78	88	111	111	117	101.0
Replication 3	111	122	91	98	86	101.6
Replication 4	98	96	119	99	107	103.8
Replication 5	105	113	103	103	98	104.4
Replication 6	81	89	93	85	114	92.4
Replication 7	100	93	108	98	133	106.4
Replication 8	107	100	105	117	85	102.8
Replication 9	86	119	108	73	116	100.4
Replication 10	95	126	112	120	76	105.8

```
> IQ.2 <- round( rnorm(n=5, mean=100, sd=15 ))
> IQ.2
[1]  78  88 111 111 117
```

This time around, the mean IQ in my sample is 101. If I repeat the experiment 10 times I obtain the results shown in Table 10.1, and as you can see the sample mean varies from one replication to the next.

Now suppose that I decided to keep going in this fashion, replicating this "five IQ scores" experiment over and over again. Every time I replicate the experiment I write down the sample mean. Over time, I'd be amassing a new data set, in which every experiment generates a single data point. The first 10 observations from my data set are the sample means listed in Table 10.1, so my data set starts out like this:

```
95.0 101.0 101.6 103.8 104.4 ...
```

What if I continued like this for 10,000 replications, and then drew a histogram? Using the magical powers of R that's exactly what I did, and you can see the results in Figure 10.5. As this picture illustrates, the average of 5 IQ scores is usually between 90 and 110. But more importantly, what it highlights is that if we replicate an experiment over and over again, what we end up with is a *distribution* of sample means! This distribution has a special name in statistics: it's called the **sampling distribution of the mean**.

Sampling distributions are another important theoretical idea in statistics, and they're crucial for understanding the behaviour of small samples. For instance, when I ran the very first "five IQ scores" experiment, the sample mean turned out to be 95. What the sampling distribution in Figure 10.5 tells us, though, is that the "five IQ scores" experiment is not very accurate. If I repeat the experiment, the sampling distribution tells me that I can expect to see a sample mean anywhere between 80 and 120.

10.3.2 Sampling distributions exist for any sample statistic!

One thing to keep in mind when thinking about sampling distributions is that *any* sample statistic you might care to calculate has a sampling distribution. For example, suppose that each time I replicated the "five IQ scores" experiment I wrote down the largest IQ score in the experiment. This would give me a data set that started out like this:

```
110 117 122 119 113 ...
```

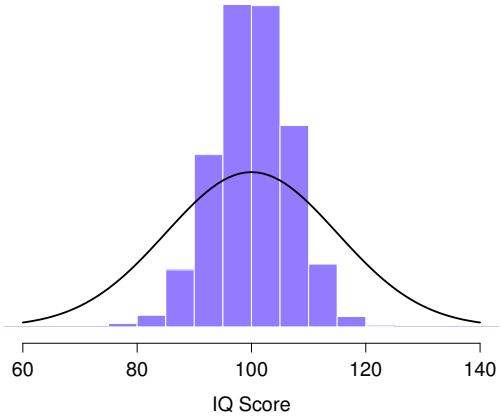


Figure 10.5: The sampling distribution of the mean for the "five IQ scores experiment". If you sample 5 people at random and calculate their *average* IQ, you'll almost certainly get a number between 80 and 120, even though there are quite a lot of individuals who have IQs above 120 or below 80. For comparison, the black line plots the population distribution of IQ scores.

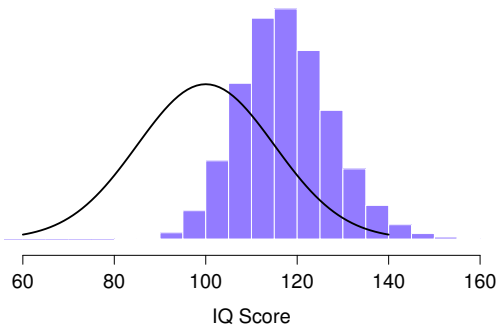
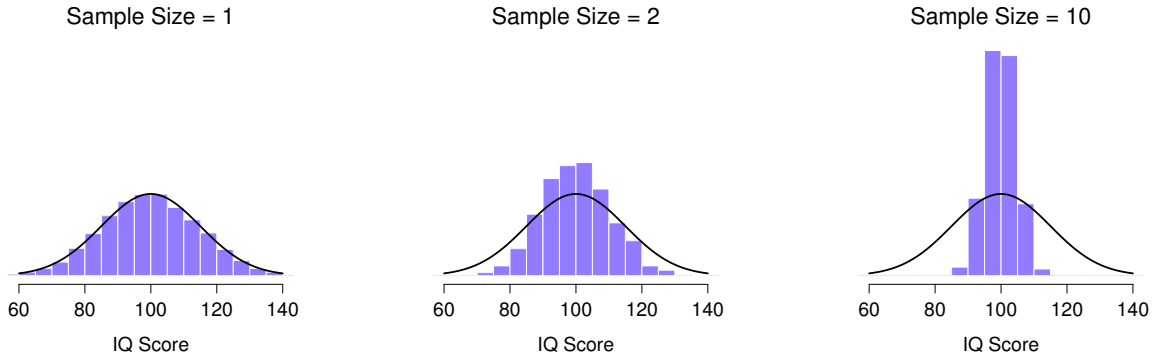


Figure 10.6: The sampling distribution of the *maximum* for the "five IQ scores experiment". If you sample 5 people at random and select the one with the highest IQ score, you'll probably see someone with an IQ between 100 and 140.



(a) (b) (c)

Figure 10.7: An illustration of the how sampling distribution of the mean depends on sample size. In each panel, I generated 10,000 samples of IQ data, and calculated the mean IQ observed within each of these data sets. The histograms in these plots show the distribution of these means (i.e., the sampling distribution of the mean). Each individual IQ score was drawn from a normal distribution with mean 100 and standard deviation 15, which is shown as the solid black line). In panel a, each data set contained only a single observation, so the mean of each sample is just one person's IQ score. As a consequence, the sampling distribution of the mean is of course identical to the population distribution of IQ scores. However, when we raise the sample size to 2, the mean of any one sample tends to be closer to the population mean than a one person's IQ score, and so the histogram (i.e., the sampling distribution) is a bit narrower than the population distribution. By the time we raise the sample size to 10 (panel c), we can see that the distribution of sample means tend to be fairly tightly clustered around the true population mean.

. . . . . .

Doing this over and over again would give me a very different sampling distribution, namely the *sampling distribution of the maximum*. The sampling distribution of the maximum of 5 IQ scores is shown in Figure 10.6. Not surprisingly, if you pick 5 people at random and then find the person with the highest IQ score, they're going to have an above average IQ. Most of the time you'll end up with someone whose IQ is measured in the 100 to 140 range.

10.3.3 The central limit theorem

At this point I hope you have a pretty good sense of what sampling distributions are, and in particular what the sampling distribution of the mean is. In this section I want to talk about how the sampling distribution of the mean changes as a function of sample size. Intuitively, you already know part of the answer: if you only have a few observations, the sample mean is likely to be quite inaccurate: if you replicate a small experiment and recalculate the mean you'll get a very different answer. In other words, the sampling distribution is quite wide. If you replicate a large experiment and recalculate the sample mean you'll probably get the same answer you got last time, so the sampling distribution will be very narrow. You can see this visually in Figure 10.7: the bigger the sample size, the narrower the sampling distribution gets. We can quantify this effect by calculating the standard deviation of the sampling distribution, which is referred to as the **standard error**. The standard error of a statistic is often denoted SE, and since we're usually interested in the standard error of the sample *mean*, we often use the acronym SEM. As you can see just by looking at the picture, as the sample size N increases, the

SEM decreases.

Okay, so that's one part of the story. However, there's something I've been glossing over so far. All my examples up to this point have been based on the "IQ scores" experiments, and because IQ scores are roughly normally distributed, I've assumed that the population distribution is normal. What if it isn't normal? What happens to the sampling distribution of the mean? The remarkable thing is this: no matter what shape your population distribution is, as N increases the sampling distribution of the mean starts to look more like a normal distribution. To give you a sense of this, I ran some simulations using R. To do this, I started with the "ramped" distribution shown in the histogram in Figure 10.8. As you can see by comparing the triangular shaped histogram to the bell curve plotted by the black line, the population distribution doesn't look very much like a normal distribution at all. Next, I used R to simulate the results of a large number of experiments. In each experiment I took $N = 2$ samples from this distribution, and then calculated the sample mean. Figure 10.8b plots the histogram of these sample means (i.e., the sampling distribution of the mean for $N = 2$). This time, the histogram produces a $\cap$-shaped distribution: it's still not normal, but it's a lot closer to the black line than the population distribution in Figure 10.8a. When I increase the sample size to $N = 4$, the sampling distribution of the mean is very close to normal (Figure 10.8c), and by the time we reach a sample size of $N = 8$ it's almost perfectly normal. In other words, as long as your sample size isn't tiny, the sampling distribution of the mean will be approximately normal no matter what your population distribution looks like!

On the basis of these figures, it seems like we have evidence for all of the following claims about the sampling distribution of the mean:

- The mean of the sampling distribution is the same as the mean of the population
- The standard deviation of the sampling distribution (i.e., the standard error) gets smaller as the sample size increases
- The shape of the sampling distribution becomes normal as the sample size increases

As it happens, not only are all of these statements true, there is a very famous theorem in statistics that proves all three of them, known as the **central limit theorem**. Among other things, the central limit theorem tells us that if the population distribution has mean μ and standard deviation σ, then the sampling distribution of the mean also has mean μ, and the standard error of the mean is

$$\text{SEM} = \frac{\sigma}{\sqrt{N}}$$

Because we divide the population standard devation σ by the square root of the sample size N, the SEM gets smaller as the sample size increases. It also tells us that the shape of the sampling distribution becomes normal.[4]

This result is useful for all sorts of things. It tells us why large experiments are more reliable than small ones, and because it gives us an explicit formula for the standard error it tells us *how much* more reliable a large experiment is. It tells us why the normal distribution is, well, *normal*. In real experiments, many of the things that we want to measure are actually averages of lots of different quantities (e.g., arguably, "general" intelligence as measured by IQ is an average of a large number of "specific" skills and abilities), and when that happens, the averaged quantity should follow a normal distribution. Because of this mathematical law, the normal distribution pops up over and over again in real data.

[4] As usual, I'm being a bit sloppy here. The central limit theorem is a bit more general than this section implies. Like most introductory stats texts, I've discussed one situation where the central limit theorem holds: when you're taking an average across lots of independent events drawn from the same distribution. However, the central limit theorem is much broader than this. There's a whole class of things called "U-statistics" for instance, all of which satisfy the central limit theorem and therefore become normally distributed for large sample sizes. The mean is one such statistic, but it's not the only one.

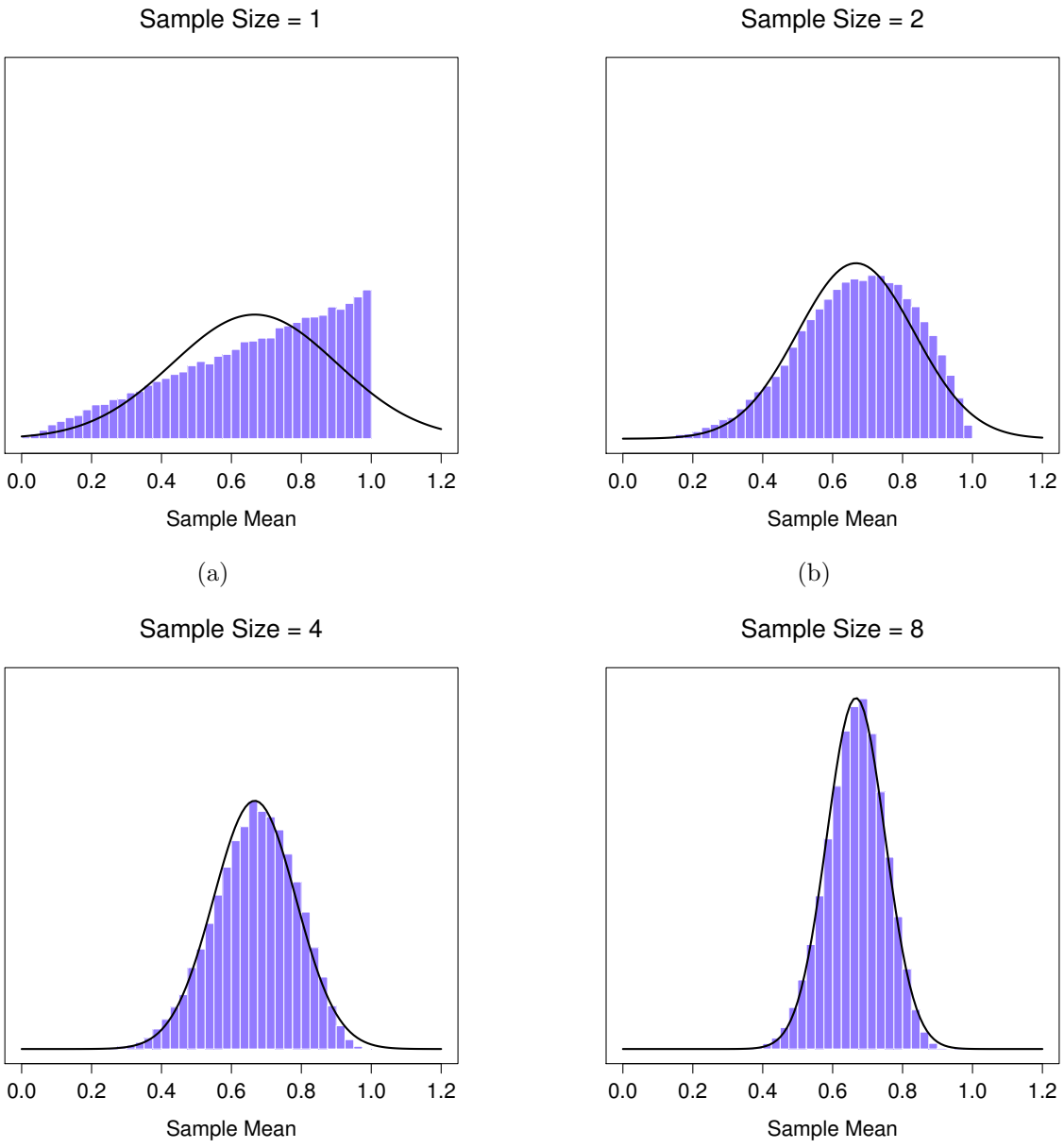


Figure 10.8: A demonstration of the central limit theorem. In panel a, we have a non-normal population distribution; and panels b-d show the sampling distribution of the mean for samples of size 2,4 and 8, for data drawn from the distribution in panel a. As you can see, even though the original population distribution is non-normal, the sampling distribution of the mean becomes pretty close to normal by the time you have a sample of even 4 observations.

. . . . . .

10.4 Estimating population parameters

In all the IQ examples in the previous sections, we actually knew the population parameters ahead of time. As every undergraduate gets taught in their very first lecture on the measurement of intelligence, IQ scores are *defined* to have mean 100 and standard deviation 15. However, this is a bit of a lie. How do we know that IQ scores have a true population mean of 100? Well, we know this because the people who designed the tests have administered them to very large samples, and have then "rigged" the scoring rules so that their sample has mean 100. That's not a bad thing of course: it's an important part of designing a psychological measurement. However, it's important to keep in mind that this theoretical mean of 100 only attaches to the population that the test designers used to design the tests. Good test designers will actually go to some lengths to provide "test norms" that can apply to lots of different populations (e.g., different age groups, nationalities etc).

This is very handy, but of course almost every research project of interest involves looking at a different population of people to those used in the test norms. For instance, suppose you wanted to measure the effect of low level lead poisoning on cognitive functioning in Port Pirie, a South Australian industrial town with a lead smelter. Perhaps you decide that you want to compare IQ scores among people in Port Pirie to a comparable sample in Whyalla, a South Australian industrial town with a steel refinery.[5] Regardless of which town you're thinking about, it doesn't make a lot of sense simply to *assume* that the true population mean IQ is 100. No-one has, to my knowledge, produced sensible norming data that can automatically be applied to South Australian industrial towns. We're going to have to **estimate** the population parameters from a sample of data. So how do we do this?

10.4.1 Estimating the population mean

Suppose we go to Port Pirie and 100 of the locals are kind enough to sit through an IQ test. The average IQ score among these people turns out to be $\bar{X} = 98.5$. So what is the true mean IQ for the entire population of Port Pirie? Obviously, we don't know the answer to that question. It could be 97.2, but if could also be 103.5. Our sampling isn't exhaustive so we cannot give a definitive answer. Nevertheless if I was forced at gunpoint to give a "best guess" I'd have to say 98.5. That's the essence of statistical estimation: giving a best guess.

In this example, estimating the unknown poulation parameter is straightforward. I calculate the sample mean, and I use that as my **estimate of the population mean**. It's pretty simple, and in the next section I'll explain the statistical justification for this intuitive answer. However, for the moment what I want to do is make sure you recognise that the sample statistic and the estimate of the population parameter are conceptually different things. A sample statistic is a description of your data, whereas the estimate is a guess about the population. With that in mind, statisticians often different notation to

[5] Please note that if you were *actually* interested in this question, you would need to be a *lot* more careful than I'm being here. You *can't* just compare IQ scores in Whyalla to Port Pirie and assume that any differences are due to lead poisoning. Even if it were true that the only differences between the two towns corresponded to the different refineries (and it isn't, not by a long shot), you need to account for the fact that people already *believe* that lead pollution causes cognitive deficits: if you recall back to Chapter 2, this means that there are different demand effects for the Port Pirie sample than for the Whyalla sample. In other words, you might end up with an illusory group difference in your data, caused by the fact that people *think* that there is a real difference. I find it pretty implausible to think that the locals wouldn't be well aware of what you were trying to do if a bunch of researchers turned up in Port Pirie with lab coats and IQ tests, and even less plausible to think that a lot of people would be pretty resentful of you for doing it. Those people won't be as co-operative in the tests. Other people in Port Pirie might be *more* motivated to do well because they don't want their home town to look bad. The motivational effects that would apply in Whyalla are likely to be weaker, because people don't have any concept of "iron ore poisoning" in the same way that they have a concept for "lead poisoning". Psychology is *hard*.

refer to them. For instance, if true population mean is denoted μ, then we would use $\hat{\mu}$ to refer to our estimate of the population mean. In contrast, the sample mean is denoted $\bar{X}$ or sometimes m. However, in simple random samples, the estimate of the population mean is identical to the sample mean: if I observe a sample mean of $\bar{X} = 98.5$, then my estimate of the population mean is also $\hat{\mu} = 98.5$. To help keep the notation clear, here's a handy table:

Symbol	What is it?	Do we know what it is?
$\bar{X}$	Sample mean	Yes, calculated from the raw data
μ	True population mean	Almost never known for sure
$\hat{\mu}$	Estimate of the population mean	Yes, identical to the sample mean

10.4.2 Estimating the population standard deviation

So far, estimation seems pretty simple, and you might be wondering why I forced you to read through all that stuff about sampling theory. In the case of the mean, our estimate of the population parameter (i.e. $\hat{\mu}$) turned out to identical to the corresponding sample statistic (i.e. $\bar{X}$). However, that's not always true. To see this, let's have a think about how to construct an **estimate of the population standard deviation**, which we'll denote $\hat{\sigma}$. What shall we use as our estimate in this case? Your first thought might be that we could do the same thing we did when estimating the mean, and just use the sample statistic as our estimate. That's almost the right thing to do, but not quite.

Here's why. Suppose I have a sample that contains a single observation. For this example, it helps to consider a sample where you have no intutions at all about what the true population values might be, so let's use something completely fictitious. Suppose the observation in question measures the *cromulence* of my shoes. It turns out that my shoes have a cromulence of 20. So here's my sample:

```
20
```

This is a perfectly legitimate sample, even if it does have a sample size of $N = 1$. It has a sample mean of 20, and because every observation in this sample is equal to the sample mean (obviously!) it has a sample standard deviation of 0. As a description of the *sample* this seems quite right: the sample contains a single observation and therefore there is no variation observed within the sample. A sample standard deviation of $s = 0$ is the right answer here. But as an estimate of the *population* standard deviation, it feels completely insane, right? Admittedly, you and I don't know anything at all about what "cromulence" is, but we know something about data: the only reason that we don't see any variability in the *sample* is that the sample is too small to display any variation! So, if you have a sample size of $N = 1$, it *feels* like the right answer is just to say "no idea at all".

Notice that you *don't* have the same intuition when it comes to the sample mean and the population mean. If forced to make a best guess about the population mean, it doesn't feel completely insane to guess that the population mean is 20. Sure, you probably wouldn't feel very confident in that guess, because you have only the one observation to work with, but it's still the best guess you can make.

Let's extend this example a little. Suppose I now make a second observation. My data set now has $N = 2$ observations of the cromulence of shoes, and the complete sample now looks like this:

```
20, 22
```

This time around, our sample is *just* large enough for us to be able to observe some variability: two observations is the bare minimum number needed for any variability to be observed! For our new data set, the sample mean is $\bar{X} = 21$, and the sample standard deviation is $s = 1$. What intuitions do we have about the population? Again, as far as the population mean goes, the best guess we can possibly make

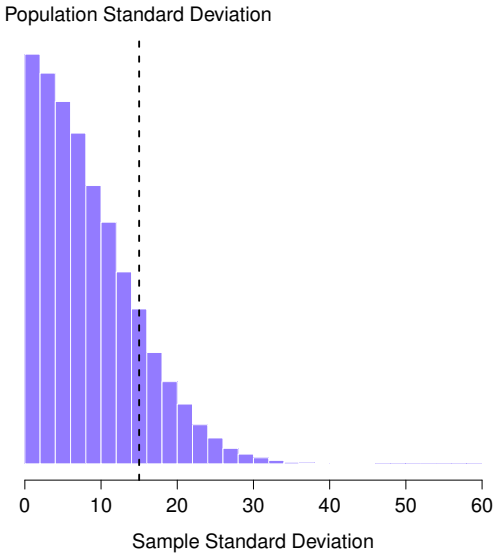
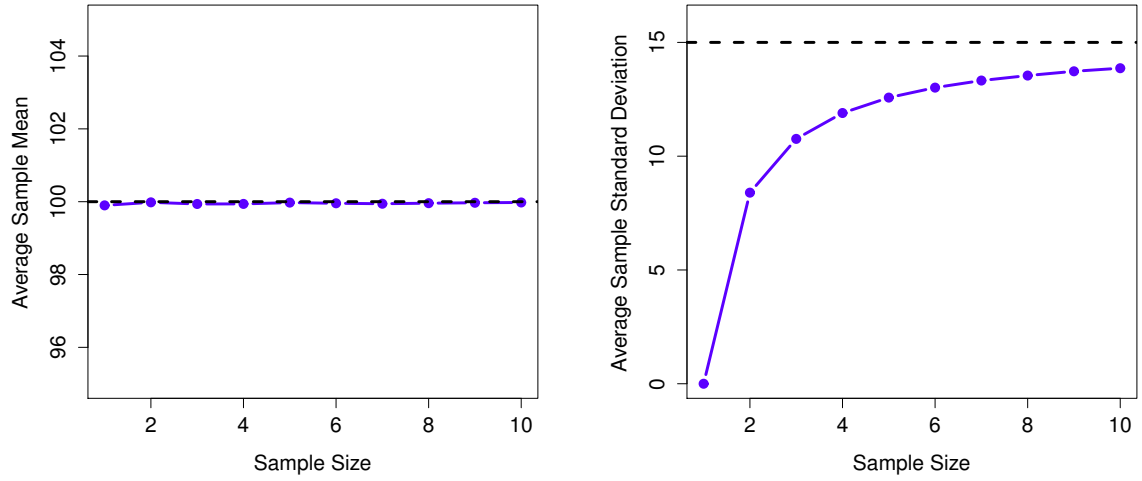


Figure 10.9: The sampling distribution of the sample standard deviation for a "two IQ scores" experiment. The true population standard deviation is 15 (dashed line), but as you can see from the histogram, the vast majority of experiments will produce a much smaller sample standard deviation than this. On average, this experiment would produce a sample standard deviation of only 8.5, well below the true value! In other words, the sample standard deviation is a *biased* estimate of the population standard deviation.

is the sample mean: if forced to guess, we'd probably guess that the population mean cromulence is 21. What about the standard deviation? This is a little more complicated. The sample standard deviation is only based on two observations, and if you're at all like me you probably have the intuition that, with only two observations, we haven't given the population "enough of a chance" to reveal its true variability to us. It's not just that we suspect that the estimate is *wrong*: after all, with only two observations we expect it to be wrong to some degree. The worry is that the error is *systematic*. Specifically, we suspect that the sample standard deviation is likely to be smaller than the population standard deviation.

This intuition feels right, but it would be nice to demonstrate this somehow. There are in fact mathematical proofs that confirm this intuition, but unless you have the right mathematical background they don't help very much. Instead, what I'll do is use R to simulate the results of some experiments. With that in mind, let's return to our IQ studies. Suppose the true population mean IQ is 100 and the standard deviation is 15. I can use the `rnorm()` function to generate the the results of an experiment in which I measure $N = 2$ IQ scores, and calculate the sample standard deviation. If I do this over and over again, and plot a histogram of these sample standard deviations, what I have is the *sampling distribution of the standard deviation*. I've plotted this distribution in Figure 10.9. Even though the true population standard deviation is 15, the average of the *sample* standard deviations is only 8.5. Notice that this is a very different result to what we found in Figure 10.7b when we plotted the sampling distribution of the mean. If you look at that sampling distribution, what you see is that the population mean is 100, and the average of the sample means is also 100.

Now let's extend the simulation. Instead of restricting ourselves to the situation where we have a sample size of $N = 2$, let's repeat the exercise for sample sizes from 1 to 10. If we plot the average sample



(a) (b)

Figure 10.10: An illustration of the fact that the sample mean is an unbiased estimator of the population mean (panel a), but the sample standard deviation is a biased estimator of the population standard deviation (panel b). To generate the figure, I generated 10,000 simulated data sets with 1 observation each, 10,000 more with 2 observations, and so on up to a sample size of 10. Each data set consisted of fake IQ data: that is, the data were normally distributed with a true population mean of 100 and standard deviation 15. *On average*, the sample means turn out to be 100, regardless of sample size (panel a). However, the sample standard deviations turn out to be systematically too small (panel b), especially for small sample sizes.

mean and average sample standard deviation as a function of sample size, you get the results shown in Figure 10.10. On the left hand side (panel a), I've plotted the average sample mean and on the right hand side (panel b), I've plotted the average standard deviation. The two plots are quite different: *on average*, the average sample mean is equal to the population mean. It is an **unbiased estimator**, which is essentially the reason why your best estimate for the population mean is the sample mean.[6] The plot on the right is quite different: on average, the sample standard deviation s is *smaller* than the population standard deviation σ. It is a **biased estimator**. In other words, if we want to make a "best guess" $\hat{\sigma}$ about the value of the population standard deviation σ, we should make sure our guess is a little bit larger than the sample standard deviation s.

The fix to this systematic bias turns out to be very simple. Here's how it works. Before tackling the standard deviation, let's look at the variance. If you recall from Section 5.2, the sample variance is defined to be the average of the squared deviations from the sample mean. That is:

$$s^2 = \frac{1}{N} \sum_{i=1}^{N} (X_i - \bar{X})^2$$

The sample variance s^2 is a biased estimator of the population variance σ^2. But as it turns out, we only

[6] I should note that I'm hiding something here. Unbiasedness is a desirable characteristic for an estimator, but there are other things that matter besides bias. However, it's beyond the scope of this book to discuss this in any detail. I just want to draw your attention to the fact that there's some hidden complexity here.

need to make a tiny tweak to transform this into an unbiased estimator. All we have to do is divide by $N-1$ rather than by N. If we do that, we obtain the following formula:

$$\hat{\sigma}^2 = \frac{1}{N-1} \sum_{i=1}^{N} (X_i - \bar{X})^2$$

This is an unbiased estimator of the population variance σ. Moreover, this finally answers the question we raised in Section 5.2. Why did R give us slightly different answers when we used the `var()` function? Because the `var()` function calculates $\hat{\sigma}^2$ not s^2, that's why. A similar story applies for the standard deviation. If we divide by $N-1$ rather than N, our estimate of the population standard deviation becomes:

$$\hat{\sigma} = \sqrt{\frac{1}{N-1} \sum_{i=1}^{N} (X_i - \bar{X})^2}$$

and when we use R's built in standard deviation function `sd()`, what it's doing is calculating $\hat{\sigma}$, not s.[7]

One final point: in practice, a lot of people tend to refer to $\hat{\sigma}$ (i.e., the formula where we divide by $N-1$) as the *sample* standard deviation. Technically, this is incorrect: the *sample* standard deviation should be equal to s (i.e., the formula where we divide by N). These aren't the same thing, either conceptually or numerically. One is a property of the sample, the other is an estimated characteristic of the population. However, in almost every real life application, what we actually care about is the estimate of the population parameter, and so people always report $\hat{\sigma}$ rather than s. This is the right number to report, of course, it's that people tend to get a little bit imprecise about terminology when they write it up, because "sample standard deviation" is shorter than "estimated population standard deviation". It's no big deal, and in practice I do the same thing everyone else does. Nevertheless, I think it's important to keep the two *concepts* separate: it's never a good idea to confuse "known properties of your sample" with "guesses about the population from which it came". The moment you start thinking that s and $\hat{\sigma}$ are the same thing, you start doing exactly that.

To finish this section off, here's another couple of tables to help keep things clear:

Symbol	What is it?	Do we know what it is?
s	Sample standard deviation	Yes, calculated from the raw data
σ	Population standard deviation	Almost never known for sure
$\hat{\sigma}$	Estimate of the population standard deviation	Yes, but not the same as the sample standard deviation

Symbol	What is it?	Do we know what it is?
s^2	Sample variance	Yes, calculated from the raw data
σ^2	Population variance	Almost never known for sure
$\hat{\sigma}^2$	Estimate of the population variance	Yes, but not the same as the sample variance

[7] Okay, I'm hiding something else here. In a bizarre and counterintuitive twist, since $\hat{\sigma}^2$ is an unbiased estimator of σ^2, you'd assume that taking the square root would be fine, and $\hat{\sigma}$ would be an unbiased estimator of σ. Right? Weirdly, it's not. There's actually a subtle, tiny bias in $\hat{\sigma}$. This is just bizarre: $\hat{\sigma}^2$ is and unbiased estimate of the population variance σ^2, but when you take the square root, it turns out that $\hat{\sigma}$ is a biased estimator of the population standard deviation σ. Weird, weird, weird, right? So, why is $\hat{\sigma}$ biased? The technical answer is "because non-linear transformations (e.g., the square root) don't commute with expectation", but that just sounds like gibberish to everyone who hasn't taken a course in mathematical statistics. Fortunately, it doesn't matter for practical purposes. The bias is small, and in real life everyone uses $\hat{\sigma}$ and it works just fine. Sometimes mathematics is just annoying.

10.5 Estimating a confidence interval

> *Statistics means never having to say you're certain*
> – Unknown origin[8]

Up to this point in this chapter, I've outlined the basics of sampling theory which statisticians rely on to make guesses about population parameters on the basis of a sample of data. As this discussion illustrates, one of the reasons we need all this sampling theory is that every data set leaves us with a some of uncertainty, so our estimates are never going to be perfectly accurate. The thing that has been missing from this discussion is an attempt to *quantify* the amount of uncertainty that attaches to our estimate. It's not enough to be able guess that, say, the mean IQ of undergraduate psychology students is 115 (yes, I just made that number up). We also want to be able to say something that expresses the degree of certainty that we have in our guess. For example, it would be nice to be able to say that there is a 95% chance that the true mean lies between 109 and 121. The name for this is a **confidence interval** for the mean.

Armed with an understanding of sampling distributions, constructing a confidence interval for the mean is actually pretty easy. Here's how it works. Suppose the true population mean is μ and the standard deviation is σ. I've just finished running my study that has N participants, and the mean IQ among those participants is $\bar{X}$. We know from our discussion of the central limit theorem (Section 10.3.3) that the sampling distribution of the mean is approximately normal. We also know from our discussion of the normal distribution Section 9.5 that there is a 95% chance that a normally-distributed quantity will fall within two standard deviations of the true mean. To be more precise, we can use the `qnorm()` function to compute the 2.5th and 97.5th percentiles of the normal distribution

```
> qnorm( p = c(.025, .975) )
[1] -1.959964  1.959964
```

Okay, so I lied earlier on. The more correct answer is that 95% chance that a normally-distributed quantity will fall within 1.96 standard deviations of the true mean. Next, recall that the standard deviation of the sampling distribution is referred to as the standard error, and the standard error of the mean is written as SEM. When we put all these pieces together, we learn that there is a 95% probability that the sample mean $\bar{X}$ that we have actually observed lies within 1.96 standard errors of the population mean. Mathematically, we write this as:

$$\mu - (1.96 \times \text{SEM}) \leqslant \bar{X} \leqslant \mu + (1.96 \times \text{SEM})$$

where the SEM is equal to $\sigma/\sqrt{N}$, and we can be 95% confident that this is true. However, that's not answering the question that we're actually interested in. The equation above tells us what we should expect about the sample mean, given that we know what the population parameters are. What we *want* is to have this work the other way around: we want to know what we should believe about the population parameters, given that we have observed a particular sample. However, it's not too difficult to do this. Using a little high school algebra, a sneaky way to rewrite our equation is like this:

$$\bar{X} - (1.96 \times \text{SEM}) \leqslant \mu \leqslant \bar{X} + (1.96 \times \text{SEM})$$

What this is telling is is that the range of values has a 95% probability of containing the population mean μ. We refer to this range as a **95% confidence interval**, denoted CI_{95}. In short, as long as N is

[8] This quote appears on a great many t-shirts and websites, and even gets a mention in a few academic papers (e.g., http://www.amstat.org/publications/jse/v10n3/friedman.html but I've never found the original source.

sufficiently large – large enough for us to believe that the sampling distribution of the mean is normal – then we can write this as our formula for the 95% confidence interval:

$$\text{CI}_{95} = \bar{X} \pm \left(1.96 \times \frac{\sigma}{\sqrt{N}} \right)$$

Of course, there's nothing special about the number 1.96: it just happens to be the multiplier you need to use if you want a 95% confidence interval. If I'd wanted a 70% confidence interval, I could have used the `qnorm()` function to calculate the 15th and 85th quantiles:

```
> qnorm( p = c(.15, .85) )
[1] -1.036433  1.036433
```

and so the formula for CI_{70} would be the same as the formula for CI_{95} except that we'd use 1.04 as our magic number rather than 1.96.

10.5.1 A slight mistake in the formula

As usual, I lied. The formula that I've given above for the 95% confidence interval is approximately correct, but I glossed over an important detail in the discussion. Notice my formula requires you to use the standard error of the mean, SEM, which in turn requires you to use the true population standard deviation σ. Yet, in Section 10.4 I stressed the fact that we don't actually *know* the true population parameters. Because we don't know the true value of σ, we have to use an estimate of the population standard deviation $\hat{\sigma}$ instead. This is pretty straightforward to do, but this has the consequence that we need to use the quantiles of the t-distribution rather than the normal distribution to calculate our magic number; and the answer depends on the sample size. When N is very large, we get pretty much the same value using `qt()` that we would if we used `qnorm()`...

```
> N <- 10000   # suppose our sample size is 10,000
> qt( p = .975, df = N-1)   # calculate the 97.5th quantile of the t-dist
[1] 1.960201
```

But when N is small, we get a much bigger number when we use the t distribution:

```
> N <- 10   # suppose our sample size is 10
> qt( p = .975, df = N-1)   # calculate the 97.5th quantile of the t-dist
[1] 2.262157
```

There's nothing too mysterious about what's happening here. Bigger values mean that the confidence interval is wider, indicating that we're more uncertain about what the true value of μ actually is. When we use the t distribution instead of the normal distribution, we get bigger numbers, indicating that we have more uncertainty. And why do we have that extra uncertainty? Well, because our estimate of the population standard deviation $\hat{\sigma}$ might be wrong! If it's wrong, it implies that we're a bit less sure about what our sampling distribution of the mean actually looks like... and this uncertainty ends up getting reflected in a wider confidence interval.

10.5.2 Interpreting a confidence interval

The hardest thing about confidence intervals is understanding what they *mean*. Whenever people first encounter confidence intervals, the first instinct is almost always to say that "there is a 95% probabaility that the true mean lies inside the confidence interval". It's simple, and it seems to capture the common

sense idea of what it means to say that I am "95% confident". Unfortunately, it's not quite right. The intuitive definition relies very heavily on your own personal *beliefs* about the value of the population mean. I say that I am 95% confident because those are my beliefs. In everyday life that's perfectly okay, but if you remember back to Section 9.2, you'll notice that talking about personal belief and confidence is a Bayesian idea. Personally (speaking as a Bayesian) I have no problem with the idea that the phrase "95% probability" is allowed to refer to a personal belief. However, confidence intervals are *not* Bayesian tools. Like everything else in this chapter, confidence intervals are *frequentist* tools, and if you are going to use frequentist methods then it's not appropriate to attach a Bayesian interpretation to them. If you use frequentist methods, you must adopt frequentist interpretations!

Okay, so if that's not the right answer, what is? Remember what we said about frequentist probability: the only way we are allowed to make "probability statements" is to talk about a sequence of events, and to count up the frequencies of different kinds of events. From that perspective, the interpretation of a 95% confidence interval must have something to do with replication. Specifically: if we replicated the experiment over and over again and computed a 95% confidence interval for each replication, then 95% of those *intervals* would contain the true mean. More generally, 95% of all confidence intervals constructed using this procedure should contain the true population mean. This idea is illustrated in Figure 10.11, which shows 50 confidence intervals constructed for a "measure 10 IQ scores" experiment (top panel) and another 50 confidence intervals for a "measure 25 IQ scores" experiment (bottom panel). A bit fortuitously, across the 100 replications that I simulated, it turned out that exactly 95 of them contained the true mean.

The critical difference here is that the Bayesian claim makes a probability statement about the population mean (i.e., it refers to our uncertainty about the population mean), which is not allowed under the frequentist interpretation of probability because you can't "replicate" a population! In the frequentist claim, the population mean is fixed and no probabilistic claims can be made about it. Confidence intervals, however, are repeatable so we can replicate experiments. Therefore a frequentist is allowed to talk about the probability that the *confidence interval* (a random variable) contains the true mean; but is not allowed to talk about the probability that the *true population mean* (not a repeatable event) falls within the confidence interval.

I know that this seems a little pedantic, but it does matter. It matters because the difference in interpretation leads to a difference in the mathematics. There is a Bayesian alternative to confidence intervals, known as *credible intervals*. In most situations credible intervals are quite similar to confidence intervals, but in other cases they are drastically different. As promised, though, I'll talk more about the Bayesian perspective in Chapter 17.

10.5.3 Calculating confidence intervals in R

As far as I can tell, the core packages in R don't include a simple function for calculating confidence intervals for the mean. They *do* include a lot of complicated, extremely powerful functions that can be used to calculate confidence intervals associated with lots of different things, such as the `confint()` function that we'll use in Chapter 15. But I figure that when you're first learning statistics, it might be useful to start with something simpler. As a consequence, the `lsr` package includes a function called `ciMean()` which you can use to calculate your confidence intervals. There are two arguments that you might want to specify:[9]

- `x`. This should be a numeric vector containing the data.
- `conf`. This should be a number, specifying the confidence level. By default, `conf = .95`, since 95% confidence intervals are the de facto standard in psychology.

[9] As of the current writing, these are the only arguments to the function. However, I am planning to add a bit more functionality to `ciMean()`. However, regardless of what those future changes might look like, the `x` and `conf` arguments will remain the same, and the commands used in this book will still work.

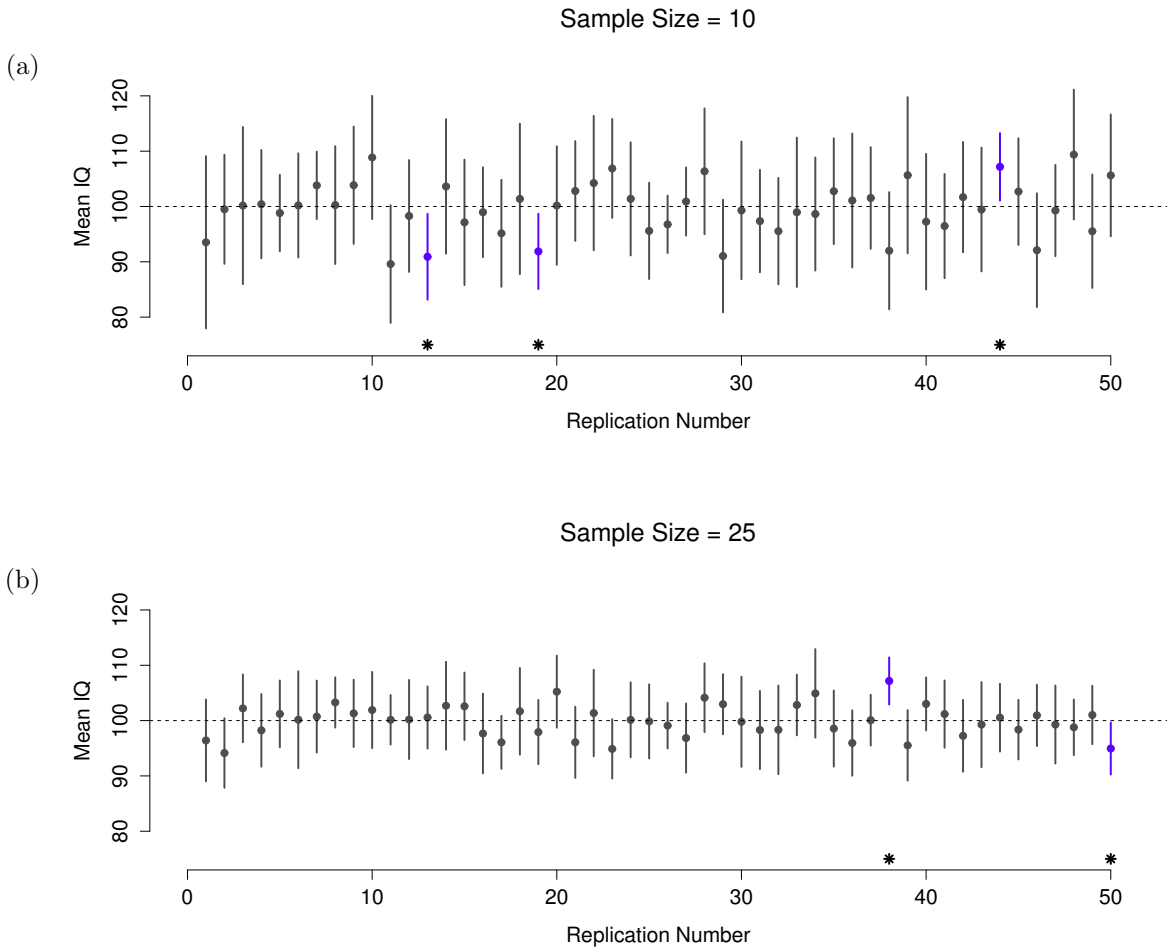


Figure 10.11: 95% confidence intervals. The top (panel a) shows 50 simulated replications of an experiment in which we measure the IQs of 10 people. The dot marks the location of the sample mean, and the line shows the 95% confidence interval. In total 47 of the 50 confidence intervals do contain the true mean (i.e., 100), but the three intervals marked with asterisks do not. The lower graph (panel b) shows a similar simulation, but this time we simulate replications of an experiment that measures the IQs of 25 people.

. . . . . .

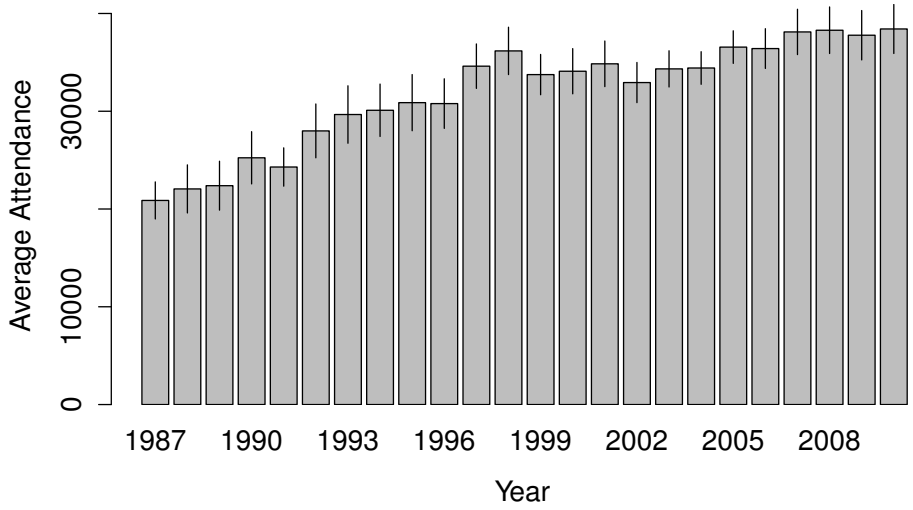


Figure 10.12: Means and 95% confidence intervals for AFL `attendance`, plotted separately for each `year` from 1987 to 2010. This graph was drawn using the `bargraph.CI()` function.

So, for example, if I load the `afl24.Rdata` file, calculate the confidence interval associated with the mean attendance:

```
> ciMean( x = afl$attendance )
    2.5%    97.5%
31597.32 32593.12
```

Hopefully that's fairly clear.

10.5.4 Plotting confidence intervals in R

There's several different ways you can draw graphs that show confidence intervals as error bars. I'll show three versions here, but this certainly doesn't exhaust the possibilities. In doing so, what I'm assuming is that you want to draw is a plot showing the means and confidence intervals for one variable, broken down by different levels of a second variable. For instance, in our `afl` data that we discussed earlier, we might be interested in plotting the average `attendance` by `year`. I'll do this using three different functions, `bargraph.CI()`, `lineplot.CI()` (both of which are in the `sciplot` package), and `plotmeans()` (which is in the `gplots`) package. Assuming that you've installed these packages on your system (see Section 4.2 if you've forgotten how to do this), you'll need to load them. You'll also need to load the `lsr` package, because we'll make use of the `ciMean()` function to actually calculate the confidence intervals

```
> library( sciplot )      # bargraph.CI() and lineplot.CI() functions
> library( gplots )       # plotmeans() function
> library( lsr )          # ciMean() function
```

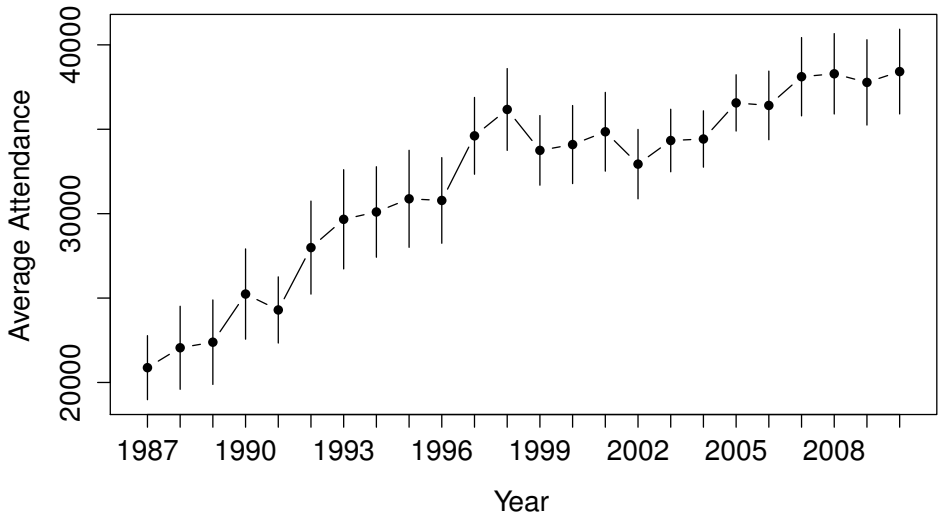


Figure 10.13: Means and 95% confidence intervals for AFL `attendance`, plotted separately for each `year` from 1987 to 2010. This graph was drawn using the `lineplot.CI()` function.

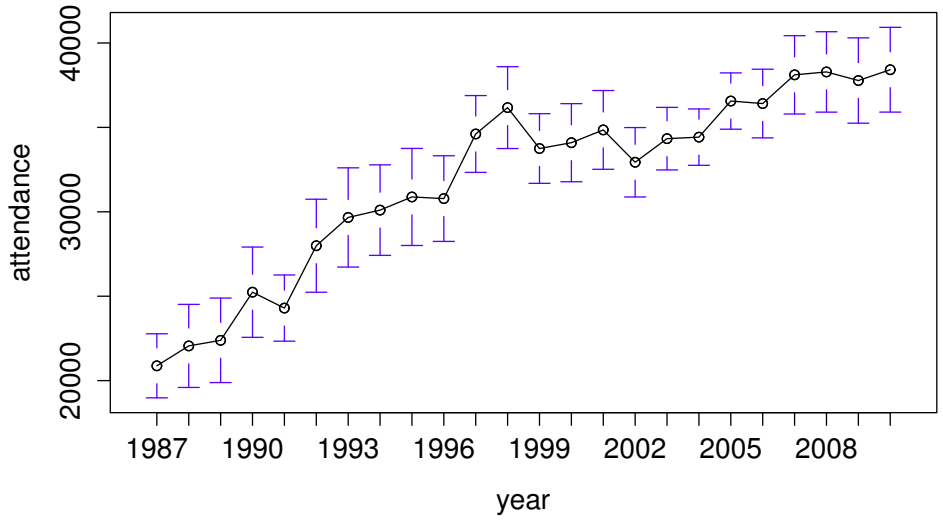


Figure 10.14: Means and 95% confidence intervals for AFL `attendance`, plotted separately for each `year` from 1987 to 2010. This graph was drawn using the `plotmeans()` function.

Here's how to plot the means and confidence intervals drawn using `bargraph.CI()`.

```
> bargraph.CI( x.factor = year,            # grouping variable
+              response = attendance,      # outcome variable
+              data = afl,                 # data frame with the variables
+              ci.fun= ciMean,             # name of the function to calculate CIs
+              xlab = "Year",              # x-axis label
+              ylab = "Average Attendance" # y-axis label
+ )
```

This produces the output shown in Figure 10.12. We can use the same arguments when calling the `lineplot.CI()` function:

```
> lineplot.CI( x.factor = year,            # grouping variable
+              response = attendance,      # outcome variable
+              data = afl,                 # data frame with the variables
+              ci.fun= ciMean,             # name of the function to calculate CIs
+              xlab = "Year",              # x-axis label
+              ylab = "Average Attendance" # y-axis label
+ )
```

And the output for this command is shown in Figure 10.13. Finally, here's how you would do it using `plotmeans()`:

```
> plotmeans( formula = attendance ~ year,  # outcome ~ group
+            data = afl,                   # data frame with the variables
+            n.label = FALSE               # don't show the sample sizes
+ )
```

This is shown in Figure 10.14.

10.6 Summary

In this chapter I've covered two main topics. The first half of the chapter talks about sampling theory, and the second half talks about how we can use sampling theory to construct estimates of the population parameters. The section breakdown looks like this:

- Basic ideas about samples, sampling and populations (Section 10.1)
- Statistical theory of sampling: the law of large numbers (Section 10.2), sampling distributions and the central limit theorem (Section 10.3).
- Estimating means and standard deviations (Section 10.4)
- Estimating a confidence interval (Section 10.5)

As always, there's a lot of topics related to sampling and estimation that aren't covered in this chapter, but for an introductory psychology class this is fairly comprehensive I think. For most applied researchers you won't need much more theory than this. One big question that I haven't touched on in this chapter is what you do when you don't have a simple random sample. There is a lot of statistical theory you can draw on to handle this situation, but it's well beyond the scope of this book.

11. Hypothesis testing

> *The process of induction is the process of assuming the simplest law that can be made to harmonize with our experience. This process, however, has no logical foundation but only a psychological one. It is clear that there are no grounds for believing that the simplest course of events will really happen. It is an hypothesis that the sun will rise tomorrow: and this means that we do not know whether it will rise.*
>
> – Ludwig Wittgenstein[1]

In the last chapter, I discussed the ideas behind estimation, which is one of the two "big ideas" in inferential statistics. It's now time to turn out attention to the other big idea, which is *hypothesis testing*. In its most abstract form, hypothesis testing really a very simple idea: the researcher has some theory about the world, and wants to determine whether or not the data actually support that theory. However, the details are messy, and most people find the theory of hypothesis testing to be the most frustrating part of statistics. The structure of the chapter is as follows. Firstly, I'll describe how hypothesis testing works, in a fair amount of detail, using a simple running example to show you how a hypothesis test is "built". I'll try to avoid being too dogmatic while doing so, and focus instead on the underlying logic of the testing procedure.[2] Afterwards, I'll spend a bit of time talking about the various dogmas, rules and heresies that surround the theory of hypothesis testing.

11.1 A menagerie of hypotheses

Eventually we all succumb to madness. For me, that day will arrive once I'm finally promoted to full professor. Safely ensconced in my ivory tower, happily protected by tenure, I will finally be able to take leave of my senses (so to speak), and indulge in that most thoroughly unproductive line of psychological research: the search for extrasensory perception (ESP).[3]

[1] The quote comes from Wittgenstein's (1922) text, *Tractatus Logico-Philosphicus*.

[2] A technical note. The description below differs subtly from the standard description given in a lot of introductory texts. The orthodox theory of null hypothesis testing emerged from the work of Sir Ronald Fisher and Jerzy Neyman in the early 20th century; but Fisher and Neyman actually had very different views about how it should work. The standard treatment of hypothesis testing that most texts use is a hybrid of the two approaches. The treatment here is a little more Neyman-style than the orthodox view, especially as regards the meaning of the p value.

[3] My apologies to anyone who actually believes in this stuff, but on my reading of the literature on ESP, it's just not reasonable to think this is real. To be fair, though, some of the studies are rigorously designed; so it's actually an interesting area for thinking about psychological research design. And of course it's a free country, so you can spend your own time and effort proving me wrong if you like, but I wouldn't think that's a terribly practical use of your intellect.

Let's suppose that this glorious day has come. My first study is a simple one, in which I seek to test whether clairvoyance exists. Each participant sits down at a table, and is shown a card by an experimenter. The card is black on one side and white on the other. The experimenter takes the card away, and places it on a table in an adjacent room. The card is placed black side up or white side up completely at random, with the randomisation occurring only after the experimenter has left the room with the participant. A second experimenter comes in and asks the participant which side of the card is now facing upwards. It's purely a one-shot experiment. Each person sees only one card, and gives only one answer; and at no stage is the participant actually in contact with someone who knows the right answer. My data set, therefore, is very simple. I have asked the question of N people, and some number X of these people have given the correct response. To make things concrete, let's suppose that I have tested $N = 100$ people, and $X = 62$ of these got the answer right... a surprisingly large number, sure, but is it large enough for me to feel safe in claiming I've found evidence for ESP? This is the situation where hypothesis testing comes in useful. However, before we talk about how to *test* hypotheses, we need to be clear about what we mean by hypotheses.

11.1.1 Research hypotheses versus statistical hypotheses

The first distinction that you need to keep clear in your mind is between research hypotheses and statistical hypotheses. In my ESP study, my overall scientific goal is to demonstrate that clairvoyance exists. In this situation, I have a clear research goal: I am hoping to discover evidence for ESP. In other situations I might actually be a lot more neutral than that, so I might say that my research goal is to determine whether or not clairvoyance exists. Regardless of how I want to portray myself, the basic point that I'm trying to convey here is that a research hypothesis involves making a substantive, testable scientific claim... if you are a psychologist, then your research hypotheses are fundamentally *about* psychological constructs. Any of the following would count as **research hypotheses**:

- *Listening to music reduces your ability to pay attention to other things.* This is a claim about the causal relationship between two psychologically meaningful concepts (listening to music and paying attention to things), so it's a perfectly reasonable research hypothesis.
- *Intelligence is related to personality.* Like the last one, this is a relational claim about two psychological constructs (intelligence and personality), but the claim is weaker: correlational not causal.
- *Intelligence is speed of information processing.* This hypothesis has a quite different character: it's not actually a relational claim at all. It's an ontological claim about the fundamental character of intelligence (and I'm pretty sure it's wrong). It's worth expanding on this one actually: It's usually easier to think about how to construct experiments to test research hypotheses of the form "does X affect Y?" than it is to address claims like "what is X?" And in practice, what usually happens is that you find ways of testing relational claims that follow from your ontological ones. For instance, if I believe that intelligence *is* speed of information processing in the brain, my experiments will often involve looking for relationships between measures of intelligence and measures of speed. As a consequence, most everyday research questions do tend to be relational in nature, but they're almost always motivated by deeper ontological questions about the state of nature.

Notice that in practice, my research hypotheses could overlap a lot. My ultimate goal in the ESP experiment might be to test an ontological claim like "ESP exists", but I might operationally restrict myself to a narrower hypothesis like "Some people can 'see' objects in a clairvoyant fashion". That said, there are some things that really don't count as proper research hypotheses in any meaningful sense:

- *Love is a battlefield.* This is too vague to be testable. While it's okay for a research hypothesis to have a degree of vagueness to it, it has to be possible to operationalise your theoretical ideas.

Maybe I'm just not creative enough to see it, but I can't see how this can be converted into any concrete research design. If that's true, then this isn't a scientific research hypothesis, it's a pop song. That doesn't mean it's not interesting – a lot of deep questions that humans have fall into this category. Maybe one day science will be able to construct testable theories of love, or to test to see if God exists, and so on; but right now we can't, and I wouldn't bet on ever seeing a satisfying scientific approach to either.

- *The first rule of tautology club is the first rule of tautology club.* This is not a substantive claim of any kind. It's true by definition. No conceivable state of nature could possibly be inconsistent with this claim. As such, we say that this is an unfalsifiable hypothesis, and as such it is outside the domain of science. Whatever else you do in science, your claims must have the possibility of being wrong.

- *More people in my experiment will say "yes" than "no".* This one fails as a research hypothesis because it's a claim about the data set, not about the psychology (unless of course your actual research question is whether people have some kind of "yes" bias!). As we'll see shortly, this hypothesis is starting to sound more like a statistical hypothesis than a research hypothesis.

As you can see, research hypotheses can be somewhat messy at times; and ultimately they are *scientific* claims. **Statistical hypotheses** are neither of these two things. Statistical hypotheses must be mathematically precise, and they must correspond to specific claims about the characteristics of the data generating mechanism (i.e., the "population"). Even so, the intent is that statistical hypotheses bear a clear relationship to the substantive research hypotheses that you care about! For instance, in my ESP study my research hypothesis is that some people are able to see through walls or whatever. What I want to do is to "map" this onto a statement about how the data were generated. So let's think about what that statement would be. The quantity that I'm interested in within the experiment is $P(\text{"correct"})$, the true-but-unknown probability with which the participants in my experiment answer the question correctly. Let's use the Greek letter θ (theta) to refer to this probability. Here are four different statistical hypotheses:

- If ESP doesn't exist and if my experiment is well designed, then my participants are just guessing. So I should expect them to get it right half of the time and so my statistical hypothesis is that the true probability of choosing correctly is $\theta = 0.5$.

- Alternatively, suppose ESP does exist and participants can see the card. If that's true, people will perform better than chance. The statistical hypotheis would be that $\theta > 0.5$.

- A third possibility is that ESP does exist, but the colours are all reversed and people don't realise it (okay, that's wacky, but you never know...). If that's how it works then you'd expect people's performance to be *below* chance. This would correspond to a statistical hypothesis that $\theta < 0.5$.

- Finally, suppose ESP exists, but I have no idea whether people are seeing the right colour or the wrong one. In that case, the only claim I could make about the data would be that the probability of making the correct answer is *not* equal to 50. This corresponds to the statistical hypothesis that $\theta \neq 0.5$.

All of these are legitimate examples of a statistical hypothesis because they are statements about a population parameter and are meaningfully related to my experiment.

What this discussion makes clear, I hope, is that when attempting to construct a statistical hypothesis test the researcher actually has two quite distinct hypotheses to consider. First, he or she has a research hypothesis (a claim about psychology), and this corresponds to a statistical hypothesis (a claim about the data generating population). In my ESP example, these might be

Dan's **research** hypothesis: "ESP exists"
Dan's **statistical** hypothesis: $\theta \neq 0.5$

And the key thing to recognise is this: *a statistical hypothesis test is a test of the statistical hypothesis, not the research hypothesis*. If your study is badly designed, then the link between your research hypothesis and your statistical hypothesis is broken. To give a silly example, suppose that my ESP study was conducted in a situation where the participant can actually see the card reflected in a window; if that happens, I would be able to find very strong evidence that $\theta \neq 0.5$, but this would tell us nothing about whether "ESP exists".

11.1.2 Null hypotheses and alternative hypotheses

So far, so good. I have a research hypothesis that corresponds to what I want to believe about the world, and I can map it onto a statistical hypothesis that corresponds to what I want to believe about how the data were generated. It's at this point that things get somewhat counterintuitive for a lot of people. Because what I'm about to do is invent a new statistical hypothesis (the "null" hypothesis, H_0) that corresponds to the exact opposite of what I want to believe, and then focus exclusively on that, almost to the neglect of the thing I'm actually interested in (which is now called the "alternative" hypothesis, H_1). In our ESP example, the null hypothesis is that $\theta = 0.5$, since that's what we'd expect if ESP *didn't* exist. My hope, of course, is that ESP is totally real, and so the *alternative* to this null hypothesis is $\theta \neq 0.5$. In essence, what we're doing here is dividing up the possible values of θ into two groups: those values that I really hope aren't true (the null), and those values that I'd be happy with if they turn out to be right (the alternative). Having done so, the important thing to recognise is that the goal of a hypothesis test is *not* to show that the alternative hypothesis is (probably) true; the goal is to show that the null hypothesis is (probably) false. Most people find this pretty weird.

The best way to think about it, in my experience, is to imagine that a hypothesis test is a criminal trial[4]... *the trial of the null hypothesis*. The null hypothesis is the defendant, the researcher is the prosecutor, and the statistical test itself is the judge. Just like a criminal trial, there is a presumption of innocence: the null hypothesis is *deemed* to be true unless you, the researcher, can prove beyond a reasonable doubt that it is false. You are free to design your experiment however you like (within reason, obviously!), and your goal when doing so is to maximise the chance that the data will yield a conviction... for the crime of being false. The catch is that the statistical test sets the rules of the trial, and those rules are designed to protect the null hypothesis – specifically to ensure that if the null hypothesis is actually true, the chances of a false conviction are guaranteed to be low. This is pretty important: after all, the null hypothesis doesn't get a lawyer. And given that the researcher is trying desperately to prove it to be false, *someone* has to protect it.

11.2 Two types of errors

Before going into details about how a statistical test is constructed, it's useful to understand the philosophy behind it. I hinted at it when pointing out the similarity between a null hypothesis test and a criminal trial, but I should now be explicit. Ideally, we would like to construct our test so that we never make any errors. Unfortunately, since the world is messy, this is never possible. Sometimes you're just really unlucky: for instance, suppose you flip a coin 10 times in a row and it comes up heads all 10 times. That feels like very strong evidence that the coin is biased (and it is!), but of course there's a 1 in 1024

[4] This analogy only works if you're from an adversarial legal system like UK/US/Australia. As I understand these things, the French inquisitorial system is quite different.

chance that this would happen even if the coin was totally fair. In other words, in real life we *always* have to accept that there's a chance that we did the wrong thing. As a consequence, the goal behind statistical hypothesis testing is not to *eliminate* errors, but to *minimise* them.

At this point, we need to be a bit more precise about what we mean by "errors". Firstly, let's state the obvious: it is either the case that the null hypothesis is true, or it is false; and our test will either reject the null hypothesis or retain it.[5] So, as the table below illustrates, after we run the test and make our choice, one of four things might have happened:

	retain H_0	reject H_0
H_0 is true	correct decision	error (type I)
H_0 is false	error (type II)	correct decision

As a consequence there are actually *two* different types of error here. If we reject a null hypothesis that is actually true, then we have made a **type I error**. On the other hand, if we retain the null hypothesis when it is in fact false, then we have made a **type II error**.

Remember how I said that statistical testing was kind of like a criminal trial? Well, I meant it. A criminal trial requires that you establish "beyond a reasonable doubt" that the defendant did it. All of the evidentiary rules are (in theory, at least) designed to ensure that there's (almost) no chance of wrongfully convicting an innocent defendant. The trial is designed to protect the rights of a defendant: as the English jurist William Blackstone famously said, it is "better that ten guilty persons escape than that one innocent suffer." In other words, a criminal trial doesn't treat the two types of error in the same way ... punishing the innocent is deemed to be much worse than letting the guilty go free. A statistical test is pretty much the same: the single most important design principle of the test is to *control* the probability of a type I error, to keep it below some fixed probability. This probability, which is denoted α, is called the **significance level** of the test (or sometimes, the *size* of the test). And I'll say it again, because it is so central to the whole set-up ... a hypothesis test is said to have significance level α if the type I error rate is no larger than α.

So, what about the type II error rate? Well, we'd also like to keep those under control too, and we denote this probability by β. However, it's much more common to refer to the **power** of the test, which is the probability with which we reject a null hypothesis when it really is false, which is $1 - \beta$. To help keep this straight, here's the same table again, but with the relevant numbers added:

	retain H_0	reject H_0
H_0 is true	$1 - \alpha$ (probability of correct retention)	α (type I error rate)
H_0 is false	β (type II error rate)	$1 - \beta$ (power of the test)

A "powerful" hypothesis test is one that has a small value of β, while still keeping α fixed at some (small) desired level. By convention, scientists make use of three different α levels: .05, .01 and .001. Notice the asymmetry here ... the tests are designed to *ensure* that the α level is kept small, but there's no corresponding guarantee regarding β. We'd certainly *like* the type II error rate to be small, and we try to design tests that keep it small, but this is very much secondary to the overwhelming need to control

[5] An aside regarding the language you use to talk about hypothesis testing. Firstly, one thing you really want to avoid is the word "prove": a statistical test really doesn't *prove* that a hypothesis is true or false. Proof implies certainty, and as the saying goes, statistics means never having to say you're certain. On that point almost everyone would agree. However, beyond that there's a fair amount of confusion. Some people argue that you're only allowed to make statements like "rejected the null", "failed to reject the null", or possibly "retained the null". According to this line of thinking, you can't say things like "accept the alternative" or "accept the null". Personally I think this is too strong: in my opinion, this conflates null hypothesis testing with Karl Popper's falsificationist view of the scientific process. While there are similarities between falsificationism and null hypothesis testing, they aren't equivalent. However, while I personally think it's fine to talk about accepting a hypothesis (on the proviso that "acceptance" doesn't actually mean that it's necessarily true, especially in the case of the null hypothesis), many people will disagree. And more to the point, you should be aware that this particular weirdness exists, so that you're not caught unawares by it when writing up your own results.

the type I error rate. As Blackstone might have said if he were a statistician, it is "better to retain 10 false null hypotheses than to reject a single true one". To be honest, I don't know that I agree with this philosophy – there are situations where I think it makes sense, and situations where I think it doesn't – but that's neither here nor there. It's how the tests are built.

11.3 Test statistics and sampling distributions

At this point we need to start talking specifics about how a hypothesis test is constructed. To that end, let's return to the ESP example. Let's ignore the actual data that we obtained, for the moment, and think about the structure of the experiment. Regardless of what the actual numbers are, the *form* of the data is that X out of N people correctly identified the colour of the hidden card. Moreover, let's suppose for the moment that the null hypothesis really is true: ESP doesn't exist, and the true probability that anyone picks the correct colour is exactly $\theta = 0.5$. What would we *expect* the data to look like? Well, obviously, we'd expect the proportion of people who make the correct response to be pretty close to 50%. Or, to phrase this in more mathematical terms, we'd say that X/N is approximately 0.5. Of course, we wouldn't expect this fraction to be *exactly* 0.5: if, for example we tested $N = 100$ people, and $X = 53$ of them got the question right, we'd probably be forced to concede that the data are quite consistent with the null hypothesis. On the other hand, if $X = 99$ of our participants got the question right, then we'd feel pretty confident that the null hypothesis is wrong. Similarly, if only $X = 3$ people got the answer right, we'd be similarly confident that the null was wrong. Let's be a little more technical about this: we have a quantity X that we can calculate by looking at our data; after looking at the value of X, we make a decision about whether to believe that the null hypothesis is correct, or to reject the null hypothesis in favour of the alternative. The name for this thing that we calculate to guide our choices is a **test statistic**.

Having chosen a test statistic, the next step is to state precisely which values of the test statistic would cause is to reject the null hypothesis, and which values would cause us to keep it. In order to do so, we need to determine what the **sampling distribution of the test statistic** would be if the null hypothesis were actually true (we talked about sampling distributions earlier in Section 10.3.1). Why do we need this? Because this distribution tells us exactly what values of X our null hypothesis would lead us to expect. And therefore, we can use this distribution as a tool for assessing how closely the null hypothesis agrees with our data.

How do we actually determine the sampling distribution of the test statistic? For a lot of hypothesis tests this step is actually quite complicated, and later on in the book you'll see me being slightly evasive about it for some of the tests (some of them I don't even understand myself). However, sometimes it's very easy. And, fortunately for us, our ESP example provides us with one of the easiest cases. Our population parameter θ is just the overall probability that people respond correctly when asked the question, and our test statistic X is the *count* of the number of people who did so, out of a sample size of N. We've seen a distribution like this before, in Section 9.4: that's exactly what the binomial distribution describes! So, to use the notation and terminology that I introduced in that section, we would say that the null hypothesis predicts that X is binomially distributed, which is written

$$X \sim \text{Binomial}(\theta, N)$$

Since the null hypothesis states that $\theta = 0.5$ and our experiment has $N = 100$ people, we have the sampling distribution we need. This sampling distribution is plotted in Figure 11.1. No surprises really: the null hypothesis says that $X = 50$ is the most likely outcome, and it says that we're almost certain to see somewhere between 40 and 60 correct responses.

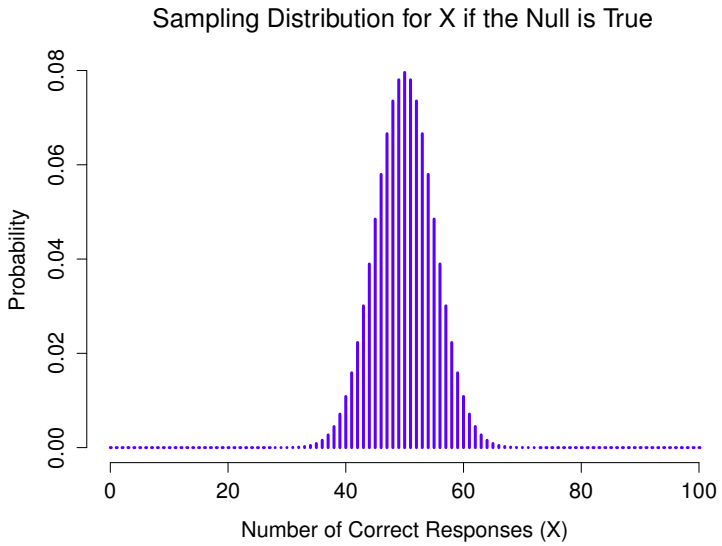


Figure 11.1: The sampling distribution for our test statistic X when the null hypothesis is true. For our ESP scenario, this is a binomial distribution. Not surprisingly, since the null hypothesis says that the probability of a correct response is $\theta = .5$, the sampling distribution says that the most likely value is 50 (our of 100) correct responses. Most of the probability mass lies between 40 and 60.

11.4 Making decisions

Okay, we're very close to being finished. We've constructed a test statistic (X), and we chose this test statistic in such a way that we're pretty confident that if X is close to $N/2$ then we should retain the null, and if not we should reject it. The question that remains is this: exactly which values of the test statistic should we associate with the null hypothesis, and which exactly values go with the alternative hypothesis? In my ESP study, for example, I've observed a value of $X = 62$. What decision should I make? Should I choose to believe the null hypothesis, or the alternative hypothesis?

11.4.1 Critical regions and critical values

To answer this question, we need to introduce the concept of a **critical region** for the test statistic X. The critical region of the test corresponds to those values of X that would lead us to reject null hypothesis (which is why the critical region is also sometimes called the rejection region). How do we find this critical region? Well, let's consider what we know:

- X should be very big or very small in order to reject the null hypothesis.
- If the null hypothesis is true, the sampling distribution of X is Binomial$(0.5, N)$.
- If $\alpha = .05$, the critical region must cover 5% of this sampling distribution.

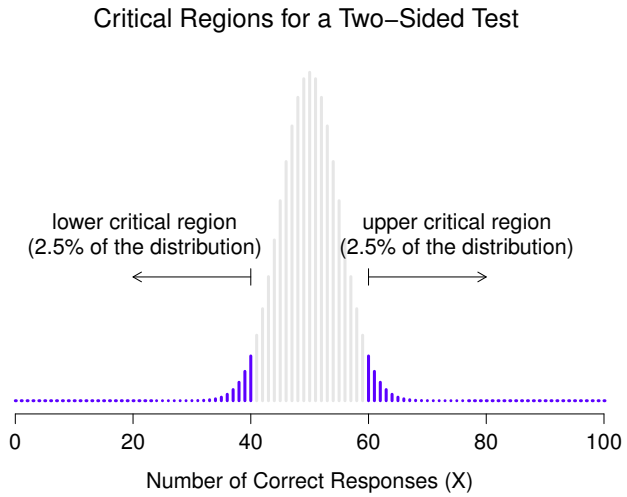


Figure 11.2: The critical region associated with the hypothesis test for the ESP study, for a hypothesis test with a significance level of $\alpha = .05$. The plot itself shows the sampling distribution of X under the null hypothesis (i.e., same as Figure 11.1): the grey bars correspond to those values of X for which we would retain the null hypothesis. The black bars show the critical region: those values of X for which we would reject the null. Because the alternative hypothesis is two sided (i.e., allows both $\theta < .5$ and $\theta > .5$), the critical region covers both tails of the distribution. To ensure an α level of .05, we need to ensure that each of the two regions encompasses 2.5% of the sampling distribution.

It's important to make sure you understand this last point: the critical region corresponds to those values of X for which we would reject the null hypothesis, and the sampling distribution in question describes the probability that we would obtain a particular value of X if the null hypothesis were actually true. Now, let's suppose that we chose a critical region that covers 20% of the sampling distribution, and suppose that the null hypothesis is actually true. What would be the probability of incorrectly rejecting the null? The answer is of course 20%. And therefore, we would have built a test that had an α level of 0.2. If we want $\alpha = .05$, the critical region is only *allowed* to cover 5% of the sampling distribution of our test statistic.

As it turns out, those three things uniquely solve the problem: our critical region consists of the most *extreme values*, known as the **tails** of the distribution. This is illustrated in Figure 11.2. As it turns out, if we want $\alpha = .05$, then our critical regions correspond to $X \leqslant 40$ and $X \geqslant 60$.[6] That is, if the number of people saying "true" is between 41 and 59, then we should retain the null hypothesis. If the number is between 0 to 40 or between 60 to 100, then we should reject the null hypothesis. The numbers 40 and 60 are often referred to as the **critical values**, since they define the edges of the critical region.

At this point, our hypothesis test is essentially complete: (1) we choose an α level (e.g., $\alpha = .05$, (2) come up with some test statistic (e.g., X) that does a good job (in some meaningful sense) of comparing H_0 to H_1, (3) figure out the sampling distribution of the test statistic on the assumption that the null hypothesis is true (in this case, binomial) and then (4) calculate the critical region that produces an

[6] Strictly speaking, the test I just constructed has $\alpha = .057$, which is a bit too generous. However, if I'd chosen 39 and 61 to be the boundaries for the critical region, then the critical region only covers 3.5% of the distribution. I figured that it makes more sense to use 40 and 60 as my critical values, and be willing to tolerate a 5.7% type I error rate, since that's as close as I can get to a value of $\alpha = .05$.

appropriate α level (0-40 and 60-100). All that we have to do now is calculate the value of the test statistic for the real data (e.g., $X = 62$) and then compare it to the critical values to make our decision. Since 62 is greater than the critical value of 60, we would reject the null hypothesis. Or, to phrase it slightly differently, we say that the test has produced a **significant** result.

11.4.2 A note on statistical "significance"

> *Like other occult techniques of divination, the statistical method has a private jargon deliberately contrived to obscure its methods from non-practitioners.*
> – Attributed to G. O. Ashley[7]

A very brief digression is in order at this point, regarding the word "significant". The concept of statistical significance is actually a very simple one, but has a very unfortunate name. If the data allow us to reject the null hypothesis, we say that "the result is *statistically significant*", which is often shortened to "the result is significant". This terminology is rather old, and dates back to a time when "significant" just meant something like "indicated", rather than its modern meaning, which is much closer to "important". As a result, a lot of modern readers get very confused when they start learning statistics, because they think that a "significant result" must be an important one. It doesn't mean that at all. All that "statistically significant" means is that the data allowed us to reject a null hypothesis. Whether or not the result is actually important in the real world is a very different question, and depends on all sorts of other things.

11.4.3 The difference between one sided and two sided tests

There's one more thing I want to point out about the hypothesis test that I've just constructed. If we take a moment to think about the statistical hypotheses I've been using,

$$\begin{array}{ll} H_0: & \theta = .5 \\ H_1: & \theta \neq .5 \end{array}$$

we notice that the alternative hypothesis covers *both* the possibility that $\theta < .5$ and the possibility that $\theta > .5$. This makes sense if I really think that ESP could produce better-than-chance performance *or* worse-than-chance performance (and there are some people who think that). In statistical language, this is an example of a **two-sided test**. It's called this because the alternative hypothesis covers the area on both "sides" of the null hypothesis, and as a consequence the critical region of the test covers both tails of the sampling distribution (2.5% on either side if $\alpha = .05$), as illustrated earlier in Figure 11.2.

However, that's not the only possibility. It might be the case, for example, that I'm only willing to believe in ESP if it produces better than chance performance. If so, then my alternative hypothesis would only covers the possibility that $\theta > .5$, and as a consequence the null hypothesis now becomes $\theta \leqslant .5$:

$$\begin{array}{ll} H_0: & \theta \leqslant .5 \\ H_1: & \theta > .5 \end{array}$$

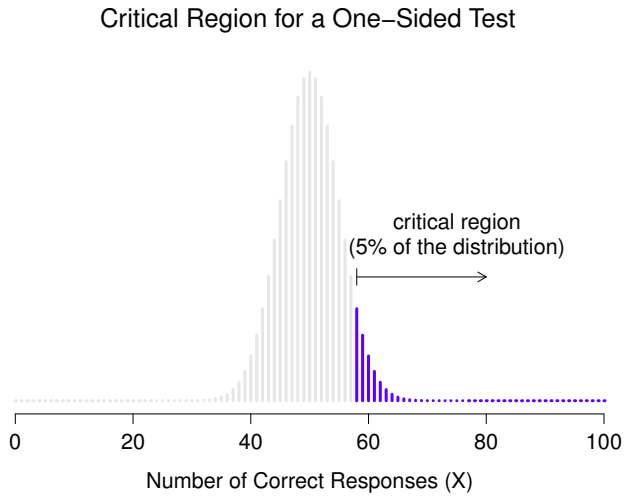


Figure 11.3: The critical region for a one sided test. In this case, the alternative hypothesis is that $\theta > .05$, so we would only reject the null hypothesis for large values of X. As a consequence, the critical region only covers the upper tail of the sampling distribution; specifically the upper 5% of the distribution. Contrast this to the two-sided version in Figure 11.2.

When this happens, we have what's called a **one-sided test**, and when this happens the critical region only covers one tail of the sampling distribution. This is illustrated in Figure 11.3.

11.5 The p value of a test

In one sense, our hypothesis test is complete; we've constructed a test statistic, figured out its sampling distribution if the null hypothesis is true, and then constructed the critical region for the test. Nevertheless, I've actually omitted the most important number of all: **the p value**. It is to this topic that we now turn. There are two somewhat different ways of interpreting a p value, one proposed by Sir Ronald Fisher and the other by Jerzy Neyman. Both versions are legitimate, though they reflect very different ways of thinking about hypothesis tests. Most introductory textbooks tend to give Fisher's version only, but I think that's a bit of a shame. To my mind, Neyman's version is cleaner, and actually better reflects the logic of the null hypothesis test. You might disagree though, so I've included both. I'll start with Neyman's version...

11.5.1 A softer view of decision making

One problem with the hypothesis testing procedure that I've described is that it makes no distinction at all between a result this "barely significant" and those that are "highly significant". For instance, in my ESP study the data I obtained only just fell inside the critical region - so I did get a significant

[7] The internet seems fairly convinced that Ashley said this, though I can't for the life of me find anyone willing to give a source for the claim.

effect, but was a pretty near thing. In contrast, suppose that I'd run a study in which $X = 97$ out of my $N = 100$ participants got the answer right. This would obviously be significant too, but my a much larger margin; there's really no ambiguity about this at all. The procedure that I described makes no distinction between the two. If I adopt the standard convention of allowing $\alpha = .05$ as my acceptable Type I error rate, then both of these are significant results.

This is where the p value comes in handy. To understand how it works, let's suppose that we ran lots of hypothesis tests on the same data set: but with a different value of α in each case. When we do that for my original ESP data, what we'd get is something like this

Value of α	0.05	0.04	0.03	0.02	0.01
Reject the null?	Yes	Yes	Yes	No	No

When we test ESP data ($X = 62$ successes out of $N = 100$ observations) using α levels of .03 and above, we'd always find ourselves rejecting the null hypothesis. For α levels of .02 and below, we always end up retaining the null hypothesis. Therefore, somewhere between .02 and .03 there must be a smallest value of α that would allow us to reject the null hypothesis for this data. This is the p value; as it turns out the ESP data has $p = .021$. In short:

> p is defined to be the smallest Type I error rate (α) that you have to be willing to tolerate if you want to reject the null hypothesis.

If it turns out that p describes an error rate that you find intolerable, then you must retain the null. If you're comfortable with an error rate equal to p, then it's okay to reject the null hypothesis in favour of your preferred alternative.

In effect, p is a summary of all the possible hypothesis tests that you could have run, taken across all possible α values. And as a consequence it has the effect of "softening" our decision process. For those tests in which $p \leqslant \alpha$ you would have rejected the null hypothesis, whereas for those tests in which $p > \alpha$ you would have retained the null. In my ESP study I obtained $X = 62$, and as a consequence I've ended up with $p = .021$. So the error rate I have to tolerate is 2.1%. In contrast, suppose my experiment had yielded $X = 97$. What happens to my p value now? This time it's shrunk to $p = 1.36 \times 10^{-25}$, which is a tiny, tiny[8] Type I error rate. For this second case I would be able to reject the null hypothesis with a lot more confidence, because I only have to be "willing" to tolerate a type I error rate of about 1 in 10 trillion trillion in order to justify my decision to reject.

11.5.2 The probability of extreme data

The second definition of the p-value comes from Sir Ronald Fisher, and it's actually this one that you tend to see in most introductory statistics textbooks. Notice how, when I constructed the critical region, it corresponded to the *tails* (i.e., extreme values) of the sampling distribution? That's not a coincidence: almost all "good" tests have this characteristic (good in the sense of minimising our type II error rate, β). The reason for that is that a good critical region almost always corresponds to those values of the test statistic that are least likely to be observed if the null hypothesis is true. If this rule is true, then we can define the p-value as the probability that we would have observed a test statistic that is at least as extreme as the one we actually did get. In other words, if the data are extremely implausible according

[8] That's $p = .00000000000000000000000136$ for folks that don't like scientific notation!

to the null hypothesis, then the null hypothesis is probably wrong.

11.5.3 A common mistake

Okay, so you can see that there are two rather different but legitimate ways to interpret the p value, one based on Neyman's approach to hypothesis testing and the other based on Fisher's. Unfortunately, there is a third explanation that people sometimes give, especially when they're first learning statistics, and it is *absolutely and completely wrong*. This mistaken approach is to refer to the p value as "the probability that the null hypothesis is true". It's an intuitively appealing way to think, but it's wrong in two key respects: (1) null hypothesis testing is a frequentist tool, and the frequentist approach to probability does *not* allow you to assign probabilities to the null hypothesis... according to this view of probability, the null hypothesis is either true or it is not; it cannot have a "5% chance" of being true. (2) even within the Bayesian approach, which does let you assign probabilities to hypotheses, the p value would not correspond to the probability that the null is true; this interpretation is entirely inconsistent with the mathematics of how the p value is calculated. Put bluntly, despite the intuitive appeal of thinking this way, there is no justification for interpreting a p value this way. Never do it.

11.6 Reporting the results of a hypothesis test

When writing up the results of a hypothesis test, there's usually several pieces of information that you need to report, but it varies a fair bit from test to test. Throughout the rest of the book I'll spend a little time talking about how to report the results of different tests (see Section 12.1.9 for a particularly detailed example), so that you can get a feel for how it's usually done. However, regardless of what test you're doing, the one thing that you always have to do is say something about the p value, and whether or not the outcome was significant.

The fact that you have to do this is unsurprising; it's the whole point of doing the test. What might be surprising is the fact that there is some contention over exactly how you're supposed to do it. Leaving aside those people who completely disagree with the entire framework underpinning null hypothesis testing, there's a certain amount of tension that exists regarding whether or not to report the exact p value that you obtained, or if you should state only that $p < \alpha$ for a significance level that you chose in advance (e.g., $p < .05$).

11.6.1 The issue

To see why this is an issue, the key thing to recognise is that p values are *terribly* convenient. In practice, the fact that we can compute a p value means that we don't actually have to specify any α level at all in order to run the test. Instead, what you can do is calculate your p value and interpret it directly: if you get $p = .062$, then it means that you'd have to be willing to tolerate a Type I error rate of 6.2% to justify rejecting the null. If you personally find 6.2% intolerable, then you retain the null. Therefore, the argument goes, why don't we just report the actual p value and let the reader make up their own minds about what an acceptable Type I error rate is? This approach has the big advantage of "softening" the decision making process – in fact, if you accept the Neyman definition of the p value, that's the whole point of the p value. We no longer have a fixed significance level of $\alpha = .05$ as a bright line separating "accept" from "reject" decisions; and this removes the rather pathological problem of being forced to treat $p = .051$ in a fundamentally different way to $p = .049$.

This flexibility is both the advantage and the disadvantage to the p value. The reason why a lot of

Table 11.1: A commonly adopted convention for reporting p values: in many places it is conventional to report one of four different things (e.g., $p < .05$) as shown below. I've included the "significance stars" notation (i.e., a * indicates $p < .05$) because you sometimes see this notation produced by statistical software. It's also worth noting that some people will write *n.s.* (not significant) rather than $p > .05$.

Usual notation	Signif. stars	English translation	The null is...
$p > .05$		The test wasn't significant	Retained
$p < .05$	*	The test was significant at $\alpha = .05$ but not at $\alpha = .01$ or $\alpha = .001$.	Rejected
$p < .01$	**	The test was significant at $\alpha = .05$ and $\alpha = .01$ but not at $\alpha = .001$.	Rejected
$p < .001$	***	The test was significant at all levels	Rejected

people don't like the idea of reporting an exact p value is that it gives the researcher a bit *too much* freedom. In particular, it lets you change your mind about what error tolerance you're willing to put up with *after* you look at the data. For instance, consider my ESP experiment. Suppose I ran my test, and ended up with a p value of .09. Should I accept or reject? Now, to be honest, I haven't yet bothered to think about what level of Type I error I'm "really" willing to accept. I don't have an opinion on that topic. But I *do* have an opinion about whether or not ESP exists, and I *definitely* have an opinion about whether my research should be published in a reputable scientific journal. And amazingly, now that I've looked at the data I'm starting to think that a 9% error rate isn't so bad, especially when compared to how annoying it would be to have to admit to the world that my experiment has failed. So, to avoid looking like I just made it up after the fact, I now say that my α is .1: a 10% type I error rate isn't too bad, and at that level my test is significant! I win.

In other words, the worry here is that I might have the best of intentions, and be the most honest of people, but the temptation to just "shade" things a little bit here and there is really, really strong. As anyone who has ever run an experiment can attest, it's a long and difficult process, and you often get *very* attached to your hypotheses. It's hard to let go and admit the experiment didn't find what you wanted it to find. And that's the danger here. If we use the "raw" p-value, people will start interpreting the data in terms of what they *want* to believe, not what the data are actually saying... and if we allow that, well, why are we bothering to do science at all? Why not let everyone believe whatever they like about anything, regardless of what the facts are? Okay, that's a bit extreme, but that's where the worry comes from. According to this view, you really *must* specify your α value in advance, and then only report whether the test was significant or not. It's the only way to keep ourselves honest.

11.6.2 Two proposed solutions

In practice, it's pretty rare for a researcher to specify a single α level ahead of time. Instead, the convention is that scientists rely on three standard significance levels: .05, .01 and .001. When reporting your results, you indicate which (if any) of these significance levels allow you to reject the null hypothesis. This is summarised in Table 11.1. This allows us to soften the decision rule a little bit, since $p < .01$ implies that the data meet a stronger evidentiary standard than $p < .05$ would. Nevertheless, since these levels are fixed in advance by convention, it does prevent people choosing their α level after looking at the data.

Nevertheless, quite a lot of people still prefer to report exact p values. To many people, the advan-

tage of allowing the reader to make up their own mind about how to interpret $p = .06$ outweighs any disadvantages. In practice, however, even among those researchers who prefer exact p values it is quite common to just write $p < .001$ instead of reporting an exact value for small p. This is in part because a lot of software doesn't actually print out the p value when it's that small (e.g., SPSS just writes $p = .000$ whenever $p < .001$), and in part because a very small p value can be kind of misleading. The human mind sees a number like .0000000001 and it's hard to suppress the gut feeling that the evidence in favour of the alternative hypothesis is a near certainty. In practice however, this is usually wrong. Life is a big, messy, complicated thing: and every statistical test ever invented relies on simplifications, approximations and assumptions. As a consequence, it's probably not reasonable to walk away from *any* statistical analysis with a feeling of confidence stronger than $p < .001$ implies. In other words, $p < .001$ is really code for "as far as *this test* is concerned, the evidence is overwhelming."

In light of all this, you might be wondering exactly what you should do. There's a fair bit of contradictory advice on the topic, with some people arguing that you should report the exact p value, and other people arguing that you should use the tiered approach illustrated in Table 11.1. As a result, the best advice I can give is to suggest that you look at papers/reports written in your field and see what the convention seems to be. If there doesn't seem to be any consistent pattern, then use whichever method you prefer.

11.7 Running the hypothesis test in practice

At this point some of you might be wondering if this is a "real" hypothesis test, or just a toy example that I made up. It's real. In the previous discussion I built the test from first principles, thinking that it was the simplest possible problem that you might ever encounter in real life. However, this test already exists: it's called the *binomial test*, and it's implemented by an R function called `binom.test()`. To test the null hypothesis that the response probability is one-half `p = .5`,[9] using data in which `x = 62` of `n = 100` people made the correct response, here's how to do it in R:

```
> binom.test( x=62, n=100, p=.5 )

        Exact binomial test

data:  62 and 100
number of successes = 62, number of trials = 100,
p-value = 0.02098
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.5174607 0.7152325
sample estimates:
probability of success
                  0.62
```

Right now, this output looks pretty unfamiliar to you, but you can see that it's telling you more or less the right things. Specifically, the p-value of 0.02 is less than the usual choice of $\alpha = .05$, so you can reject the null. We'll talk a lot more about how to read this sort of output as we go along; and after a while you'll hopefully find it quite easy to read and understand. For now, however, I just wanted to make the point that R contains a whole lot of functions corresponding to different kinds of hypothesis test. And while I'll usually spend quite a lot of time explaining the logic behind how the tests are built, every time

[9] Note that the `p` here has nothing to do with a p value. The `p` argument in the `binom.test()` function corresponds to the probability of making a correct response, according to the null hypothesis. In other words, it's the θ value.

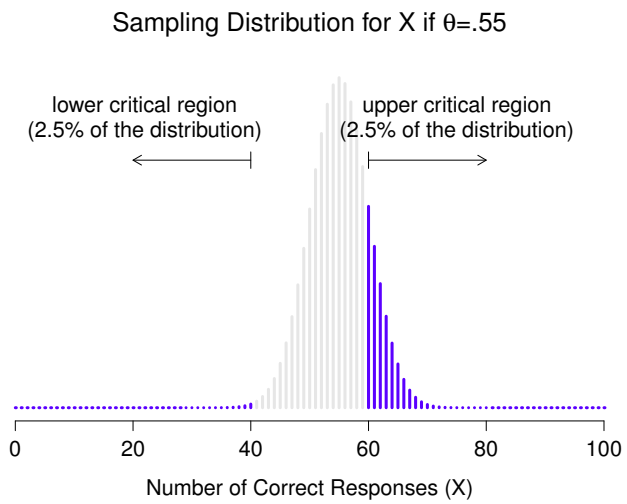


Figure 11.4: Sampling distribution under the *alternative* hypothesis, for a population parameter value of $\theta = 0.55$. A reasonable proportion of the distribution lies in the rejection region.

I discuss a hypothesis test the discussion will end with me showing you a fairly simple R command that you can use to run the test in practice.

11.8 Effect size, sample size and power

In previous sections I've emphasised the fact that the major design principle behind statistical hypothesis testing is that we try to control our Type I error rate. When we fix $\alpha = .05$ we are attempting to ensure that only 5% of true null hypotheses are incorrectly rejected. However, this doesn't mean that we don't care about Type II errors. In fact, from the researcher's perspective, the error of failing to reject the null when it is actually false is an extremely annoying one. With that in mind, a secondary goal of hypothesis testing is to try to minimise β, the Type II error rate, although we don't usually *talk* in terms of minimising Type II errors. Instead, we talk about maximising the *power* of the test. Since power is defined as $1 - \beta$, this is the same thing.

11.8.1 The power function

Let's take a moment to think about what a Type II error actually is. A Type II error occurs when the alternative hypothesis is true, but we are nevertheless unable to reject the null hypothesis. Ideally, we'd be able to calculate a single number β that tells us the Type II error rate, in the same way that we can set $\alpha = .05$ for the Type I error rate. Unfortunately, this is a lot trickier to do. To see this, notice that in my ESP study the alternative hypothesis actually corresponds to lots of possible values of θ. In fact, the alternative hypothesis corresponds to every value of θ *except* 0.5. Let's suppose that the true probability of someone choosing the correct response is 55% (i.e., $\theta = .55$). If so, then the *true* sampling distribution

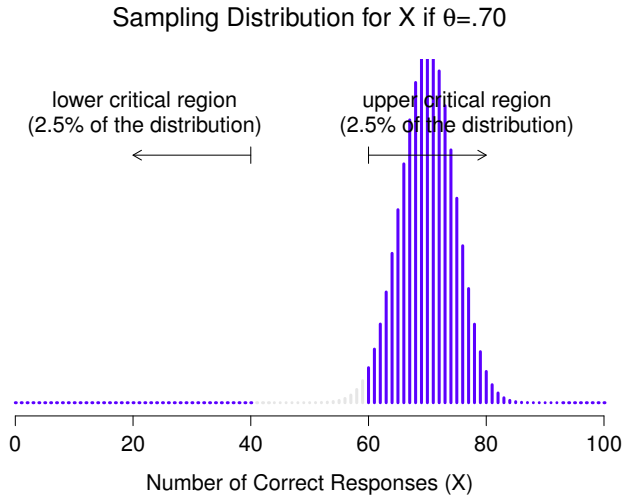


Figure 11.5: Sampling distribution under the *alternative* hypothesis, for a population parameter value of $\theta = 0.70$. Almost all of the distribution lies in the rejection region.

for X is not the same one that the null hypothesis predicts: the most likely value for X is now 55 out of 100. Not only that, the whole sampling distribution has now shifted, as shown in Figure 11.4. The critical regions, of course, do not change: by definition, the critical regions are based on what the null hypothesis predicts. What we're seeing in this figure is the fact that when the null hypothesis is wrong, a much larger proportion of the sampling distribution distribution falls in the critical region. And of course that's what should happen: the probability of rejecting the null hypothesis is larger when the null hypothesis is actually false! However $\theta = .55$ is not the only possibility consistent with the alternative hypothesis. Let's instead suppose that the true value of θ is actually 0.7. What happens to the sampling distribution when this occurs? The answer, shown in Figure 11.5, is that almost the entirety of the sampling distribution has now moved into the critical region. Therefore, if $\theta = 0.7$ the probability of us correctly rejecting the null hypothesis (i.e., the power of the test) is much larger than if $\theta = 0.55$. In short, while $\theta = .55$ and $\theta = .70$ are both part of the alternative hypothesis, the Type II error rate is different.

What all this means is that the power of a test (i.e., $1 - \beta$) depends on the true value of θ. To illustrate this, I've calculated the expected probability of rejecting the null hypothesis for all values of θ, and plotted it in Figure 11.6. This plot describes what is usually called the **power function** of the test. It's a nice summary of how good the test is, because it actually tells you the power $(1 - \beta)$ for all possible values of θ. As you can see, when the true value of θ is very close to 0.5, the power of the test drops very sharply, but when it is further away, the power is large.

11.8.2 Effect size

> *Since all models are wrong the scientist must be alert to what is importantly wrong. It is inappropriate to be concerned with mice when there are tigers abroad*
> – George Box (1976, p. 792)

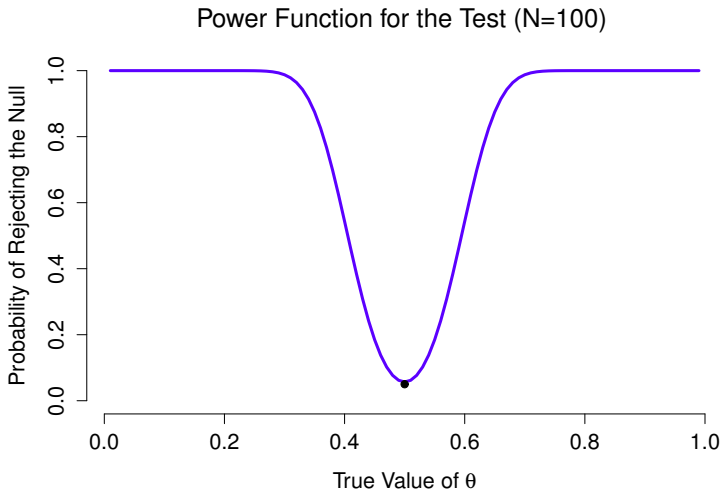


Figure 11.6: The probability that we will reject the null hypothesis, plotted as a function of the true value of θ. Obviously, the test is more powerful (greater chance of correct rejection) if the true value of θ is very different from the value that the null hypothesis specifies (i.e., $\theta = .5$). Notice that when θ actually is equal to .05 (plotted as a black dot), the null hypothesis is in fact true: rejecting the null hypothesis in this instance would be a Type I error.

The plot shown in Figure 11.6 captures a fairly basic point about hypothesis testing. If the true state of the world is very different from what the null hypothesis predicts, then your power will be very high; but if the true state of the world is similar to the null (but not identical) then the power of the test is going to be very low. Therefore, it's useful to be able to have some way of quantifying how "similar" the true state of the world is to the null hypothesis. A statistic that does this is called a measure of **effect size** (e.g., Cohen, 1988; Ellis, 2010). Effect size is defined slightly differently in different contexts,[10] (and so this section just talks in general terms) but the qualitative idea that it tries to capture is always the same: how big is the difference between the *true* population parameters, and the parameter values that are assumed by the null hypothesis? In our ESP example, if we let $\theta_0 = 0.5$ denote the value assumed by the null hypothesis, and let θ denote the true value, then a simple measure of effect size could be something like the difference between the true value and null (i.e., $\theta - \theta_0$), or possibly just the magnitude of this difference, $\text{abs}(\theta - \theta_0)$.

Why calculate effect size? Let's assume that you've run your experiment, collected the data, and gotten a significant effect when you ran your hypothesis test. Isn't it enough just to say that you've gotten a significant effect? Surely that's the *point* of hypothesis testing? Well, sort of. Yes, the point of doing a hypothesis test is to try to demonstrate that the null hypothesis is wrong, but that's hardly the only thing we're interested in. If the null hypothesis claimed that $\theta = .5$, and we show that it's wrong, we've only really told half of the story. Rejecting the null hypothesis implies that we believe that $\theta \neq .5$, but there's a big difference between $\theta = .51$ and $\theta = .8$. If we find that $\theta = .8$, then not only have we found that the null hypothesis is wrong, it appears to be *very* wrong. On the other hand, suppose we've successfully rejected the null hypothesis, but it looks like the true value of θ is only .51 (this would

[10] There's an R package called `compute.es` that can be used for calculating a very broad range of effect size measures; but for the purposes of the current book we won't need it: all of the effect size measures that I'll talk about here have functions in the `lsr` package

Table 11.2: A crude guide to understanding the relationship between statistical significance and effect sizes. Basically, if you don't have a significant result, then the effect size is pretty meaningless; because you don't have any evidence that it's even real. On the other hand, if you do have a significant effect but your effect size is small, then there's a pretty good chance that your result (although real) isn't all that interesting. However, this guide is very crude: it depends a lot on what exactly you're studying. Small effects can be of massive practical importance in some situations. So don't take this table too seriously. It's a rough guide at best.

	big effect size	small effect size
significant result	difference is real, and of practical importance	difference is real, but might not be interesting
non-significant result	no effect observed	no effect observed

only be possible with a large study). Sure, the null hypothesis is wrong, but it's not at all clear that we actually *care*, because the effect size is so small. In the context of my ESP study we might still care, since any demonstration of real psychic powers would actually be pretty cool[11], but in other contexts a 1% difference isn't very interesting, even if it is a real difference. For instance, suppose we're looking at differences in high school exam scores between males and females, and it turns out that the female scores are 1% higher on average than the males. If I've got data from thousands of students, then this difference will almost certainly be *statistically significant*, but regardless of how small the p value is it's just not very interesting. You'd hardly want to go around proclaiming a crisis in boys education on the basis of such a tiny difference would you? It's for this reason that it is becoming more standard (slowly, but surely) to report some kind of standard measure of effect size along with the the results of the hypothesis test. The hypothesis test itself tells you whether you should believe that the effect you have observed is real (i.e., not just due to chance); the effect size tells you whether or not you should care.

11.8.3 Increasing the power of your study

Not surprisingly, scientists are fairly obsessed with maximising the power of their experiments. We want our experiments to work, and so we want to maximise the chance of rejecting the null hypothesis if it is false (and of course we usually want to believe that it is false!) As we've seen, one factor that influences power is the effect size. So the first thing you can do to increase your power is to increase the effect size. In practice, what this means is that you want to design your study in such a way that the effect size gets magnified. For instance, in my ESP study I might believe that psychic powers work best in a quiet, darkened room; with fewer distractions to cloud the mind. Therefore I would try to conduct my experiments in just such an environment: if I can strengthen people's ESP abilities somehow, then the true value of θ will go up[12] and therefore my effect size will be larger. In short, clever experimental design is one way to boost power; because it can alter the effect size.

Unfortunately, it's often the case that even with the best of experimental designs you may have

[11] Although in practice a very small effect size is worrying, because even very minor methodological flaws might be responsible for the effect; and in practice no experiment is perfect, so there are always methodological issues to worry about.

[12] Notice that the true population parameter θ doesn't necessarily correspond to an immutable fact of nature. In this context θ is just the true probability that people would correctly guess the colour of the card in the other room. As such the population parameter can be influenced by all sorts of things. Of course, this is all on the assumption that ESP actually exists!

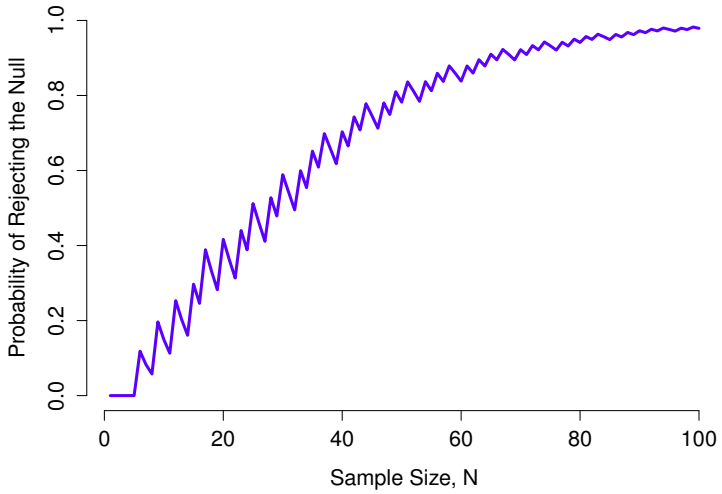


Figure 11.7: The power of our test, plotted as a function of the sample size N. In this case, the true value of θ is 0.7, but the null hypothesis is that $\theta = 0.5$. Overall, larger N means greater power. (The small zig-zags in this function occur because of some odd interactions between θ, α and the fact that the binomial distribution is discrete; it doesn't matter for any serious purpose)

only a small effect. Perhaps, for example, ESP really does exist, but even under the best of conditions it's very very weak. Under those circumstances, your best bet for increasing power is to increase the sample size. In general, the more observations that you have available, the more likely it is that you can discriminate between two hypotheses. If I ran my ESP experiment with 10 participants, and 7 of them correctly guessed the colour of the hidden card, you wouldn't be terribly impressed. But if I ran it with 10,000 participants and 7,000 of them got the answer right, you would be much more likely to think I had discovered something. In other words, power increases with the sample size. This is illustrated in Figure 11.7, which shows the power of the test for a true parameter of $\theta = 0.7$, for all sample sizes N from 1 to 100, where I'm assuming that the null hypothesis predicts that $\theta_0 = 0.5$.

Because power is important, whenever you're contemplating running an experiment it would be pretty useful to know how much power you're likely to have. It's never possible to know for sure, since you can't possibly know what your effect size is. However, it's often (well, sometimes) possible to guess how big it should be. If so, you can guess what sample size you need! This idea is called **power analysis**, and if it's feasible to do it, then it's very helpful, since it can tell you something about whether you have enough time or money to be able to run the experiment successfully. It's increasingly common to see people arguing that power analysis should be a required part of experimental design, so it's worth knowing about. I don't discuss power analysis in this book, however. This is partly for a boring reason and partly for a substantive one. The boring reason is that I haven't had time to write about power analysis yet. The substantive one is that I'm still a little suspicious of power analysis. Speaking as a researcher, I have very rarely found myself in a position to be able to do one – it's either the case that (a) my experiment is a bit non-standard and I don't know how to define effect size properly, (b) I literally have so little idea about what the effect size will be that I wouldn't know how to interpret the answers. Not only that, after extensive conversations with someone who does stats consulting for a living (my wife, as it happens), I can't help but notice that in practice the *only* time anyone ever asks her for a

power analysis is when she's helping someone write a grant application. In other words, the only time any scientist ever seems to want a power analysis in real life is when they're being forced to do it by bureaucratic process. It's not part of anyone's day to day work. In short, I've always been of the view that while power is an important concept, power *analysis* is not as useful as people make it sound, except in the rare cases where (a) someone has figured out how to calculate power for your actual experimental design and (b) you have a pretty good idea what the effect size is likely to be. Maybe other people have had better experiences than me, but I've personally never been in a situation where both (a) and (b) were true. Maybe I'll be convinced otherwise in the future, and probably a future version of this book would include a more detailed discussion of power analysis, but for now this is about as much as I'm comfortable saying about the topic.

11.9 Some issues to consider

What I've described to you in this chapter is the orthodox framework for null hypothesis significance testing (NHST). Understanding how NHST works is an absolute necessity, since it has been the dominant approach to inferential statistics ever since it came to prominence in the early 20th century. It's what the vast majority of working scientists rely on for their data analysis, so even if you hate it you need to know it. However, the approach is not without problems. There are a number of quirks in the framework, historical oddities in how it came to be, theoretical disputes over whether or not the framework is right, and a lot of practical traps for the unwary. I'm not going to go into a lot of detail on this topic, but I think it's worth briefly discussing a few of these issues.

11.9.1 Neyman versus Fisher

The first thing you should be aware of is that orthodox NHST is actually a mash-up of two rather different approaches to hypothesis testing, one proposed by Sir Ronald Fisher and the other proposed by Jerzy Neyman (see Lehmann, 2011, for a historical summary). The history is messy because Fisher and Neyman were real people whose opinions changed over time, and at no point did either of them offer "the definitive statement" of how we should interpret their work many decades later. That said, here's a quick summary of what I take these two approaches to be.

First, let's talk about Fisher's approach. As far as I can tell, Fisher assumed that you only had the one hypothesis (the null), and what you want to do is find out if the null hypothesis is inconsistent with the data. From his perspective, what you should do is check to see if the data are "sufficiently unlikely" according to the null. In fact, if you remember back to our earlier discussion, that's how Fisher defines the p-value. According to Fisher, if the null hypothesis provided a very poor account of the data, you could safely reject it. But, since you don't have any other hypotheses to compare it to, there's no way of "accepting the alternative" because you don't necessarily have an explicitly stated alternative. That's more or less all that there was to it.

In contrast, Neyman thought that the point of hypothesis testing was as a guide to action, and his approach was somewhat more formal than Fisher's. His view was that there are multiple things that you could *do* (accept the null or accept the alternative) and the point of the test was to tell you which one the data support. From this perspective, it is critical to specify your alternative hypothesis properly. If you don't know what the alternative hypothesis is, then you don't know how powerful the test is, or even which action makes sense. His framework genuinely requires a competition between different hypotheses. For Neyman, the p value didn't directly measure the probability of the data (or data more extreme) under the null, it was more of an abstract description about which "possible tests" were telling you to accept the null, and which "possible tests" were telling you to accept the alternative.

As you can see, what we have today is an odd mishmash of the two. We talk about having both a null hypothesis and an alternative (Neyman), but usually[13] define the p value in terms of exreme data (Fisher), but we still have α values (Neyman). Some of the statistical tests have explicitly specified alternatives (Neyman) but others are quite vague about it (Fisher). And, according to some people at least, we're not allowed to talk about accepting the alternative (Fisher). It's a mess: but I hope this at least explains why it's a mess.

11.9.2 Bayesians versus frequentists

Earlier on in this chapter I was quite emphatic about the fact that you *cannot* interpret the p value as the probability that the null hypothesis is true. NHST is fundamentally a frequentist tool (see Chapter 9) and as such it does not allow you to assign probabilities to hypotheses: the null hypothesis is either true or it is not. The Bayesian approach to statistics interprets probability as a degree of belief, so it's totally okay to say that there is a 10% chance that the null hypothesis is true: that's just a reflection of the degree of confidence that you have in this hypothesis. You aren't allowed to do this within the frequentist approach. Remember, if you're a frequentist, a probability can only be defined in terms of what happens after a large number of independent replications (i.e., a long run frequency). If this is your interpretation of probability, talking about the "probability" that the null hypothesis is true is complete gibberish: a null hypothesis is either true or it is false. There's no way you can talk about a long run frequency for this statement. To talk about "the probability of the null hypothesis" is as meaningless as "the colour of freedom". It doesn't have one!

Most importantly, this *isn't* a purely ideological matter. If you decide that you are a Bayesian and that you're okay with making probability statements about hypotheses, you have to follow the Bayesian rules for calculating those probabilities. I'll talk more about this in Chapter 17, but for now what I want to point out to you is the p value is a *terrible* approximation to the probability that H_0 is true. If what you want to know is the probability of the null, then the p value is not what you're looking for!

11.9.3 Traps

As you can see, the theory behind hypothesis testing is a mess, and even now there are arguments in statistics about how it "should" work. However, disagreements among statisticians are not our real concern here. Our real concern is practical data analysis. And while the "orthodox" approach to null hypothesis significance testing has many drawbacks, even an unrepentant Bayesian like myself would agree that they can be useful if used responsibly. Most of the time they give sensible answers, and you can use them to learn interesting things. Setting aside the various ideologies and historical confusions that we've discussed, the fact remains that the biggest danger in all of statistics is *thoughtlessness*. I don't mean stupidity, here: I literally mean thoughtlessness. The rush to interpret a result without spending time thinking through what each test actually says about the data, and checking whether that's consistent with how you've interpreted it. That's where the biggest trap lies.

To give an example of this, consider the following example (see Gelman & Stern, 2006). Suppose I'm running my ESP study, and I've decided to analyse the data separately for the male participants and the female participants. Of the male participants, 33 out of 50 guessed the colour of the card correctly. This is a significant effect ($p = .03$). Of the female participants, 29 out of 50 guessed correctly. This is not a significant effect ($p = .32$). Upon observing this, it is extremely tempting for people to start wondering why there is a difference between males and females in terms of their psychic abilities. However, this is wrong. If you think about it, we haven't *actually* run a test that explicitly compares males to females. All

[13] Although this book describes both Neyman's and Fisher's definition of the p value, most don't. Most introductory textbooks will only give you the Fisher version.

we have done is compare males to chance (binomial test was significant) and compared females to chance (binomial test was non significant). If we want to argue that there is a real difference between the males and the females, we should probably run a test of the null hypothesis that there is no difference! We can do that using a different hypothesis test,[14] but when we do that it turns out that we have no evidence that males and females are significantly different ($p = .54$). *Now* do you think that there's anything fundamentally different between the two groups? Of course not. What's happened here is that the data from both groups (male and female) are pretty borderline: by pure chance, one of them happened to end up on the magic side of the $p = .05$ line, and the other one didn't. That doesn't actually imply that males and females are different. This mistake is so common that you should always be wary of it: the difference between significant and not-significant is *not* evidence of a real difference – if you want to say that there's a difference between two groups, then you have to test for that difference!

The example above is just that: an example. I've singled it out because it's such a common one, but the bigger picture is that data analysis can be tricky to get right. Think about what it is you want to test, why you want to test it, and whether or not the answers that your test gives could possibly make any sense in the real world.

11.10 Summary

Null hypothesis testing is one of the most ubiquitous elements to statistical theory. The vast majority of scientific papers report the results of some hypothesis test or another. As a consequence it is almost impossible to get by in science without having at least a cursory understanding of what a p-value means, making this one of the most important chapters in the book. As usual, I'll end the chapter with a quick recap of the key ideas that we've talked about:

- Research hypotheses and statistical hypotheses. Null and alternative hypotheses. (Section 11.1).
- Type 1 and Type 2 errors (Section 11.2)
- Test statistics and sampling distributions (Section 11.3)
- Hypothesis testing as a decision making process (Section 11.4)
- p-values as "soft" decisions (Section 11.5)
- Writing up the results of a hypothesis test (Section 11.6)
- Effect size and power (Section 11.8)
- A few issues to consider regarding hypothesis testing (Section 11.9)

Later in the book, in Chapter 17, I'll revisit the theory of null hypothesis tests from a Bayesian perspective, and introduce a number of new tools that you can use if you aren't particularly fond of the orthodox approach. But for now, though, we're done with the abstract statistical theory, and we can start discussing specific data analysis tools.

[14] In this case, the Pearson chi-square test of independence (Chapter 12; `chisq.test()` in R) is what we use; see also the `prop.test()` function.